

STIC-Biotech/ChemLib

174294

From: Duffy, Patricia
Sent: Thursday, December 15, 2005 8:29 AM
To: STIC-Biotech/ChemLib
Subject: SPDI SEARCH

IN RE:10/063,549

PLEASE SEARCH SEQ ID NO:46 AND OLIGOMERS THEREOF.

Patricia A. Duffy, Ph.D.
Art Unit 1645
Remsen 3B05; Mailbox 3C18
571-272-0855

RECEIVED
DEC 15 2005
STIC/BIOTECH DIV.
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6

OM protein - protein search, using sw model
Run on: December 16, 2005, 10:31:21 ; Search time 81 Seconds(without alignments)
1817.184 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 1772

Sequence: 1 MAGSPCTLTLYIYMQTGS.....PHSLTWDPFRLFAVENVI 335

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : A_Geneseq_21:*

```
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description

RESULT 1 ID AAY66701 standard; protein; 335 AA.

DE Membrane-bound protein PRO1138.

PN WO9963088-A2.

PD 09-DEC-1999.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 3; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 2 ID AAY70431 standard; protein; 335 AA.

DE Human cell surface immunomodulator-1 (CSIMM-1).

PN WO20001150-A1.

PD 02-MAR-2000.

PA (INCY-) INCYTE PHARM INC.

Query Match 100.0%; Score 1772; DB 3; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 3 ID AAY4609 standard; protein; 335 AA.

DE Human myocardiium protein-7.

PN WO9967387-A2.

PD 29-DEC-1999.

PA (MILL-) MILLENNITUM PHARM INC.

Query Match 100.0%; Score 1772; DB 3; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 4 ID AAU29119 standard; protein; 335 AA.

DE Human PRO polypeptide sequence #96.

PN WO200168848-A2.

PD 20-SEP-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 5 ID AAB87548 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 6 ID AAB47321 standard; protein; 335 AA.

DE APEX-1.

PN WO200146260-A2.

PD 28-JUN-2001.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 7 ID AAB65224 standard; protein; 335 AA.

DE Human PRO1138 (UNQ576) protein sequence SEQ ID NO:253.

PN WO200073454-A1.

PD 07-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 8 ID AAB95873 standard; protein; 335 AA.

DE Human secreted/transmembrane protein PRO1138.

PN US2002119130-A1.

PD 29-AUG-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 5; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 9 ID AAB58495 standard; protein; 335 AA.

DE Human PRO polypeptide #96.

PN US2003027272-A1.

PD 06-FEB-2003.

Query Match 100.0%; Score 1772; DB 6; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 10 ID AAB88043 standard; protein; 335 AA.

DE Novel human secreted and transmembrane protein PRO1138.

PN US2003032127-A1.

PD 13-FEB-2003.

Query Match 100.0%; Score 1772; DB 6; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 11 ID AAB84358 standard; protein; 335 AA.

DE Human secreted/transmembrane protein (PRO) #96.

PN US2003032112-A1.

PD 13-FEB-2003.

Query Match 100.0%; Score 1772; DB 6; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 12 ID AAB66232 standard; protein; 335 AA.

DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003027278-A1.

PD 06-FEB-2003.

Query Match 100.0%; Score 1772; DB 6; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 13 ID AAB65622 standard; protein; 335 AA.

DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003036159-A1.

PD 20-FEB-2003.

Query Match 100.0%; Score 1772; DB 6; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 14 ID AAB09562 standard; protein; 335 AA.

DE Human secreted/transmembrane protein (PRO) #96.

PN US2003040070-A1.

PD 27-FEB-2003.

Query Match 100.0%; Score 1772; DB 6; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 15 ID AAB58039 standard; protein; 335 AA.

DE Human PRO polypeptide #71.

PN US2003027163-A1.

PD 06-FEB-2003.

Query Match 100.0%; Score 1772; DB 6; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 16 ID AAB59117 standard; protein; 335 AA.

DE Novel human secreted or transmembrane protein PRO1138.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 17
ID ABU82629 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 18
ID ABU82801 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 19
ID ABU89922 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 20
ID ABR68171 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 21
ID ABU60548 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, #100.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 22
ID ABU96224 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 23
ID ABU92655 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 24
ID AB008732 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 25
ID AB002784 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 26
ID ABR74938 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 27
ID ABR94700 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 28
ID ABU13930 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 29
ID ABU85673 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 30
ID ABU98833 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 31
ID ABU98048 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 32
ID ABU91754 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 33
ID ABU89447 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 34
ID ABU86288 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 35
ID ABU67501 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 36
ID ABU80529 standard; protein; 335 AA.

```
DE Human PRO protein #96.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 37
ID ABR72515 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 38
ID ABR90898 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 39
ID ABO33957 standard; protein; 335 AA.
DE Human secreted/cranmembrane protein PRO138.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 40
ID ABR99447 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 41
ID ABR98837 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 42
ID ABO16360 standard; protein; 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 43
ID ABR92260 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 44
ID ABO18901 standard; protein; 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 45
ID ABR78322 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 46
ID ABR71974 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO138.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 47
ID ABR85058 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 48
ID ABO00197 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 49
ID ABO11529 standard; protein; 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 50
ID ABO02174 standard; protein; 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 51
ID ABR8748 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 52
ID ABR83443 standard; protein; 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 53
ID ABO06244 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 54
ID ABR59280 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 55
ID ABO09342 standard; protein; 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 56
ID ABO19206 standard; protein; 335 AA.
```

```
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 57
ID ABO11224 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 58
ID ABR66842 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 59
ID ABO16055 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 60
ID ABO13761 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 61
ID ABU71528 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 62
ID ABU65664 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, SEQ ID 192.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 63
ID ABO07512 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 64
ID ABO03699 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 65
ID ABR67147 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 66
ID ABO15750 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 67
ID ABU56031 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, PRO1138.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 68
ID ABU72309 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 69
ID ABU65359 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 70
ID ABU95304 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 71
ID ABU71207 standard; protein; 335 AA.
DE Human PRO1138 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 72
ID ABO07817 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 73
ID ABR70058 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 74
ID ABR69391 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 75
ID ABO01532 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US200308353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 76
ID ABU81334 standard; protein; 335 AA.
```

```
DE Human PRO polypeptide #96.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 77
ID ABR60131 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 78
ID ABU90982 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 79
ID ABR67866 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 80
ID ABR65254 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 81
ID ABR68476 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 82
ID ABR71888 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 83
ID ABUS9264 standard; protein; 335 AA.
DE Human secreted/transmembrane protein; #100.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 84
ID ABUS368 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 85
ID ABUS9058 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 86
ID ABUS3138 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 87
ID ABUS9494 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 88
ID ABUS90542 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 89
ID ABUS4053 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 90
ID ABUS93704 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 91
ID ABO25961 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 92
ID ABR64949 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 93
ID ABO27303 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO138.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 94
ID ABR68781 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 95
ID ABO06597 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 96
ID ABR99142 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
```

PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 97
ID ABU57026 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 98
ID ABU85978 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 99
ID ABU8265 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 100
ID ABU87276 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 101
ID ABU83748 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 102
ID ABO08122 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 103
ID ABU92498 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 104
ID ABU81833 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 105
ID ABU65997 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 106
ID ABU8168 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138.
PN US2003027212-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 107
ID ABR59826 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 108
ID ABU94014 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 109
ID ABU99867 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 110
ID ABR6537 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 111
ID ABR90955 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 112
ID ABO53283 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO138.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 113
ID ABU58970 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, #100.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 114
ID ABU94382 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 115
ID ABU79264 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 116
ID ABU86593 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032129-A1.

PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 117
ID ABU86698 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 118
ID ABU94687 standard; protein, 335 AA.
DE Human PRO polypeptide #96.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 119
ID ABO04614 standard; protein, 335 AA.
DE Human PRO polypeptide #96.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 120
ID ABR70363 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 121
ID ABU92348 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 122
ID ABU98528 standard; protein, 335 AA.
DE Human PRO polypeptide #96.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 123
ID ABR65927 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 124
ID ABR64644 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 125
ID ABU59413 standard; protein, 335 AA.
DE Novel human secreted or transmembrane protein PRO1054.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 126
ID ABU79569 standard; protein, 335 AA.
DE Human PRO polypeptide #96.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 127
ID ABU92960 standard; protein, 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 128
ID ABU95919 standard; protein, 335 AA.
DE Human PRO polypeptide #96.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 129
ID ABU91139 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 130
ID ABU90332 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 131
ID ABO09647 standard; protein, 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 132
ID ABR58417 standard; protein, 335 AA.
DE Human NOV27a.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 133
ID ABO10919 standard; protein, 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 134
ID ABR70973 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 135
ID ABU198285 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GRTH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 136
ID ABU87581 standard; protein, 335 AA.
DE Human PRO polypeptide #96.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;

RESULT 137
ID ABU91449 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 138
ID ABU89290 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 139
ID ABU84663 standard; protein; 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 140
ID ABR69753 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 141
ID ABU80130 standard; protein; 335 AA.
DE Human PRO protein #96.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 142
ID ABU82497 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 143
ID ABU92179 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 144
ID ABU9339 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 145
ID ABO09952 standard; protein; 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 146
ID ABO09037 standard; protein; 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 147
ID ABO06427 standard; protein; 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003044922-A1.

ID ABU96461 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 148
ID ABU10885 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 149
ID ABU10605 standard; protein; 335 AA.
DE Human secreted/cranmembrane protein #96.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 150
ID ABU81637 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 151
ID ABU72131 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 152
ID ABU95614 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 153
ID ABU96823 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 154
ID ABR70668 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 155
ID ABO05019 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
Pred. No. 1.1e-162;
RESULT 156
ID ABO06427 standard; protein; 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003044922-A1.


```
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 157
ID ABU8576 standard; protein; 335 AA.
DE Human secreted and transmembrane polypeptide PRO1138.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 158
ID ABO34090 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 159
ID ABO05634 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 160
ID ABR74023 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 161
ID ABR95615 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 162
ID ABR80912 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 163
ID ABR81217 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 164
ID ABR00913 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 165
ID ABR88515 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 166
ID ABM77336 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 167
ID ABO28820 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 168
ID ABO31565 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 169
ID ABM07982 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 170
ID ABO40462 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 171
ID ABO35887 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 172
ID ABO44026 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 173
ID ADA77944 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 174
ID ABM24621 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 175
ID ABO03089 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
```


ID ABM1642 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US200306447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 195
ID ABM02743 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 196
ID ABM16039 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 197
ID ABO27600 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 198
ID ABM29091 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 199
ID ABM07067 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068659-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 200
ID ABM21161 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 201
ID ABM09507 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 202
ID ABO41377 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 203
ID ABO36192 standard; protein; 335 AA.

DE Human PRO polypeptide #96.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 204
ID ABO43721 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 205
ID ABM76421 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 206
ID ABM76117 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 207
ID ABM25736 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 208
ID ABM26041 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 209
ID ADA21450 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO1138.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 210
ID ABO03394 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 211
ID ABO02479 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 212
ID ABO44261 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO 1138.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 213

```
ID ABR90650 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 03-APR-2003.  
RESULT 214  
ID ABR73718 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 215  
ID ABO16970 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 216  
ID ABR94395 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 217  
ID ABR75902 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 218  
ID ABR71278 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 219  
ID ABR93175 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 220  
ID ABR93480 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 221  
ID ADA10237 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein, PRO1138.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 222  
ID ABR87905 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 223  
ID ABO27905 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 224  
ID ABO30040 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 225  
ID ABO33249 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 226  
ID ABO4937 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 227  
ID ABO08897 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 228  
ID ABO36497 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 229  
ID ABO35582 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 230  
ID ABO39547 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 231  
ID ABO10422 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
```

Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 232
ID ABM11947 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 233
ID ABO52093 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 234
ID ABO52398 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 235
ID ADH19908 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 236
ID ABO23716 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 237
ID ADB17291 standard; protein; 335 AA.
DE Human transmembrane PRO polypeptide (SegID 46).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 238
ID ADA17781 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 239
ID ABR97202 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 240
ID ABR86990 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 241
ID ABM11032 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 242
ID ABM28176 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 243
ID ABO32175 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 244
ID ABM15302 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 245
ID ABM06457 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 246
ID ABM04268 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 247
ID ABM22381 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 248
ID ABM07677 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 249
ID ABO40767 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 250
ID ABM35414 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003073179-A1.
PA 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 251
ID ABM33177 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003087374-A1.
PD 08-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 252
ID ABO52703 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 253
ID ABO50263 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 254
ID ABU99257 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 255
ID ABO04309 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 256
ID ABO05939 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 257
ID ABM18479 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 258
ID ADA27889 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 259
ID ABR97507 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 260

ID ABR80607 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 261
ID ABM01218 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 262
ID ABR88820 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 263
ID ABM13472 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 264
ID ABM20856 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 265
ID ABO41987 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003048745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 266
ID ABO42597 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 267
ID ABM10117 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 268
ID ABO38632 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 269
ID ABM32872 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 270
ID ABM22686 standard; protein; 335 AA.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 271
ID ABM74897 standard; protein; 335 AA.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 272
ID ADA79736 standard; protein; 335 AA.
PN Human secreted/cranmembrane protein (PRO) #96.
PD 17-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 273
ID ABR96287 standard; protein; 335 AA.
PN Human secreted polypeptide PRO1138, SEQ ID NO:192.
PD 20-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 274
ID ABM02338 standard; protein; 335 AA.
PN US2003059886-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 275
ID ABR86380 standard; protein; 335 AA.
PN Human secreted polypeptide PRO1138, SEQ ID NO:192.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 276
ID ABR86685 standard; protein; 335 AA.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 277
ID ABM16649 standard; protein; 335 AA.
PN Human secreted polypeptide PRO1138, SEQ ID NO:192.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 278
ID ABM29701 standard; protein; 335 AA.
PN Human secreted polypeptide PRO1138, SEQ ID NO:192.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 279
ID ABO29125 standard; protein; 335 AA.
PN Human secreted/cranmembrane protein (PRO) #96.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 280
ID ABM23906 standard; protein; 335 AA.
PN Human secreted polypeptide PRO1138, SEQ ID NO:192.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 281
ID ABM23296 standard; protein; 335 AA.
PN Human secreted polypeptide PRO1138, SEQ ID NO:192.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 282
ID ABM22076 standard; protein; 335 AA.
PN Human secreted polypeptide PRO1138, SEQ ID NO:192.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 283
ID ABO37717 standard; protein; 335 AA.
PN Human secreted/cranmembrane protein (PRO) #96.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 284
ID ABM28481 standard; protein; 335 AA.
PN Human secreted polypeptide PRO1138, SEQ ID NO:192.
PD 01-MAY-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 285
ID ABM28786 standard; protein; 335 AA.
PN Human secreted polypeptide PRO1138, SEQ ID NO:192.
PD 01-MAY-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 286
ID ABM66430 standard; protein; 335 AA.
PN Human secreted polypeptide PRO1138, SEQ ID NO:192.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 287
ID ABM75812 standard; protein; 335 AA.
PN Human secreted polypeptide PRO1138, SEQ ID NO:192.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 288
ID ABM34092 standard; protein; 335 AA.
PN Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003096359-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 289
ID ABM34397 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 290
ID ABO20328 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 291
ID ABO21243 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 292
ID ABO22158 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 293
ID ADA20080 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 294
ID ABO34189 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO 1138.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 295
ID ABR96592 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 296
ID ADA94469 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 297
ID ABR85770 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 298
ID ABR9752 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 299
ID ABM0608 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 300
ID ABM0303 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 301
ID ABO29735 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 302
ID ABM23601 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 303
ID ABM29396 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 304
ID ABO38327 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 305
ID ABO45627 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 306
ID ABM20551 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 307
ID ADA81463 standard; protein; 335 AA.

DE Human secreted/transmembrane protein (PRO) #96.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 308
ID ABO16665 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 309
ID ABO18291 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 310
ID ABO22718 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 311
ID ABO23023 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 312
ID ABR92565 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 313
ID ABR81522 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 314
ID ABM77946 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 315
ID ABR89735 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 316
ID ABM26651 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 317
ID ABM13777 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 318
ID ABO28515 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 319
ID ABO30345 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 320
ID ABM07372 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 321
ID ABM03963 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 322
ID ABO37107 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 323
ID ABO41682 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 324
ID ABO35277 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 325
ID ABM25126 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 326
ID ABO47518 standard; protein; 335 AA.

DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 327
ID ABO47823 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 328
ID ABO48433 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 329
ID ABO51483 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 330
ID ABO51788 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 331
ID ABO50568 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 332
ID ABR79692 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 333
ID ABM16954 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 334
ID ABO17986 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 335
ID ABO20938 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032132-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 336
ID ABR68697 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 337
ID ADA38694 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 338
ID ABM12252 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 339
ID ABM16344 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 340
ID ABM24211 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 341
ID ABM14692 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 342
ID ABM04573 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 343
ID ABM06762 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 344
ID ABM09202 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 345
ID ABO39242 standard; protein; 335 AA.

DE Human secreted/transmembrane protein (PRO) #96.
PN US200306875-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 346
ID ABR75507 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 347
ID ABR25431 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 348
ID ABR19941 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 349
ID ABO46847 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 350
ID ABO47152 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 351
ID ADA83261 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 352
ID ABR71563 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 353
ID ABR72193 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 354
ID ABR8532 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 355
ID ABR94090 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 355
ID ABO06902 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 356
ID ABR84855 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 357
ID ABR73413 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 358
ID ABR76507 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 359
ID ABR73108 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 360
ID ABR18174 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 361
ID ABO20633 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 362
ID ABO25376 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 363
ID ABO25681 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 364
ID ABR94090 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 365
ID ADA92815 standard; protein, 335 AA.
DE Human secreted/cranmembrane protein PRO1138.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 366
ID ABR79997 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 367
ID ABM11337 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064469-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 368
ID ABO32944 standard; protein, 335 AA.
DE Human PRO polypeptide #96.
PN US2003064453-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 369
ID ABO30650 standard; protein, 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003064466-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 370
ID ABO30955 standard; protein, 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003064468-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 371
ID ABM27261 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068760-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 372
ID ABM30006 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068769-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 373
ID ABM05542 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003045700-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 374
ID ABM15607 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068698-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 375
ID ABM08592 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068759-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 376
ID ABO42292 standard; protein, 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003049748-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 377
ID ABO38022 standard; protein, 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003068765-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 378
ID ABO45932 standard; protein, 335 AA.
DE Human PRO polypeptide #96.
PN US2003049754-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 379
ID ABM66735 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068688-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 380
ID ADB20304 standard; protein, 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 381
ID ABM19636 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104552-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 382
ID ABO49348 standard; protein, 335 AA.
DE Human secreted/cranmembrane protein (PRO) #96.
PN US2003049774-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 383
ID ABO49653 standard; protein, 335 AA.

DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 384
ID ADA78556 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 385
ID ABR88210 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 386
ID ADA00377 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO 138.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 387
ID ABM26956 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 388
ID ABM03353 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 389
ID ABO39852 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 390
ID ABO49958 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 391
ID ABO50873 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 392
ID ABO05329 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.

PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 393
ID ABR74633 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 394
ID ABR77112 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 395
ID ABM17869 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 396
ID ABR95920 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 397
ID ABO21853 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 398
ID ABO20023 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 399
ID ABO24326 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 400
ID ABR86075 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 401
ID ABM10727 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 402
ID ABM76726 standard; protein; 335 AA.

DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054465-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 403
ID ABR89430 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 404
ID ABR12557 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 405
ID ABR05847 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 406
ID ABR034972 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 407
ID ABR03048 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 408
ID ABR19026 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 409
ID ABR19331 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 410
ID ABR046542 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 411
ID ABR049043 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 412
ID ABR69086 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 413
ID ABR89125 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 414
ID ABR72498 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 415
ID ABR74328 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 416
ID ABR018596 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 417
ID ABR80302 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 418
ID ABR01523 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 419
ID ABR02133 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 420
ID ABR87295 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 421

ID ABM12862 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 422
ID ABM30616 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 423
ID ABM24516 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 424
ID ABO29430 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 425
ID ABO31260 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 426
ID ABM14387 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 427
ID ABM09812 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 428
ID ABO38937 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 429
ID ABM34702 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US200304538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 430
ID ABO51178 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.

PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 431
ID ABO04004 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 432
ID ABO10474 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 433
ID ABO53176 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 434
ID ABR7717 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 435
ID ABR78927 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 436
ID ABO24021 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 437
ID ABR93785 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 438
ID ABM01828 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 439
ID ABM78251 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 440

ID ABR90040 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 441
ID AD2376 standard; protein, 335 AA.
DE Human secreted/transmembrane polypeptide PRO1138.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 442
ID ABM27566 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 443
ID ABM13167 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 444
ID ABO31870 standard; protein, 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 445
ID ABM14082 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 446
ID ABM08287 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 447
ID ABO40157 standard; protein, 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 448
ID ABM74592 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 449
ID ABM33787 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003096358-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 450
ID ABM20246 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 451
ID ABO48738 standard; protein, 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 452
ID ABO2546 standard; protein, 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 453
ID ABR72803 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 454
ID ABO15445 standard; protein, 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 455
ID ABR85160 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 456
ID ABO15140 standard; protein, 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 457
ID ABO17275 standard; protein, 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 458
ID ABM17564 standard; protein, 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 459
ID ADA06542 standard; protein, 335 AA.
DE Human secreted/transmembrane PRO polypeptide #71.
PN US2003049638-A1.

PD 13-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 460
ID ADJ39235 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 461
ID ABH85465 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 462
ID ABW77031 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 463
ID ABO28210 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 464
ID ABM22991 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 465
ID ABM30311 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 466
ID ABM21771 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 467
ID ABM21466 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 468
ID ABM14997 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 469
ID ABO41072 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 470
ID ABO36802 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 471
ID ABO37412 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 472
ID ABM75202 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 473
ID ABM33482 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 474
ID ABO46237 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 475
ID ADA82627 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 476
ID ADB85619 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 477
ID ADB96261 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 478

ID AEM31836 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 479
ID AEM31226 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 480
ID ADB85935 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 481
ID AEM32141 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 482
ID AEM32446 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 483
ID ADB68298 standard; protein; 335 AA.
DE Human PRO1138 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 484
ID ADB68105 standard; protein; 335 AA.
DE Human PRO1138 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 485
ID AEM31531 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 486
ID AEM30921 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 487
ID ADB90922 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.

PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 488
ID ADC57733 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 489
ID ADC55097 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 490
ID ADC11964 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 491
ID ADC07002 standard; protein; 335 AA.
DE Human PRO1138 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 492
ID ADC56386 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 493
ID ADC17181 standard; protein; 335 AA.
DE Mammalian PRO polypeptide (SeqID 46).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 494
ID ADC07441 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 495
ID ADC11431 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 496
ID ADC14879 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
Pred. No. 1.1e-162;
RESULT 497
ID ADC52374 standard; protein; 335 AA.

DE Novel human secreted and transmembrane protein PRO1138.
PN US200313882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 498
ID ADC1453 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 499
ID ADD08085 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 500
ID ADC81910 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 501
ID ADD07552 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US200219329-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 502
ID ADC82443 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 503
ID ADD0565 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 504
ID ADD08623 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 505
ID ADD06872 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 506
ID ADC95903 standard; protein; 335 AA.
DE Human natural killer cell surface receptor CSL.
PN US2003113332-A1.
PD 19-JUN-2003.
PA (UNVT-) UNIV NORTH TEXAS HEALTH SCI CENT.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 507
ID ADC83119 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 508
ID ADD67525 standard; protein; 335 AA.
DE Human ly1728P protein SEQ ID NO:2.
PN WO2003062401-A2.
PD 31-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 509
ID ADD55226 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 510
ID ADD36050 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 511
ID ADD56184 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 512
ID ADD54622 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 513
ID ADS26776 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 514
ID ADS26243 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 515
ID ADF67180 standard; protein; 335 AA.
DE Human PRO1138 amino acid sequence SEQ ID NO:253.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 516
ID ADC01051 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

```
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 517
ID ADG08604 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 518
ID ADG02660 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 519
ID ADG01367 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 520
ID ADF95542 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 521
ID ADF95225 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 522
ID ADG12357 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 523
ID ADH24078 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 524
ID ADH34104 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 525
ID ADH29337 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 526
ID ADH23908 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 527
ID ADH09017 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 528
ID ADG85312 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 529
ID ADH24588 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 530
ID ADH37444 standard; protein; 335 AA.
DE Human secreted and transmembrane protein PRO138 CDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 531
ID ADH02033 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 532
ID ADH37614 standard; protein; 335 AA.
DE Human secreted and transmembrane protein PRO138 CDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 533
ID ADG85652 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 534
ID ADH24248 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 535
```

ID ADH38542 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 536
ID ADH83663 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 537
ID ADH29471 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 538
ID ADH27587 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 539
ID ADH37784 standard; protein; 335 AA.
DE Human secreted and transmembrane protein PRO1138 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 540
ID ADH37961 standard; protein; 335 AA.
DE Human secreted and transmembrane protein PRO1138 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 541
ID ADH57381 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 542
ID ADH53523 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 543
ID ADH53693 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 544
ID ADH52029 standard; protein; 335 AA.

DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 545
ID ADH49884 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 546
ID ADI25394 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 547
ID ADH90187 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 548
ID ADI25564 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 549
ID ADH97738 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 550
ID ADI35434 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 551
ID ADI03586 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 552
ID ADI11943 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 553
ID ADH90017 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181697-A1.

Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 572
ID AD103246 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 573
ID AD111433 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 574
ID AD102335 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 575
ID AD111773 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 576
ID AD105410 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 577
ID ADH79482 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 578
ID AD119439 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 579
ID AD105240 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 580
ID ADH79652 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 581
ID AD101478 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 582
ID AD101648 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 583
ID AD101818 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 584
ID ADH79822 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 585
ID AD104640 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 586
ID AD102776 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 587
ID ADH78095 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 588
ID AD125734 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 589
ID AD125904 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 590

ID ADK65416 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 591
ID ADH98758 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 592
ID ADH79999 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 593
ID ADJ32798 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 594
ID ADM30332 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 595
ID ADJ93730 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 596
ID ADC52184 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 597
ID ADH74432 standard; protein, 335 AA.
DE Human secreted and transmembrane protein (PRO) #96.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 598
ID ADH74941 standard; protein, 335 AA.
DE Human secreted and transmembrane protein (PRO) #96.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 599
ID ADH35379 standard; protein, 335 AA.
DE Human secreted and transmembrane protein PRO1138.
PN US2003194760-A1.
PD 13-NOV-2003.

PD 16-OCT-2003.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 600
ID ADG11629 standard; protein, 335 AA.
DE Human PRO1138 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 601
ID ADP96154 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 602
ID ADG04425 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 603
ID ADG00585 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 604
ID ADH06616 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 605
ID ADH06446 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 606
ID ADG68867 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 607
ID ADH27757 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 608
ID ADH25098 standard; protein, 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 609
ID ADH35379 standard; protein, 335 AA.
DE Human secreted and transmembrane protein PRO1138.
PN US2003194760-A1.
PD 13-NOV-2003.

Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 609
ID ADH33730 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 610
ID ADG82841 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 611
ID ADH02373 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 612
ID ADH07980 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 613
ID ADG69377 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 614
ID ADH39198 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 615
ID ADH26122 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 616
ID ADG83938 standard; protein; 335 AA.
DE Human PRO polypeptide #33.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 617
ID ADH19499 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;

RESULT 618
ID ADG85482 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 619
ID ADH06276 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 620
ID ADH30106 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 621
ID ADH24418 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 622
ID ADH33091 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 623
ID ADG69547 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 624
ID ADH07810 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 625
ID ADG85822 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 626
ID ADH39368 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 627

ID ADH33560 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 628
ID ADH33900 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 629
ID ADH0110 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 630
ID ADG69717 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 631
ID ADH20992 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US200324358-A1.
PD 04-DEC-2003.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 632
ID ADH02203 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 633
ID ADG69207 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 634
ID ADG85992 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 635
ID ADH24928 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 636
ID ADH39545 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.

PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 637
ID ADH20032 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 638
ID ADH02543 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 639
ID ADG69037 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 640
ID ADH07640 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 641
ID ADG86162 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 642
ID ADH24758 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 643
ID ADH25806 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 644
ID ADH38372 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Best Local Similarity 100.0%; Score 1772; DB 8; Length 335;
Pred. No. 1.1e-162;
RESULT 645
ID ADH57211 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181642-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 646
ID ADH52199 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 647
ID ADH49565 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 648
ID ADH90527 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 649
ID ADH11263 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 650
ID ADH98928 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 651
ID ADH102158 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 652
ID ADH90697 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 653
ID ADH54830 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 654
ID ADH98572 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 655
ID ADH98742 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 656
ID ADH78901 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 657
ID ADH99135 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 658
ID ADH99305 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 659
ID ADH98923 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 660
ID ADH79071 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 661
ID ADH00931 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 662
ID ADH14452 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 663
ID ADH64601 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 664
ID ADM3197 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 665
ID ADM3644 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 666
ID ADM40349 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 667
ID ADM80901 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 668
ID ADN37957 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 669
ID ADU87689 standard; protein; 335 AA.
DE Human CSI (SLAMF7) protein.
PN WO2004100898-A2.
PD 25-NOV-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 670
ID ADY19131 standard; protein; 335 AA.
DE PRO polypeptide SEQ ID NO 4937.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 671
ID ADY77741 standard; protein; 335 AA.
DE Neoplastic disease detection protein PRO1138.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FLIV/) FLIVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1772; DB 9; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 672
ID AEA38506 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, #139.
PN US200512725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 673
ID AAB32373 standard; protein; 336 AA.
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:59.
PN WO200047602-A1.
PD 17-AUG-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1772; DB 3; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 674
ID ADS98579 standard; protein; 340 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 843.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 100.0%; Score 1772; DB 8; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
RESULT 675
ID ADD18672 standard; protein; 335 AA.
DE Human disease related protein SegID103.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 99.8%; Score 1769; DB 7; Length 335;
Best Local Similarity 99.7%; Pred. No. 2.1e-162;
RESULT 676
ID ADI69599 standard; protein; 335 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID1405.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 99.8%; Score 1769; DB 7; Length 335;
Best Local Similarity 99.7%; Pred. No. 2.1e-162;
RESULT 677
ID ABR58418 standard; protein; 348 AA.
DE Human NOV27b.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 99.1%; Score 1755.5; DB 6; Length 348;
Best Local Similarity 96.3%; Pred. No. 4.5e-161;
RESULT 678
ID AAY44610 standard; protein; 312 AA.
DE Mature human myocardium protein-7.
PN WO9967387-A2.
PD 29-DEC-1999.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 93.3%; Score 1653; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 3.3e-151;
RESULT 679
ID ABB97473 standard; protein; 328 AA.
DE Novel human protein SEQ ID NO: 741.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 78.6%; Score 1392.5; DB 5; Length 328;
Best Local Similarity 86.4%; Pred. No. 6.4e-126;
RESULT 680
ID ADS98765 standard; protein; 328 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 1029.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.

PA (DEMA/) DEMANAC R T.
Query Match 78.6%; Score 1392.5; DB 8; Length 328;
Best Local Similarity 86.4%; Pred. No. 6.4e-126;
RESULT 681
ID ADS97998 standard; protein: 236 AA.
DE Protein factor discovery related isolated human polypeptide, SEQ ID 262.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NIVE-) NIVELO INC.
PA (DEMA/) DEMANAC R T.
Query Match 76.1%; Score 1349; DB 8; Length 296;
Best Local Similarity 100.0%; Pred. No. 9.1e-122;
RESULT 682
ID ADN02731 standard; protein: 204 AA.
DE Human receptor and membrane-associated protein #34.
PN WO2004029218-A2.
PD 08-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 56.3%; Score 997.5; DB 8; Length 204;
Best Local Similarity 60.9%; Pred. No. 6.4e-88;
RESULT 683
ID ABG11697 standard; protein: 684 AA.
DE Novel human diagnostic protein #11688.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 52.7%; Score 933.5; DB 4; Length 684;
Best Local Similarity 64.9%; Pred. No. 6e-81;
RESULT 684
ID ABG12169 standard; protein: 684 AA.
DE Novel human diagnostic protein #12160.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 52.7%; Score 933.5; DB 4; Length 684;
Best Local Similarity 64.9%; Pred. No. 6e-81;
RESULT 685
ID ADS98714 standard; protein: 684 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 978.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NIVE-) NIVELO INC.
PA (DEMA/) DEMANAC R T.
Query Match 52.7%; Score 933.5; DB 8; Length 684;
Best Local Similarity 64.9%; Pred. No. 6e-81;
RESULT 686
ID ADR20055 standard; protein: 165 AA.
DE Human immune response associated protein (IRAP), seq id 15.
PN WO2004048550-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 36.9%; Score 653; DB 8; Length 165;
Best Local Similarity 90.9%; Pred. No. 1.2e-54;
RESULT 687
ID AAY12645 standard; protein: 124 AA.
DE Human 5' EST secreted protein SEQ ID NO: 310 from WO 9906553.
PN WO9906553-A2.
PD 11-FEB-1999.
PA (GENST-) GENSET.
Query Match 35.1%; Score 622; DB 2; Length 124;
Best Local Similarity 97.6%; Pred. No. 8e-52;
RESULT 688
ID AAW67811 standard; protein: 110 AA.
DE Human secreted protein encoded by gene 5 clone HASAV70.
PN WO9842738-A1.
PD 01-OCT-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 582; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 5e-48;
RESULT 689
ID AAB32405 standard; protein: 110 AA.
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:91.
PN WO20047602-A1.
PD 17-AUG-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 582; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 5e-48;
RESULT 690
ID ADA57321 standard; protein: 110 AA.
DE Human secreted protein #32.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 582; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 5e-48;
RESULT 691
ID ADA6750 standard; protein: 110 AA.
DE Human secreted protein #32.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 582; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 5e-48;
RESULT 692
ID ADA40601 standard; protein: 110 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 582; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 5e-48;
RESULT 693
ID ADA41198 standard; protein: 110 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 582; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 5e-48;
RESULT 694
ID AAG00391 standard; protein: 97 AA.
DE Human secreted protein, SEQ ID NO: 4472.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GENST-) GENSET.
Query Match 28.1%; Score 498; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.9e-40;
RESULT 695
ID AAY11662 standard; protein: 98 AA.
DE Human 5' EST secreted protein SEQ ID NO:314.
PN WO9906439-A2.
PD 11-FEB-1999.
PA (GENST-) GENSET.
Query Match 28.1%; Score 498; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.9e-40;
RESULT 696
ID AAM21122 standard; protein: 91 AA.
DE Peptide #7556 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
RESULT 697
ID ABA43438 standard; peptide: 91 AA.
DE Peptide #10944 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
RESULT 698
ID AAM37326 standard; protein: 91 AA.
DE Peptide #11363 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
RESULT 699
ID ABB26408 standard; protein; 91 AA.
DE Protein #8407 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
RESULT 700
ID AAM77190 standard; protein; 91 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 37496.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
RESULT 701
ID AAM64367 standard; protein; 91 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 36472.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
RESULT 702
ID ABG58815 standard; peptide; 91 AA.
DE Human liver peptide, SEQ ID NO 37463.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
RESULT 703
ID AAG46203 standard; peptide; 91 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 35868.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
RESULT 704
ID AAB32404 standard; protein; 90 AA.
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:90.
PN WO200047602-A1.
PD 17-AUG-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.1%; Score 445; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 7.2e-35;
RESULT 705
ID AAB47878 standard; protein; 328 AA.
DE SCZ/CD84.
PN WO200202054-A2.
PD 10-JAN-2002.
PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.
Query Match 20.5%; Score 362.5; DB 5; Length 328;
Best Local Similarity 31.5%; Pred. No. 4.8e-26;
RESULT 706
ID AAB26238 standard; protein; 328 AA.
DE Human CD84 protein.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILT-) MILLENNIUM PHARM INC.
Query Match 20.5%; Score 362.5; DB 5; Length 328;
Best Local Similarity 31.5%; Pred. No. 4.8e-26;
RESULT 707
ID ADI82907 standard; protein; 328 AA.
DE Human PRO24934, SEQ ID 109.
PN WO2004024097-A2.
PD 25-MAR-2004.
PA (GERTH) GENENTECH INC.

Query Match 20.5%; Score 362.5; DB 8; Length 328;
Best Local Similarity 31.5%; Pred. No. 4.8e-26;
RESULT 708
ID ADO05708 standard; protein; 328 AA.
DE Human leukocyte differentiation antigen CD84.
PN WO2004032867-A2.
PD 22-APR-2004.
PA (TOLR-) TOLLERX INC.
Query Match 20.5%; Score 362.5; DB 8; Length 328;
Best Local Similarity 31.5%; Pred. No. 4.8e-26;
RESULT 709
ID ADQ19067 standard; protein; 328 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1886.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 20.5%; Score 362.5; DB 8; Length 328;
Best Local Similarity 31.5%; Pred. No. 4.8e-26;
RESULT 710
ID ADP23943 standard; protein; 328 AA.
DE PRO polypeptide SEQ ID NO:1121.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GERTH) GENENTECH INC.
Query Match 20.5%; Score 362.5; DB 8; Length 328;
Best Local Similarity 31.5%; Pred. No. 4.8e-26;
RESULT 711
ID ADY16548 standard; protein; 328 AA.
DE PRO polypeptide SEQ ID NO 2354.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GERTH) GENENTECH INC.
Query Match 20.5%; Score 362.5; DB 9; Length 328;
Best Local Similarity 31.5%; Pred. No. 4.8e-26;
RESULT 712
ID ADY16566 standard; protein; 328 AA.
DE PRO polypeptide SEQ ID NO 1462.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GERTH) GENENTECH INC.
Query Match 20.5%; Score 362.5; DB 9; Length 328;
Best Local Similarity 31.5%; Pred. No. 4.8e-26;
RESULT 713
ID AAW74891 standard; protein; 329 AA.
DE Human secreted protein encoded by gene 164 clone HSAWP26.
PN WO9839448-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.5%; Score 362.5; DB 2; Length 329;
Best Local Similarity 31.5%; Pred. No. 4.8e-26;
RESULT 714
ID ABG95343 standard; protein; 329 AA.
DE Human novel secreted protein #164.
PN US6420526-B1.
PD 16-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.5%; Score 362.5; DB 5; Length 329;
Best Local Similarity 31.5%; Pred. No. 4.8e-26;
RESULT 715
ID ABQ34537 standard; protein; 329 AA.
DE Region of human secreted protein encoded by cDNA sequence #164.
PN US2003049618-A1.
PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPE/) SOPERT D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NITU/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.

PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJI/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIT/) SHI Y.
PA (LAFI/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 20.5%; Score 362.5; DB 6; Length 329;
Best Local Similarity 31.5%; Pred. No. 4.8e-26;
RESULT 716
ID ADI23198 standard; protein; 329 AA.
DE Novel human secreted protein seq id 483.
PN US2003175858-A1.
PD 18-SEP-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPF/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BRDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJG/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJI/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIT/) SHI Y.
PA (LAFI/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 20.5%; Score 362.5; DB 7; Length 329;
Best Local Similarity 31.5%; Pred. No. 4.8e-26;
RESULT 717
ID ADH74200 standard; protein; 329 AA.
DE Human secreted protein #164.
PN US2003225248-A1.
PD 04-DEC-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.5%; Score 362.5; DB 8; Length 329;
Best Local Similarity 31.5%; Pred. No. 4.8e-26;
RESULT 718
ID AAU74424 standard; protein; 629 AA.
DE Mouse protein sequence #3, related to isolation of genes within SLE-1B.
PN WO000188200-A2.
PD 22-NOV-2001.
PA (TEXA-) UNIV TEXAS SYSTEM.
Query Match 19.4%; Score 343; DB 5; Length 629;
Best Local Similarity 29.3%; Pred. No. 9.7e-24;
RESULT 719
ID AAE26250 standard; protein; 289 AA.
DE Human CD2001 protein #2.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.8%; Score 333.5; DB 5; Length 289;
Best Local Similarity 31.0%; Pred. No. 2.6e-23;

RESULT 720
ID ABW01830 standard; protein; 289 AA.
DE Human CD2001 protein #3.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.8%; Score 333.5; DB 7; Length 289;
Best Local Similarity 31.0%; Pred. No. 2.6e-23;
RESULT 721
ID AAE12078 standard; protein; 289 AA.
DE Dendritic cell (DC) DC1XR protein.
PN WO200172773-A2.
PD 04-OCT-2001.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 18.7%; Score 330.5; DB 4; Length 289;
Best Local Similarity 30.6%; Pred. No. 5e-23;
RESULT 722
ID AAE26243 standard; protein; 289 AA.
DE Human CD2001 protein.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.7%; Score 330.5; DB 5; Length 289;
Best Local Similarity 30.6%; Pred. No. 5e-23;
RESULT 723
ID AAE26253 standard; protein; 289 AA.
DE Human CD2001 protein #5.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.7%; Score 330.5; DB 5; Length 289;
Best Local Similarity 30.6%; Pred. No. 5e-23;
RESULT 724
ID ABP65110 standard; protein; 289 AA.
DE Hypoxia-induced protein #36.
PN WO200246465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 18.7%; Score 330.5; DB 5; Length 289;
Best Local Similarity 30.6%; Pred. No. 5e-23;
RESULT 725
ID ABW01823 standard; protein; 289 AA.
DE Human CD2001 protein #1.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.7%; Score 330.5; DB 7; Length 289;
Best Local Similarity 30.6%; Pred. No. 5e-23;
RESULT 726
ID ABW01833 standard; protein; 289 AA.
DE Human CD2001 protein #6.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.7%; Score 330.5; DB 7; Length 289;
Best Local Similarity 30.6%; Pred. No. 5e-23;
RESULT 727
ID AAE26251 standard; protein; 289 AA.
DE Human CD2001 protein #3.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.5%; Score 327.5; DB 5; Length 289;
Best Local Similarity 30.3%; Pred. No. 9.9e-23;
RESULT 728
ID AAE26252 standard; protein; 289 AA.
DE Human CD2001 protein #4.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.5%; Score 327.5; DB 5; Length 289;
Best Local Similarity 30.3%; Pred. No. 9.9e-23;

RESULT 729
ID ABW01831 standard; protein; 289 AA.
DE Human CD2001 protein #4.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.5%; Score 327.5; DB 7; Length 289;
Best Local Similarity 30.3%; Pred. No. 9.9e-23;
RESULT 730
ID ABW01832 standard; protein; 289 AA.
DE Human CD2001 protein #5.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.5%; Score 327.5; DB 7; Length 289;
Best Local Similarity 30.3%; Pred. No. 9.9e-23;
RESULT 731
ID AAE26244 standard; protein; 270 AA.
DE Human CD2001 mature protein.
PN EP1232318-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.5%; Score 327; DB 5; Length 270;
Best Local Similarity 31.4%; Pred. No. 1e-22;
RESULT 732
ID ABW01824 standard; protein; 270 AA.
DE Human CD2001 mature protein.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.5%; Score 327; DB 7; Length 270;
Best Local Similarity 31.4%; Pred. No. 1e-22;
RESULT 733
ID ADS98002 standard; protein; 632 AA.
DE Protein factor discovery related isolated human polypeptide, SEQ ID 266.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
(DRMA/) DRMANAC R T.
Query Match 18.2%; Score 323; DB 8; Length 632;
Best Local Similarity 30.3%; Pred. No. 8.5e-22;
RESULT 734
ID ADS97999 standard; protein; 655 AA.
DE Protein factor discovery related isolated human polypeptide, SEQ ID 263.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
(DRMA/) DRMANAC R T.
Query Match 18.2%; Score 323; DB 8; Length 655;
Best Local Similarity 30.3%; Pred. No. 8.9e-22;
RESULT 735
ID ADS98003 standard; protein; 669 AA.
DE Protein factor discovery related isolated human polypeptide, SEQ ID 267.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
(DRMA/) DRMANAC R T.
Query Match 18.2%; Score 323; DB 8; Length 669;
Best Local Similarity 30.3%; Pred. No. 9.2e-22;
RESULT 736
ID AAE26239 standard; protein; 331 AA.
DE Human CD2000 protein #3.
PN EP1232318-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.0%; Score 319.5; DB 5; Length 331;
Best Local Similarity 29.9%; Pred. No. 7.2e-22;
RESULT 737
ID ABW01818 standard; protein; 331 AA.
DE Human CD2000 protein #2.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 18.0%; Score 319.5; DB 7; Length 331;
Best Local Similarity 29.9%; Pred. No. 7.2e-22;
RESULT 738
ID ADL57103 standard; protein; 615 AA.
DE Human NOV5a protein SEQ ID NO:46.
PN WO2004022723-A2.
PD 18-MAR-2004.
PA (CURA-) CURAGEN CORP.
Query Match 17.9%; Score 318; DB 8; Length 615;
Best Local Similarity 30.3%; Pred. No. 2.5e-21;
RESULT 739
ID AD063782 standard; protein; 654 AA.
DE Human Ly-9 polypeptide.
PN US2004109862-A1.
PD 10-JUN-2004.
PA (EMTA/) EMTAGE P C R.
Query Match 17.9%; Score 318; DB 8; Length 654;
Best Local Similarity 30.3%; Pred. No. 2.7e-21;
RESULT 740
ID AD078174 standard; protein; 654 AA.
DE Human Ly-9 polypeptide.
PN US2004109863-A1.
PD 10-JUN-2004.
PA (EMTA/) EMTAGE P.
Query Match 17.9%; Score 318; DB 8; Length 654;
Best Local Similarity 30.3%; Pred. No. 2.7e-21;
RESULT 741
ID ADK41513 standard; protein; 331 AA.
DE Anti-cell surface antigen related protein #1.
PN WO2003068935-A2.
PD 21-AUG-2003.
PA (NUVE-) NUVELO INC.
Query Match 17.9%; Score 316.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.4e-21;
RESULT 742
ID AAE26222 standard; protein; 309 AA.
DE Human CD2000 mature protein.
PN EP1232318-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.8%; Score 315.5; DB 5; Length 309;
Best Local Similarity 29.6%; Pred. No. 1.6e-21;
RESULT 743
ID ABW01801 standard; protein; 309 AA.
DE Human CD2000 mature protein.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.8%; Score 315.5; DB 5; Length 309;
Best Local Similarity 29.6%; Pred. No. 1.6e-21;
RESULT 744
ID ABB90183 standard; protein; 331 AA.
DE Human polypeptide SEQ ID NO 2559.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMANA GENOME SCI INC.
Query Match 17.8%; Score 315.5; DB 5; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 745
ID AAE26220 standard; protein; 331 AA.
DE Human CD2000 protein.
PN EP1232318-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.8%; Score 315.5; DB 5; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 746
ID ABR39107 standard; protein; 331 AA.
DE Human NTB-A protein SEQ ID NO:2.
PN WO2003008449-A1.
PD 30-JAN-2003.
PA (INNA-) INNATE PHARMA.
(DYGE-) UNIV GENOVA.


```
Query Match 17.8%; Score 315.5; DB 6; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 747
ID AB003145 standard; protein; 331 AA.
DE Human Immunoglobulin (Ig) APEX4 protein.
PN WO200277173-A2.
PD 03-OCT-2002.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match 17.8%; Score 315.5; DB 6; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 748
ID ADC52556 standard; protein; 331 AA.
DE human dendritic cell membrane protein #SEQ ID 9.
PN JP2003052374-A.
PD 25-FEB-2003.
PA (KIRI ) KIRIN BREWERY KK.
Query Match 17.8%; Score 315.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 749
ID ABW01799 standard; protein; 331 AA.
DE Human CD2000 protein #1.
PN US200318088-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.8%; Score 315.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 750
ID AD137022 standard; protein; 331 AA.
DE Novel human secreted and transmembrane protein PRO 71240.
PN WO2004004649-A2.
PD 15-JAN-2004.
PA (GERTH ) GENENTECH INC.
Query Match 17.8%; Score 315.5; DB 8; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 751
ID AD066345 standard; protein; 331 AA.
DE Novel human protein sequence #1318.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (RRAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 17.8%; Score 315.5; DB 8; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 752
ID ADY19430 standard; protein; 331 AA.
DE PRO polypeptide SEQ ID NO 5236.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GERTH ) GENENTECH INC.
Query Match 17.8%; Score 315.5; DB 9; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 753
ID AD213231 standard; protein; 331 AA.
DE Human cancer-associated protein #235.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR ) CHIRON CORP.
Query Match 17.8%; Score 315.5; DB 9; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 754
ID AEB98756 standard; protein; 331 AA.
DE Human dendritic cell membrane molecule, SEQ ID 2.
PN JP2005206478-A.
PD 04-AUG-2005.
PA (KIRI ) KIRIN BREWERY KK.
Query Match 17.8%; Score 315.5; DB 9; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.8e-21;
RESULT 755
ID AAU09868 standard; protein; 346 AA.
DE Novel human secreted protein #9.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (SMIK ) SMITHKLINE BEECHAM PLC.

Query Match 17.8%; Score 315.5; DB 5; Length 346;
Best Local Similarity 29.6%; Pred. No. 1.9e-21;
RESULT 756
ID AAE26241 standard; protein; 331 AA.
DE Human CD2000 protein #5.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.7%; Score 314.5; DB 5; Length 331;
Best Local Similarity 29.6%; Pred. No. 2.2e-21;
RESULT 757
ID ABW01820 standard; protein; 331 AA.
DE Human CD2000 protein #4.
PN US200318088-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.7%; Score 314.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 2.2e-21;
RESULT 758
ID AAE26240 standard; protein; 331 AA.
DE Human CD2000 protein #4.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.7%; Score 313.5; DB 5; Length 331;
Best Local Similarity 29.6%; Pred. No. 2.7e-21;
RESULT 759
ID ABW01819 standard; protein; 331 AA.
DE Human CD2000 protein #3.
PN US200318088-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.7%; Score 313.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 2.7e-21;
RESULT 760
ID AAU74425 standard; protein; 610 AA.
DE Human protein sequence #3, related to isolation of genes within SLF-1B.
PN WO200188200-A2.
PD 22-NOV-2001.
PA (TEXA ) UNIV TEXAS SYSTEM.
Query Match 17.6%; Score 312.5; DB 5; Length 610;
Best Local Similarity 25.7%; Pred. No. 8.4e-21;
RESULT 761
ID ADS98001 standard; protein; 641 AA.
DE Protein factor discovery related isolated human polypeptide, SEQ ID 265.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R.T.
Query Match 17.6%; Score 312.5; DB 8; Length 641;
Best Local Similarity 25.7%; Pred. No. 9e-21;
RESULT 762
ID AAE26242 standard; protein; 331 AA.
DE Human CD2000 protein #6.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.6%; Score 311.5; DB 5; Length 331;
Best Local Similarity 29.6%; Pred. No. 4.3e-21;
RESULT 763
ID ABW01821 standard; protein; 331 AA.
DE Human CD2000 protein #5.
PN US200318088-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.6%; Score 311.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 4.3e-21;
RESULT 764
ID AAG63166 standard; protein; 332 AA.
DE Amino acid sequence of a CD84-like polypeptide.
PN WO200155336-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
```

Query Match 17.6%; Score 311; DB 4; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 765
ID ABB96267 standard; protein; 332 AA.
DE Human immunoglobulin superfamily protein IGSFP-5.
PN W0200272794-A2.
PD 19-SEP-2002.
PA (INCYTE) INCYTE GENOMICS INC.
Query Match 17.6%; Score 311; DB 5; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 766
ID ABB34067 standard; protein; 332 AA.
DE Human Pro peptide #38.
PN W0200224868-A2.
PD 28-MAR-2002.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 5; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 767
ID ABU03170 standard; protein; 332 AA.
DE Human immunoglobulin (Ig) APEX4v1 protein.
PN W0200277173-A2.
PD 03-OCT-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 17.6%; Score 311; DB 6; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 768
ID ADA37159 standard; protein; 332 AA.
DE Human PRO20080 protein SEQ ID NO.2.
PN W02003055440-A2.
PD 10-JUL-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 6; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 769
ID ADA01344 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 6; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 770
ID ADA43773 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 6; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 771
ID ADA43541 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 6; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 772
ID ADA01216 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 6; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 773
ID ADA01100 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
Query Match 17.6%; Score 311; DB 7; Length 332;

Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 774
ID ADA43657 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 775
ID ADA06919 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 776
ID ADA08407 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 777
ID ADB99700 standard; protein; 332 AA.
DE Human PRO polypeptide SEQ ID 76.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 778
ID ADB6983 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 779
ID ADB6138 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 780
ID ADB99816 standard; protein; 332 AA.
DE Human PRO polypeptide SEQ ID 76.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 781
ID ADB99471 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 782
ID ADB66022 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GENTH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
Query Match 17.6%; Score 311; DB 7; Length 332;

```
RESULT 783
ID ADC23420 standard; protein; 332 AA.
DE Human transmembrane PRO polypeptide (Segid 76).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 784
ID ADC26113 standard; protein; 332 AA.
DE Human PRO20080 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 785
ID ADB04940 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 786
ID ADE11246 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 787
ID ADB8177 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 788
ID ADD95472 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 789
ID ADE06402 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 790
ID ADE38177 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 791
ID ADB8293 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 792
ID ADD95356 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 793
ID ADP9429 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 794
ID ADG06522 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 795
ID ADG05473 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 796
ID ADG82474 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 797
ID ADE31727 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 798
ID ADE31843 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 799
ID ADE37701 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 800
ID ADE37585 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 801
ID ADD95356 standard; protein; 332 AA.
```

DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
ID ADE52379 standard; protein; 332 AA.
DE Human PRO20080.
PN US2003099661-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 803
ID ADE38056 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 804
ID ADE76145 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 805
ID ADE39468 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 806
ID ADE04472 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 807
ID ADE39869 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 808
ID ADE19734 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 809
ID ADE77312 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 810
ID ADE65420 standard; protein; 332 AA.
DE Human PRO polypeptide #38.

PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
ID ADE76029 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 812
ID ADE37940 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 813
ID ADE64550 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 814
ID ADE38885 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 815
ID ADE51959 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 816
ID ADD90990 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 817
ID ADE38769 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 818
ID ADE37469 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 819
ID ADE06286 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003138898-A1.

PD 24-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 820
ID AD90145 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003138904-A1.
PD 24-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 821
ID AD38653 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 822
ID AD39584 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 823
ID AD89189 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003138897-A1.
PD 24-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 824
ID AD88956 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003138899-A1.
PD 24-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 825
ID AD819850 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003138900-A1.
PD 24-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 826
ID AD877428 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003124667-A1.
PD 03-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 827
ID AD865304 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 828
ID AD839352 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 829
ID AD38537 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 830
ID AD81090 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 831
ID AD810974 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 832
ID AD81502 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 833
ID AD838750 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 834
ID AD829385 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 835
ID AD823688 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 836
ID AD827018 standard; protein; 332 AA.
DE Human secreted/cranmembrane polypeptide PRO20080.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 837
ID AD838286 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 838
ID ADH26902 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 839
ID ADH38170 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 840
ID ADH38866 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 841
ID ADH23804 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 842
ID ADH40179 standard; protein; 332 AA.
DE Human PRO20080 protein.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 843
ID ADH40064 standard; protein; 332 AA.
DE Human PRO20080 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 844
ID ADH31386 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 845
ID ADH29264 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 846
ID ADH49479 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;

Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 847
ID ADH51943 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 848
ID ADH49798 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 849
ID ADH52399 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 850
ID ADH52515 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 851
ID ADH58512 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 852
ID ADH51827 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 853
ID ADH58388 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 854
ID ADH13585 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 855
ID ADK00841 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;

RESULT 856
ID AD08582 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 857
ID ADS10567 standard; protein; 332 AA.
DE Human therapeutic protein - SEQ ID 804.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.8e-21;
RESULT 858
ID ADY16550 standard; protein; 280 AA.
DE PRO polypeptide SEQ ID NO 2356.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 17.4%; Score 308; DB 9; Length 280;
Best Local Similarity 32.3%; Pred. No. 7.3e-21;
RESULT 859
ID AAE26249 standard; protein; 236 AA.
DE Human CD2001 protein #1.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.0%; Score 301.5; DB 5; Length 236;
Best Local Similarity 32.6%; Pred. No. 2.4e-20;
RESULT 860
ID AEW01829 standard; protein; 236 AA.
DE Human CD2001 protein #2.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.0%; Score 301.5; DB 7; Length 236;
Best Local Similarity 32.6%; Pred. No. 2.4e-20;
RESULT 861
ID AAE26246 standard; protein; 217 AA.
DE Human CD2001 protein transmembrane domain.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 16.8%; Score 298; DB 5; Length 217;
Best Local Similarity 33.8%; Pred. No. 4.7e-20;
RESULT 862
ID AEW01826 standard; protein; 217 AA.
DE Human CD2001 protein extracellular domain.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 16.8%; Score 298; DB 7; Length 217;
Best Local Similarity 33.8%; Pred. No. 4.7e-20;
RESULT 863
ID ABE96270 standard; protein; 551 AA.
DE Human immunoglobulin superfamily protein IGSFP-8.
PN WO2002272794-A2.
PD 19-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 16.6%; Score 294.5; DB 5; Length 551;
Best Local Similarity 30.4%; Pred. No. 4e-19;
RESULT 864
ID ADK98560 standard; protein; 565 AA.
DE Human immune response associated protein IRAF-23 protein.
PN WO2004020593-A2.
PD 11-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 16.6%; Score 294.5; DB 8; Length 565;
Best Local Similarity 30.4%; Pred. No. 4.2e-19;
RESULT 865
ID ADS98832 standard; protein; 284 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 1096.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
Query Match 16.5%; Score 291.5; DB 8; Length 284;
Best Local Similarity 32.3%; Pred. No. 3e-19;
RESULT 866
ID AEA20174 standard; protein; 284 AA.
DE Novel human polypeptide SEQ ID NO 868.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 16.5%; Score 291.5; DB 9; Length 284;
Best Local Similarity 32.3%; Pred. No. 3e-19;
RESULT 867
ID ADL57243 standard; protein; 526 AA.
DE Human NOV5c protein SEQ ID NO:188.
PN WO2004022723-A2.
PD 18-MAR-2004.
PA (CURA-) CURAGEN CORP.
Query Match 15.9%; Score 282.5; DB 8; Length 526;
Best Local Similarity 31.5%; Pred. No. 5.5e-16;
RESULT 868
ID ADL57105 standard; protein; 526 AA.
DE Human NOV5c protein SEQ ID NO:50.
PN WO2004022723-A2.
PD 18-MAR-2004.
PA (CURA-) CURAGEN CORP.
Query Match 15.9%; Score 282.5; DB 8; Length 526;
Best Local Similarity 31.5%; Pred. No. 5.5e-16;
RESULT 869
ID ADR20041 standard; protein; 91 AA.
DE Human immune response associated protein (IRAP), seq id 1.
PN WO2004048550-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.3%; Score 272; DB 8; Length 91;
Best Local Similarity 100.0%; Pred. No. 4.4e-18;
RESULT 870
ID ADL13233 standard; protein; 271 AA.
DE Human cancer-associated protein #236.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.1%; Score 267; DB 9; Length 271;
Best Local Similarity 31.2%; Pred. No. 6.6e-17;
RESULT 871
ID ADL13235 standard; protein; 317 AA.
DE Human cancer-associated protein #237.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 14.8%; Score 263; DB 9; Length 317;
Best Local Similarity 31.0%; Pred. No. 2e-16;
RESULT 872
ID ABE98758 standard; protein; 445 AA.
DE Dendritic cell membrane molecule-immunoglobulin (Ig) Fc fusion protein.
PN JP2005206478-A.
PD 04-AUG-2005.
PA (KIRI) KIRIN BREWERY KK.
Query Match 14.3%; Score 254; DB 9; Length 445;
Best Local Similarity 29.1%; Pred. No. 2.5e-15;
RESULT 873
ID AAU09867 standard; protein; 220 AA.
DE Novel human secreted protein #8.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 14.2%; Score 251; DB 5; Length 220;
Best Local Similarity 35.4%; Pred. No. 1.7e-15;

RESULT 874
ID ABB53269 standard; protein; 310 AA.
DE Human polypeptide #9.
PN WO200181363-A1.
PD 01-NOV-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 13.9%; Score 247; DB 5; Length 310;
Best Local Similarity 26.7%; Pred. No. 7e-15;
RESULT 875
ID AAB26231 standard; protein; 195 AA.
DE Human CD2000 protein #2.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 13.8%; Score 245; DB 5; Length 195;
Best Local Similarity 35.1%; Pred. No. 5.5e-15;
RESULT 876
ID ABW01810 standard; protein; 195 AA.
DE Human CD2000 protein extracellular domain #4.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 13.8%; Score 245; DB 7; Length 195;
Best Local Similarity 35.1%; Pred. No. 5.5e-15;
RESULT 877
ID AAB26232 standard; protein; 203 AA.
DE Human CD2000 protein transmembrane domain.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 13.8%; Score 245; DB 7; Length 203;
Best Local Similarity 35.1%; Pred. No. 5.9e-15;
RESULT 878
ID ABW01811 standard; protein; 203 AA.
DE Human CD2000 protein extracellular domain #5.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 13.8%; Score 245; DB 7; Length 203;
Best Local Similarity 35.1%; Pred. No. 5.9e-15;
RESULT 879
ID ABA23943 standard; protein; 423 AA.
DE Human PRO polypeptide SEQ ID NO 485.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (SETH) GENENTECH INC.
Query Match 13.5%; Score 238.5; DB 9; Length 423;
Best Local Similarity 32.1%; Pred. No. 7.3e-14;
RESULT 880
ID ABB53268 standard; protein; 229 AA.
DE Human polypeptide #8.
PN WO200181363-A1.
PD 01-NOV-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 13.3%; Score 236.5; DB 5; Length 229;
Best Local Similarity 28.6%; Pred. No. 4.7e-14;
RESULT 881
ID AD21328 standard; protein; 331 AA.
DE Murine cancer-associated protein #79.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 12.7%; Score 225.5; DB 9; Length 331;
Best Local Similarity 26.0%; Pred. No. 9.3e-13;
RESULT 882
ID AAB47322 standard; protein; 351 AA.
DE APEX-2.
PN WO200146260-A2.
PD 28-JUN-2001.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 12.7%; Score 225.5; DB 4; Length 351;

Best Local Similarity 26.0%; Pred. No. 1e-12;
RESULT 883
ID ABB89245 standard; protein; 168 AA.
DE Human polypeptide SEQ ID NO 1621.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.4%; Score 219; DB 5; Length 168;
Best Local Similarity 32.3%; Pred. No. 1.5e-12;
RESULT 884
ID ABU03171 standard; protein; 220 AA.
DE Human immunoglobulin (Ig) APEX4sv1 protein.
PN WO20027173-A2.
PD 03-OCT-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 11.6%; Score 206; DB 6; Length 220;
Best Local Similarity 28.3%; Pred. No. 4e-11;
RESULT 885
ID AAE26225 standard; protein; 159 AA.
DE Human CD2000 protein #1.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 200.5; DB 5; Length 159;
Best Local Similarity 35.2%; Pred. No. 8.5e-11;
RESULT 886
ID ABW01804 standard; protein; 159 AA.
DE Human CD2000 protein cytoplasmic domain #1.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 200.5; DB 7; Length 159;
Best Local Similarity 35.2%; Pred. No. 8.5e-11;
RESULT 887
ID AAG96266 standard; protein; 221 AA.
DE Human immunoglobulin superfamily protein IGSPF-4.
PN WO200272794-A2.
PD 19-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.3%; Score 199.5; DB 5; Length 221;
Best Local Similarity 28.3%; Pred. No. 1.7e-10;
RESULT 888
ID AAB85690 standard; protein; 275 AA.
DE Mouse protein sequence MCP1591.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.8%; Score 190.5; DB 7; Length 275;
Best Local Similarity 29.1%; Pred. No. 1.8e-09;
RESULT 889
ID AAR97632 standard; protein; 343 AA.
DE Mouse SLAMF1 T-cell co-stimulatory protein.
PN WO9617060-A1.
PD 06-JUN-1996.
PA (SCHE) SCHERING CORP.
Query Match 10.5%; Score 186; DB 2; Length 343;
Best Local Similarity 24.3%; Pred. No. 6.7e-09;
RESULT 890
ID AAR97628 standard; protein; 335 AA.
DE Human SLAMF1 T-cell co-stimulatory protein.
PN WO9617060-A1.
PD 06-JUN-1996.
PA (SCHE) SCHERING CORP.
Query Match 10.3%; Score 182.5; DB 2; Length 335;
Best Local Similarity 22.5%; Pred. No. 1.4e-08;
RESULT 891
ID AAB71853 standard; protein; 335 AA.
DE Human SLAM Protein.
PN WO200111046-A1.
PD 15-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 182.5; DB 4; Length 335;
Best Local Similarity 22.5%; Pred. No. 1.4e-08;

RESULT 892
ID AAU11927 standard; protein; 335 AA.
DE Human protein sequence #1, related to isolation of genes within SLR-1B.
PN WO200188200-A2.
PD 22-NOV-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 10.3%; Score 182.5; DB 5; Length 335;
Best Local Similarity 22.5%; Pred. No. 1.4e-08;
RESULT 893
ID ABB90776 standard; protein; 335 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 285.
PN WO200210217-A2.
PD 07-FEB-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 10.3%; Score 182.5; DB 5; Length 335;
Best Local Similarity 22.5%; Pred. No. 1.4e-08;
RESULT 894
ID ABU54483 standard; protein; 335 AA.
DE Human normal endothelial marker NEM 23.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 10.3%; Score 182.5; DB 6; Length 335;
Best Local Similarity 22.5%; Pred. No. 1.4e-08;
RESULT 895
ID ADL82887 standard; protein; 335 AA.
DE Human PRO12612, SEQ ID 89.
PN WO2004024097-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 182.5; DB 8; Length 335;
Best Local Similarity 22.5%; Pred. No. 1.4e-08;
RESULT 896
ID ADP54607 standard; protein; 335 AA.
DE Human PRO protein sequence SEQ ID NO:583.
PN WO200403956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 182.5; DB 9; Length 335;
Best Local Similarity 22.5%; Pred. No. 1.4e-08;
RESULT 897
ID ADY19726 standard; protein; 335 AA.
DE PRO polypeptide SEQ ID NO 5532.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 182.5; DB 9; Length 335;
Best Local Similarity 22.5%; Pred. No. 1.4e-08;
RESULT 898
ID ADY15680 standard; protein; 335 AA.
DE PRO polypeptide SEQ ID NO 1486.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 182.5; DB 9; Length 335;
Best Local Similarity 22.5%; Pred. No. 1.4e-08;
RESULT 899
ID AAG7978 standard; protein; 334 AA.
DE Human signalling lymphocytic activation molecule (SLAMF)/SCZ.
PN WO200180717-A2.
PD 01-NOV-2001.
PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
Query Match 10.2%; Score 181.5; DB 5; Length 334;
Best Local Similarity 22.6%; Pred. No. 1.7e-08;
RESULT 900
ID AAR97631 standard; protein; 307 AA.
DE Human SLAMF T-cell co-stimulatory protein.
PN WO9617060-A1.
PD 06-JUN-1996.
PA (SCHE) SCHERING CORP.
Query Match 10.2%; Score 180; DB 2; Length 307;
Best Local Similarity 22.6%; Pred. No. 2.2e-08;
RESULT 901

ID AAY92181 standard; protein; 278 AA.
DE Murine TANGO 195.
PN WO200018800-A1.
PD 06-APR-2000.
PA (MILL-) MILENNIUM BIOTHERAPEUTICS INC.
Query Match 10.1%; Score 179; DB 3; Length 278;
Best Local Similarity 25.9%; Pred. No. 2.3e-08;
RESULT 902
ID ABG74266 standard; protein; 278 AA.
DE Human transmembrane protein TANGO 195 form 2.
PN US2002155526-A1.
PD 24-OCT-2002.
PA (BUSF/) BUSFIELD S J.
Query Match 10.1%; Score 179; DB 6; Length 278;
Best Local Similarity 25.9%; Pred. No. 2.3e-08;
RESULT 903
ID ABW01426 standard; protein; 278 AA.
DE Murine TANGO 195 protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILENNIUM PHARM INC.
Query Match 10.1%; Score 179; DB 7; Length 278;
Best Local Similarity 25.9%; Pred. No. 2.3e-08;
RESULT 904
ID ABW01428 standard; protein; 258 AA.
DE Murine TANGO 195 mature protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILENNIUM PHARM INC.
Query Match 10.0%; Score 177.5; DB 7; Length 258;
Best Local Similarity 27.0%; Pred. No. 2.9e-08;
RESULT 905
ID AAW67933 standard; protein; 33 AA.
DE Fragment of human secreted protein encoded by gene 5.
PN WO9842738-A1.
PD 01-OCT-1998.
PA (HUMA-) HUMA GENOME SCI INC.
Query Match 9.9%; Score 175; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 906
ID ADS11838 standard; protein; 148 AA.
DE Human therapeutic contig protein - SEQ ID 2075.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 9.6%; Score 170.5; DB 8; Length 148;
Best Local Similarity 29.9%; Pred. No. 6.2e-08;
RESULT 907
ID AAY43138 standard; protein; 365 AA.
DE Human NAIL protein sequence.
PN WO9950297-A1.
PD 07-OCT-1999.
PA (IMMV) IMMUNEX CORP.
Query Match 9.6%; Score 170; DB 2; Length 365;
Best Local Similarity 21.9%; Pred. No. 2.6e-07;
RESULT 908
ID AAW23942 standard; protein; 365 AA.
DE Human EST encoded protein SEQ ID NO: 1467.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.6%; Score 170; DB 4; Length 365;
Best Local Similarity 21.9%; Pred. No. 2.6e-07;
RESULT 909
ID AAU11929 standard; protein; 365 AA.
DE Human protein sequence #2, related to isolation of genes within SLR-1B.
PN WO200188200-A2.
PD 22-NOV-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 9.6%; Score 170; DB 5; Length 365;
Best Local Similarity 21.9%; Pred. No. 2.6e-07;
RESULT 910
ID ADP56168 standard; protein; 365 AA.

DE Human PRO protein sequence SEQ ID NO:2144.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 9.6%; Score 170; DB 8; Length 365;
Best Local Similarity 21.9%; Pred. No. 2.6e-07;
RESULT 911
ID ADP25183 standard; protein; 365 AA.
DE PRO polypeptide SEQ ID NO:2361.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 9.6%; Score 170; DB 8; Length 365;
Best Local Similarity 21.9%; Pred. No. 2.6e-07;
RESULT 912
ID ABP41447 standard; protein; 391 AA.
DE Human ovarian antigen HMAGN71, SEQ ID NO:2579.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 170; DB 5; Length 391;
Best Local Similarity 21.9%; Pred. No. 2.9e-07;
RESULT 913
ID AAR97630 standard; protein; 305 AA.
DE Human SLAMF3 T-cell co-stimulatory protein.
PN WO9617060-A1.
PD 06-JUN-1996.
PA (SCHE) SCHERING CORP.
Query Match 9.3%; Score 164.5; DB 2; Length 305;
Best Local Similarity 21.7%; Pred. No. 6.8e-07;
RESULT 914
ID ABB90777 standard; protein; 305 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 286.
PN WO200210217-A2.
PD 07-FEB-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 9.3%; Score 164.5; DB 5; Length 305;
Best Local Similarity 21.7%; Pred. No. 6.8e-07;
RESULT 915
ID ABU54484 standard; protein; 305 AA.
DE Human normal endothelial marker NEM 23 secreted.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 9.3%; Score 164.5; DB 6; Length 305;
Best Local Similarity 21.7%; Pred. No. 6.8e-07;
RESULT 916
ID AAR97633 standard; protein; 329 AA.
DE Mouse SLAMF2 T-cell co-stimulatory protein.
PN WO9617060-A1.
PD 06-JUN-1996.
PA (SCHE) SCHERING CORP.
Query Match 8.9%; Score 158.5; DB 2; Length 329;
Best Local Similarity 27.0%; Pred. No. 2.9e-06;
RESULT 917
ID AAU11928 standard; protein; 329 AA.
DE Mouse protein sequence #1, related to isolation of genes within SLF-1B.
PN WO200188200-A2.
PD 22-NOV-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 8.9%; Score 158.5; DB 5; Length 329;
Best Local Similarity 27.0%; Pred. No. 2.9e-06;
RESULT 918
ID AAR97629 standard; protein; 298 AA.
DE Human SLAMF2 T-cell co-stimulatory protein.
PN WO9617060-A1.
PD 06-JUN-1996.
PA (SCHE) SCHERING CORP.
Query Match 8.6%; Score 152; DB 2; Length 298;
Best Local Similarity 23.4%; Pred. No. 1.1e-05;
RESULT 919
ID ABB90778 standard; protein; 298 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 287.
PN WO200210217-A2.
PD 07-FEB-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 8.6%; Score 152; DB 5; Length 298;
Best Local Similarity 23.4%; Pred. No. 1.1e-05;
RESULT 920
ID ABU54485 standard; protein; 298 AA.
DE Human normal endothelial marker NEM 23 short.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 8.6%; Score 152; DB 6; Length 298;
Best Local Similarity 23.4%; Pred. No. 1.1e-05;
RESULT 921
ID AAY52479 standard; protein; 285 AA.
DE Human D-SLAM.
PN WO9940184-A1.
PD 12-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.5%; Score 150.5; DB 3; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 922
ID AAM93287 standard; protein; 285 AA.
DE Human polypeptide, SEQ ID NO: 2773.
PN EP113094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 8.5%; Score 150.5; DB 4; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 923
ID AAB71852 standard; protein; 285 AA.
DE Human D-SLAM protein.
PN WO20011046-A1.
PD 15-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.5%; Score 150.5; DB 4; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 924
ID AAB47323 standard; protein; 285 AA.
DE APEX-3.
PN WO200146260-A2.
PD 28-JUN-2001.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 8.5%; Score 150.5; DB 4; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 925
ID AAR12075 standard; protein; 285 AA.
DE Dendritic cell (DC) DCIGR protein.
PN WO200172773-A2.
PD 04-OCT-2001.
PA (NOVS) NOVARTIS AG.
Query Match 8.5%; Score 150.5; DB 4; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 926
ID ABG32412 standard; protein; 285 AA.
DE Dendritic enriched secreted lymphocyte activation molecule (D-SLAM).
PN WO200262955-A2.
PD 15-AUG-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.5%; Score 150.5; DB 5; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 927
ID ADC78929 standard; protein; 285 AA.
DE Human PRO protein #79.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 150.5; DB 7; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 928
ID ADD18914 standard; protein; 285 AA.
DE Human disease related protein SegId403.

PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 8.5%; Score 150.5; DB 7; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 929
ID ADP15146 standard; protein; 285 AA.
DE Human albumin fusion protein-related protein SegID444.
PN WO2003060071-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ-) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPAL PHARM CORP.
Query Match 8.5%; Score 150.5; DB 7; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 930
ID ADL30740 standard; protein; 285 AA.
DE Human protein encoded by a full length cDNA clone SeqID 2773.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.5%; Score 150.5; DB 8; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 931
ID ADQ21161 standard; protein; 285 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3981.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 8.5%; Score 150.5; DB 8; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 932
ID ADP14157 standard; protein; 285 AA.
DE Human NF-kappaB pathway-associated protein SegID158.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 8.5%; Score 150.5; DB 8; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 933
ID ADP25075 standard; protein; 285 AA.
DE PRO polypeptide SEQ ID NO:2253.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 8.5%; Score 150.5; DB 8; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 934
ID ADU06615 standard; protein; 285 AA.
DE Novel bronchial cancer-associated human protein SegID841.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 8.5%; Score 150.5; DB 8; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 935
ID ADY17598 standard; protein; 285 AA.
DE PRO polypeptide SEQ ID NO 3404.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH-) GENENTECH INC.
Query Match 8.5%; Score 150.5; DB 9; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 936
ID ADZ10066 standard; protein; 285 AA.
DE Human breast cancer marker BLMB protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB-) BAYER HEALTHCARE AG.
Query Match 8.5%; Score 150.5; DB 9; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.4e-05;
RESULT 937
ID AEW01429 standard; protein; 211 AA.
DE Murine TANGO 195 protein extracellular domain.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 146.5; DB 7; Length 211;
Best Local Similarity 28.6%; Pred. No. 2.2e-05;
RESULT 938
ID AAY92180 standard; protein; 312 AA.
DE Partial human TANGO 195 protein.
PN WO200108800-A1.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 8.2%; Score 146; DB 3; Length 312;
Best Local Similarity 24.5%; Pred. No. 4.4e-05;
RESULT 939
ID ABG74265 standard; protein; 312 AA.
DE Human transmembrane protein TANGO 195 form 1.
PN US2002155526-A1.
PD 24-OCT-2002.
PA (BUSF/) BUSFIELD S J.
Query Match 8.2%; Score 146; DB 6; Length 312;
Best Local Similarity 24.5%; Pred. No. 4.4e-05;
RESULT 940
ID AEW01412 standard; protein; 312 AA.
DE Human TANGO 195 form 1 protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.2%; Score 146; DB 7; Length 312;
Best Local Similarity 24.5%; Pred. No. 4.4e-05;
RESULT 941
ID AAM24013 standard; protein; 318 AA.
DE Human EST encoded protein SEQ ID NO: 1538.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.2%; Score 146; DB 4; Length 318;
Best Local Similarity 24.5%; Pred. No. 4.5e-05;
RESULT 942
ID AAY92182 standard; protein; 320 AA.
DE Human partial TANGO 195 from clone T195Atbpb93f1.
PN WO200018800-A1.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 8.2%; Score 146; DB 3; Length 320;
Best Local Similarity 24.5%; Pred. No. 4.5e-05;
RESULT 943
ID ABG74267 standard; protein; 320 AA.
DE Human transmembrane protein TANGO 195, full length.
PN US2002155526-A1.
PD 24-OCT-2002.
PA (BUSF/) BUSFIELD S J.
Query Match 8.2%; Score 146; DB 6; Length 320;
Best Local Similarity 24.5%; Pred. No. 4.5e-05;
RESULT 944
ID ABW01436 standard; protein; 320 AA.
DE Human TANGO 195 form 2 protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.2%; Score 146; DB 7; Length 320;
Best Local Similarity 24.5%; Pred. No. 4.5e-05;
RESULT 945
ID ADL10254 standard; protein; 211 AA.
DE Human protein useful for treating neurological disease Seq 3760.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.2%; Score 145; DB 8; Length 211;
Best Local Similarity 30.2%; Pred. No. 3.1e-05;
RESULT 946

ID AAY92183 standard; protein; 285 AA.
 DE Full-length human TANGO 195 protein.
 PN W0200018800-A1.
 PD 06-APR-2000.
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 Query Match 8.2%; Score 144.5; DB 3; Length 285;
 Best Local Similarity 22.5%; Pred. No. 5.4e-05;
 RESULT 947
 ID ABG74268 standard; protein; 285 AA.
 DE Mouse transmembrane protein TANGO 195.
 PN US2002155526-A1.
 PD 24-OCT-2002.
 PA (BUSEF) BUSEFIELD S J.
 Query Match 8.2%; Score 144.5; DB 6; Length 285;
 Best Local Similarity 22.5%; Pred. No. 5.4e-05;
 RESULT 948
 ID ABW01442 standard; protein; 285 AA.
 DE Human TANGO 195 protein.
 PN US2003113865-A1.
 PD 19-JUN-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 8.2%; Score 144.5; DB 7; Length 285;
 Best Local Similarity 22.5%; Pred. No. 5.4e-05;
 RESULT 949
 ID ADI3290 standard; protein; 344 AA.
 DE Murine cancer-associated protein #90.
 PN W02005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 8.1%; Score 144; DB 9; Length 344;
 Best Local Similarity 21.4%; Pred. No. 7.9e-05;
 RESULT 950
 ID AEM85810 standard; protein; 358 AA.
 DE Mouse protein sequence MCP3002.
 PN W02003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 8.1%; Score 144; DB 7; Length 358;
 Best Local Similarity 21.4%; Pred. No. 8.4e-05;
 RESULT 951
 ID ABG75379 standard; protein; 416 AA.
 DE Predicted INSP052 protein.
 PN W02003093316-A2.
 PD 13-NOV-2003.
 PA (ARES-) ARES TRADING SA.
 Query Match 8.0%; Score 142.5; DB 7; Length 416;
 Best Local Similarity 22.1%; Pred. No. 0.00015;
 RESULT 952
 ID ABG75377 standard; protein; 416 AA.
 DE Human INSP052 complete protein.
 PN W02003093316-A2.
 PD 13-NOV-2003.
 PA (ARES-) ARES TRADING SA.
 Query Match 8.0%; Score 142.5; DB 8; Length 416;
 Best Local Similarity 22.1%; Pred. No. 0.00015;
 RESULT 953
 ID ADO47892 standard; protein; 416 AA.
 DE Human protein SEQ ID NO:9.
 PN W02004007672-A2.
 PD 22-JAN-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 8.0%; Score 142.5; DB 8; Length 416;
 Best Local Similarity 22.1%; Pred. No. 0.00015;
 RESULT 954
 ID ADS11056 standard; protein; 416 AA.
 DE Human therapeutic protein - SEQ ID 1293.
 PN W02004080148-A2.
 PD 23-SEP-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 8.0%; Score 142.5; DB 8; Length 416;
 Best Local Similarity 22.1%; Pred. No. 0.00015;
 RESULT 955
 ID AEA27921 standard; protein; 416 AA.

DE Cell surface recognition molecule INSP052.
 PN W02005046714-A2.
 PD 26-MAY-2005.
 PA (ARES-) ARES TRADING SA.
 Query Match 8.0%; Score 142.5; DB 9; Length 416;
 Best Local Similarity 22.1%; Pred. No. 0.00015;
 RESULT 956
 ID ADQ65357 standard; protein; 367 AA.
 DE Novel human protein sequence #330.
 PN EP1440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 8.0%; Score 142; DB 8; Length 367;
 Best Local Similarity 22.2%; Pred. No. 0.00014;
 RESULT 957
 ID ADA07622 standard; peptide; 149 AA.
 DE Human secreted protein from gene 43, peptide #2.
 PN US2003064412-A1.
 PD 03-APR-2003.
 PA (FISC/) FISCHER C L.
 PA (ROSE/) ROSEN C A.
 PA (SOPP/) SOPPET D R.
 PA (RUBE/) RUBEN S M.
 PA (KYAW/) KYAW H.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (LAFL/) LAFLEUR D W.
 PA (MOOR/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (OLSE/) OLSEN H S.
 PA (EBNE/) EBNER R.
 PA (BREW/) BREWER L A.
 Query Match 8.0%; Score 141; DB 7; Length 149;
 Best Local Similarity 30.7%; Pred. No. 4.5e-05;
 RESULT 958
 ID ADN41449 standard; protein; 149 AA.
 DE Novel human secreted protein fragment seqid 571.
 PN US2004044191-A1.
 PD 04-MAR-2004.
 PA (FISC/) FISCHER C L.
 PA (ROSE/) ROSEN C A.
 PA (SOPP/) SOPPET D R.
 PA (RUBE/) RUBEN S M.
 PA (KYAW/) KYAW H.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (LAFL/) LAFLEUR D W.
 PA (MOOR/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (OLSE/) OLSEN H.
 PA (EBNE/) EBNER R.
 PA (BIRS/) BIRSE C E.
 Query Match 8.0%; Score 141; DB 8; Length 149;
 Best Local Similarity 30.7%; Pred. No. 4.5e-05;
 RESULT 959
 ID ADA57556 standard; protein; 142 AA.
 DE Human secreted protein #504.
 PN W02002102994-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 7.9%; Score 140.5; DB 6; Length 142;
 Best Local Similarity 31.0%; Pred. No. 4.7e-05;
 RESULT 960
 ID ADA41448 standard; protein; 142 AA.
 DE Human secreted protein.
 PN W02002102993-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 7.9%; Score 140.5; DB 6; Length 142;
 Best Local Similarity 31.0%; Pred. No. 4.7e-05;
 RESULT 961
 ID ADC74567 standard; protein; 142 AA.
 DE Human secreted protein - SEQ ID 1200.

PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 7.9%; Score 140.5; DB 7; Length 142;
RESULT 962
ID ADD38086 standard; protein; 142 AA.
DE Human secreted protein #269.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 7.9%; Score 140.5; DB 7; Length 142;
RESULT 963
ID ADN41130 standard; protein; 142 AA.
DE Novel human secreted protein seqid 252.
PN US200404191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAFL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIT/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match
Best Local Similarity 7.9%; Score 140.5; DB 8; Length 142;
RESULT 964
ID AAY02692 standard; protein; 143 AA.
DE Human secreted protein encoded by gene 43 clone HTADX17.
PN WO9902546-A1.
PD 21-JAN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 7.9%; Score 140.5; DB 2; Length 143;
RESULT 965
ID ADA07371 standard; protein; 143 AA.
DE Human secreted protein from gene 43.
PN US2003064412-A1.
PD 03-APR-2003.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAFL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIT/) SHI Y.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
Query Match
Best Local Similarity 7.9%; Score 140.5; DB 7; Length 143;
RESULT 966
ID ABW01419 standard; protein; 290 AA.
DE Human TANGO 195 form 1 mature protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.9%; Score 140.5; DB 7; Length 290;
RESULT 967
ID ABW01438 standard; protein; 298 AA.
DE Human TANGO 195 form 2 mature protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.8%; Score 139; DB 2; Length 28;
RESULT 969
ID ABW01444 standard; protein; 263 AA.
DE Human TANGO 195 mature protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.8%; Score 139; DB 7; Length 263;
RESULT 970
ID ABG75378 standard; protein; 418 AA.
DE Murine INSP052 complete protein.
PN WO2003093316-A2.
PD 13-NOV-2003.
PA (ARES-) ARES TRADING SA.
Query Match
Best Local Similarity 7.8%; Score 138.5; DB 7; Length 418;
RESULT 971
ID AEA27923 standard; protein; 418 AA.
DE Cell surface recognition molecule INSP055.
PN WO2005046714-A2.
PD 26-MAY-2005.
PA (ARES-) ARES TRADING SA.
Query Match
Best Local Similarity 7.8%; Score 138.5; DB 9; Length 418;
RESULT 972
ID AAR26255 standard; protein; 70 AA.
DE Human CD2001 protein Ig domain.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.8%; Score 138; DB 5; Length 70;
RESULT 973
ID AEW01635 standard; protein; 70 AA.
DE Human CD2001 protein immunoglobulin (Ig) domain.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.8%; Score 138; DB 7; Length 70;
RESULT 974
ID ADO47895 standard; protein; 383 AA.
DE Human mature protein SEQ ID NO:12.
PN WO2004007672-A2.
PD 22-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match
Best Local Similarity 7.8%; Score 137.5; DB 8; Length 383;
RESULT 975
ID AEA27931 standard; protein; 383 AA.
DE Human INSP052 mature polypeptide.
PN WO2005046714-A2.
PD 26-MAY-2005.
PA (ARES-) ARES TRADING SA.
Query Match
Best Local Similarity 7.8%; Score 137.5; DB 9; Length 383;
RESULT 976
ID ADW72195 standard; protein; 327 AA.
DE Human CD2 amino acid sequence.
PN WO2004022097-A1.
PD 18-MAR-2004.

PA (MEDI-) MEDIMUNE INC.
 PA (USSH) US NAT CANCER INST.
 Query Match 7.7%; Score 136.5; DB 8; Length 327;
 Best Local Similarity 23.9%; Pred. No. 0.00039;
 RESULT 977
 ID AAY8135 standard; protein; 351 AA.
 DE Human CD2.
 PN W0200012113-A2.
 PD 09-MAR-2000.
 PA (BIOC) BIOGEN INC.
 Query Match 7.7%; Score 136.5; DB 3; Length 351;
 Best Local Similarity 23.9%; Pred. No. 0.00043;
 RESULT 978
 ID AAB61159 standard; protein; 351 AA.
 DE Human CD2.
 PN US6162432-A.
 PD 19-DEC-2000.
 PA (UNMT) UNIV MICHIGAN.
 Query Match 7.7%; Score 136.5; DB 4; Length 351;
 Best Local Similarity 23.9%; Pred. No. 0.00043;
 RESULT 979
 ID ABB81993 standard; protein; 351 AA.
 DE Human CD2 polypeptide.
 PN W0200260480-A1.
 PD 08-AUG-2002.
 PA (BIOC) BIOGEN INC.
 Query Match 7.7%; Score 136.5; DB 5; Length 351;
 Best Local Similarity 23.9%; Pred. No. 0.00043;
 RESULT 980
 ID AAU76227 standard; protein; 351 AA.
 DE Mammalian CD2 antigen protein.
 PN US2002009449-A1.
 PD 24-JAN-2002.
 PA (BIOC) BIOGEN INC.
 Query Match 7.7%; Score 136.5; DB 8; Length 351;
 Best Local Similarity 23.9%; Pred. No. 0.00043;
 RESULT 981
 ID ABM8581 standard; protein; 351 AA.
 DE Human protein sequence hcp48906.
 PN W02003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 7.7%; Score 136.5; DB 7; Length 351;
 Best Local Similarity 23.9%; Pred. No. 0.00043;
 RESULT 982
 ID ADQ60208 standard; protein; 351 AA.
 DE Human CD2 protein.
 PN US2004136987-A1.
 PD 15-JUL-2004.
 PA (BIOC) BIOGEN INC.
 Query Match 7.7%; Score 136.5; DB 8; Length 351;
 Best Local Similarity 23.9%; Pred. No. 0.00043;
 RESULT 983
 ID ADZ13293 standard; protein; 351 AA.
 DE Human cancer-associated protein #249.
 PN W02005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 7.7%; Score 136.5; DB 9; Length 351;
 Best Local Similarity 23.9%; Pred. No. 0.00043;
 RESULT 984
 ID AAR06365 standard; protein; 353 AA.
 DE Soluble two domain human CD2 glycoprotein.
 PN W09008187-A.
 PD 26-JUL-1990.
 PA (DAND) DANA FARBER CANCER INST INC.
 Query Match 7.7%; Score 136.5; DB 2; Length 353;
 Best Local Similarity 23.9%; Pred. No. 0.00044;
 RESULT 985
 ID AAU29274 standard; protein; 198 AA.
 DE Human PRO polypeptide sequence #251.
 PN W0200168848-A2.
 PD 20-SEP-2001.
 PA (GENT) GENENTECH INC.
 Query Match 7.6%; Score 134.5; DB 4; Length 198;
 Best Local Similarity 30.7%; Pred. No. 0.00029;
 RESULT 986
 ID ABU58650 standard; protein; 198 AA.
 DE Human PRO polypeptide #251.
 PN US2003027272-A1.
 PD 06-FEB-2003.
 Query Match 7.6%; Score 134.5; DB 6; Length 198;
 Best Local Similarity 30.7%; Pred. No. 0.00029;
 RESULT 987
 ID ABU88198 standard; protein; 198 AA.
 DE Novel human secreted and transmembrane protein PRO4421.
 PN US2003032127-A1.
 PD 13-FEB-2003.
 Query Match 7.6%; Score 134.5; DB 6; Length 198;
 Best Local Similarity 30.7%; Pred. No. 0.00029;
 RESULT 988
 ID ABU84513 standard; protein; 198 AA.
 DE Human secreted/transmembrane protein (PRO) #251.
 PN US2003032112-A1.
 PD 13-FEB-2003.
 Query Match 7.6%; Score 134.5; DB 6; Length 198;
 Best Local Similarity 30.7%; Pred. No. 0.00029;
 RESULT 989
 ID ABR66387 standard; protein; 198 AA.
 DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
 PN US2003027278-A1.
 PD 06-FEB-2003.
 Query Match 7.6%; Score 134.5; DB 6; Length 198;
 Best Local Similarity 30.7%; Pred. No. 0.00029;
 RESULT 990
 ID ABR65777 standard; protein; 198 AA.
 DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
 PN US2003036159-A1.
 PD 20-FEB-2003.
 Query Match 7.6%; Score 134.5; DB 6; Length 198;
 Best Local Similarity 30.7%; Pred. No. 0.00029;
 RESULT 991
 ID ABU99717 standard; protein; 198 AA.
 DE Human secreted/transmembrane protein (PRO) #251.
 PN US2003040070-A1.
 PD 27-FEB-2003.
 Query Match 7.6%; Score 134.5; DB 6; Length 198;
 Best Local Similarity 30.7%; Pred. No. 0.00029;
 RESULT 992
 ID ABU82956 standard; protein; 198 AA.
 DE Human PRO polypeptide #251.
 PN US2003032113-A1.
 PD 13-FEB-2003.
 Query Match 7.6%; Score 134.5; DB 6; Length 198;
 Best Local Similarity 30.7%; Pred. No. 0.00029;
 RESULT 993
 ID ABU90077 standard; protein; 198 AA.
 DE Novel human secreted and transmembrane protein PRO4421.
 PN US2003036147-A1.
 PD 20-FEB-2003.
 Query Match 7.6%; Score 134.5; DB 6; Length 198;
 Best Local Similarity 30.7%; Pred. No. 0.00029;
 RESULT 994
 ID ABR68326 standard; protein; 198 AA.
 DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
 PN US2003027264-A1.
 PD 06-FEB-2003.
 Query Match 7.6%; Score 134.5; DB 6; Length 198;
 Best Local Similarity 30.7%; Pred. No. 0.00029;
 RESULT 995
 ID ABU96379 standard; protein; 198 AA.
 DE Novel human secreted and transmembrane protein PRO4421.
 PN US2003036144-A1.
 PD 20-FEB-2003.

Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 996				
ID ABU92810 standard; protein; 198 AA.				
DE Human secreted/transmembrane protein (PRO) #251.				
PN US2003036149-A1.				
PN 20-FEB-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 997				
ID ABC08887 standard; protein; 198 AA.				
DE Human secreted/transmembrane protein (PRO) #251.				
PN US2003044923-A1.				
PN 06-MAR-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 998				
ID ABO02939 standard; protein; 198 AA.				
DE Human secreted/transmembrane protein (PRO) #251.				
PN US2003040062-A1.				
PN 27-FEB-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 999				
ID ABR75093 standard; protein; 198 AA.				
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.				
PN US2003040056-A1.				
PN 27-FEB-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1000				
ID ABR94855 standard; protein; 198 AA.				
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.				
PN US2003044926-A1.				
PN 06-MAR-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1001				
ID ABU85828 standard; protein; 198 AA.				
DE Human PRO polypeptide #251.				
PN US2003036140-A1.				
PN 20-FEB-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1002				
ID ABU89898 standard; protein; 198 AA.				
DE Novel human secreted and transmembrane protein PRO4421.				
PN US2003013153-A1.				
PN 16-JAN-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1003				
ID ABU98203 standard; protein; 198 AA.				
DE Novel human secreted and transmembrane protein PRO4421.				
PN US2003017544-A1.				
PN 23-JAN-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1004				
ID ABU91909 standard; protein; 198 AA.				
DE Novel human secreted and transmembrane protein PRO4421.				
PN US2003027277-A1.				
PN 06-FEB-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1005				
ID ABU89602 standard; protein; 198 AA.				
DE Human PRO polypeptide #251.				
PN US2003036141-A1.				
PN 20-FEB-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		
RESULT 1006				
ID ABU89602 standard; protein; 198 AA.				
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.				
PN US2003036141-A1.				
PN 20-FEB-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;
Best Local Similarity	30.7%;	Pred. No. 0.00029;		

ID	ABU86443 standard; protein; 198 AA.
ID	Human secreted/transmembrane protein (PRO) #251.
PN	US2003036146-AI.
PD	20-FEB-2003.
PA	(GENETH) GENENTECH INC.
Query Match	7.6%; Score 134.5; DB 6;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1007	
ID	ABU67656 standard; protein; 198 AA.
DN	Human secreted/cransmembrane protein (PRO) #251.
PD	US2003036162-AA.
PD	20-FEB-2003.
PA	(GENTH) GENENTECH INC.
Query Match	7.6%; Score 134.5; DB 6;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1008	
ID	ABU80684 standard; protein; 198 AA.
DN	Human PRO protein #251.
PN	US2003036137-AA.
PD	20-FEB-2003.
PA	(GERTH) GENENTECH INC.
Query Match	7.6%; Score 134.5; DB 6;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1009	
ID	ABR93602 standard; protein; 198 AA.
DN	Humam secreted polypeptide PRO4421, SEQ ID NO:502.
PN	US2003040063-AA.
PD	27-FEB-2003.
Query Match	7.6%; Score 134.5; DB 6;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1010	
ID	AHR89892 standard; protein; 198 AA.
DN	Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN	US2003040064-AA.
PD	27-FEB-2003.
Query Match	7.6%; Score 134.5; DB 6;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1011	
ID	ABO16515 standard; protein; 198 AA.
DN	Human secreted/transmembrane protein (PRO) #251.
PN	US2003027267-AA.
PD	06-FEB-2003.
Query Match	7.6%; Score 134.5; DB 6;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1012	
ID	ABR92415 standard; protein; 198 AA.
DN	Humun secreted polypeptide PRO4421, SEQ ID NO:502.
PN	US2003036160-AA.
PD	20-FEB-2003.
Query Match	7.6%; Score 134.5; DB 6;
Best Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1013	
ID	ABOI9056 standard; protein; 198 AA.
DN	Humun secreted/cransmembrane protein (PRO) #251.
PN	US2003044925-AA.
PD	06-MAR-2003.
Query Match	7.6%; Score 134.5; DB 6;
Beet Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1014	
ID	ABR78477 standard; protein; 198 AA.
DN	Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN	US2003054474-AA.
PD	20-MAR-2003.
Query Match	7.6%; Score 134.5; DB 6;
Beet Local Similarity	30.7%; Pred. No. 0.00029;
RESULT 1015	
ID	ABU85213 standard; protein; 198 AA.
DN	Novel human secreted and transmembrane protein PRO4421.
PN	US2003032114-AA.
PD	13-FEB-2003.
Query Match	7.6%; Score 134.5; DB 6;

Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1016
ID ABO00352 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1017
ID ABO11684 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1018
ID ABO02329 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1019
ID AB088903 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1020
ID AB083598 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1021
ID ABO06399 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1022
ID ABR59435 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1023
ID ABO09497 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1024
ID ABO19361 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GERTH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1025
ID ABO11379 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1026

ID ABR66997 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1027
ID ABO16210 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1028
ID ABO13916 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1029
ID AB065819 standard; protein: 198 AA.
DE Human secreted/transmembrane protein, SEQ ID 502.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1030
ID ABO07667 standard; protein: 198 AA.
DE Human PRO polypeptide #251.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1031
ID ABO03854 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1032
ID ABR67302 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1033
ID ABO15905 standard; protein: 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GERTH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1034
ID ABUS6186 standard; protein: 198 AA.
DE Human secreted/transmembrane protein, PRO4421.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1035
ID ABUS5514 standard; protein: 198 AA.
DE Human PRO polypeptide #251.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1036
ID ABUS4549 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.


```

PN      US2003036117-A1.
Query Match
Best Local Similarity      7.6%; Score 134.5; DB 6; Length 198;
RESULT 1037
ID      ABUT71362 standard; protein; 198 AA.
DE      Human PRO4421 protein.
PN      US2003036143-A1.
Query Match
Best Local Similarity      7.6%; Score 134.5; DB 6; Length 198;
RESULT 1038
ID      ABO07972 standard; protein; 198 AA.
DE      Human PRO polypeptide #251.
PN      US2003032130-A1.
Query Match
Best Local Similarity      7.6%; Score 134.5; DB 6; Length 198;
RESULT 1039
ID      ABR70213 standard; protein; 198 AA.
DE      Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN      US2003032138-A1.
PD      13-FEB-2003.
PA      (GETH ) GENENTECH INC.
Query Match
Best Local Similarity      7.6%; Score 134.5; DB 6; Length 198;
RESULT 1040
ID      ABR69546 standard; protein; 198 AA.
DE      Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN      US2003036132-A1.
PD      20-FEB-2003.
Query Match
Best Local Similarity      7.6%; Score 134.5; DB 6; Length 198;
RESULT 1041
ID      ABO01687 standard; protein; 198 AA.
DE      Human PRO polypeptide #251.
PN      US2003008353-A1.
PD      09-JAN-2003.
PA      (GETH ) GENENTECH INC.
Query Match
Best Local Similarity      7.6%; Score 134.5; DB 6; Length 198;
RESULT 1042
ID      ABUS1489 standard; protein; 198 AA.
DE      Human PRO polypeptide #251.
PN      US2003017542-A1.
PD      23-JAN-2003.
Query Match
Best Local Similarity      7.6%; Score 134.5; DB 6; Length 198;
RESULT 1043
ID      ABR60286 standard; protein; 198 AA.
DE      Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN      US2003032137-A1.
PD      13-FEB-2003.
Query Match
Best Local Similarity      7.6%; Score 134.5; DB 6; Length 198;
RESULT 1044
ID      ABR68021 standard; protein; 198 AA.
DE      Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN      US2003027269-A1.
PD      06-FEB-2003.
Query Match
Best Local Similarity      7.6%; Score 134.5; DB 6; Length 198;
RESULT 1045
ID      ABR55409 standard; protein; 198 AA.
DE      Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN      US2003027268-A1.
PD      06-FEB-2003.
Query Match
Best Local Similarity      7.6%; Score 134.5; DB 6; Length 198;
RESULT 1046
ID      ABR68631 standard; protein; 198 AA.
DE      Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN      US2003027274-A1.

```

[illegible]

Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1057
ID ABO06752 standard; protein: 198 AA.
DE Human secreted/cranmembrane protein (PRO) #251.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1058
ID ABR99297 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1059
ID ABR57181 standard; protein: 198 AA.
DE Human PRO polypeptide #251.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1060
ID ABO86133 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1061
ID ABR82420 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1062
ID ABR87431 standard; protein: 198 AA.
DE Human PRO polypeptide #251.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1063
ID ABR83903 standard; protein: 198 AA.
DE Human secreted/cranmembrane protein (PRO) #251.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1064
ID ABO08277 standard; protein: 198 AA.
DE Human PRO polypeptide #251.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1065
ID ABR8198 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1066
ID ABR66152 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1067

ID ABR5981 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1068
ID ABR94169 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1069
ID ABO00042 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1070
ID ABR6692 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027281-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1071
ID ABR9110 standard; protein: 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1072
ID ABR94537 standard; protein: 198 AA.
DE Human PRO polypeptide #251.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1073
ID ABR79419 standard; protein: 198 AA.
DE Human PRO polypeptide #251.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1074
ID ABR86748 standard; protein: 198 AA.
DE Human secreted/cranmembrane protein (PRO) #251.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1075
ID ABR87053 standard; protein: 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1076
ID ABR94842 standard; protein: 198 AA.
DE Human PRO polypeptide #251.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1077
ID ABO04769 standard; protein: 198 AA.
DE Human PRO polypeptide #251.

PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1078
ID ABR70518 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1079
ID ABR98683 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1080
ID ABR66082 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1081
ID ABR64799 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1082
ID ABR79724 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1083
ID ABR93115 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1084
ID ABR96074 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1085
ID ABR91294 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1086
ID ABR90367 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1087
ID ABR09802 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044931-A1.
PD 06-MAR-2003.

Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1088
ID ABR11074 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1089
ID ABR71128 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1090
ID ABR87736 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1091
ID ABR91604 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1092
ID ABR84818 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1093
ID ABR69908 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1094
ID ABR80285 standard; protein; 198 AA.
DE Human PRO protein #251.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1095
ID ABR93554 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1096
ID ABR10107 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1097
ID ABR09192 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1098

ID ABU10760 standard; protein; 198 AA.
DE Human secreted/transmembrane protein #251.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1099
ID ABU95769 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003032115-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1100
ID ABU96978 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1101
ID ABR70823 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1102
ID ABO05174 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1103
ID ABO08582 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1104
ID ABO05789 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1105
ID ABR74178 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1106
ID ABR5770 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1107
ID ABR1067 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;

Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1108
ID ABR81372 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1109
ID ABM01068 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1110
ID ABR86670 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1111
ID ABM77491 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1112
ID ABO28975 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1113
ID ABO31720 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1114
ID ABM08137 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1115
ID ABO40617 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1116
ID ABO36042 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;

```
RESULT 1117
ID ABO44181 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1118
ID ADA78254 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1119
ID ABM24976 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1120
ID ABO03244 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1121
ID ABR0500 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1122
ID ABM17414 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1123
ID ABR95160 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1124
ID ABR95465 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1125
ID ABO21703 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1126
ID ABR97967 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1127
ID ABR87755 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1128
ID ABM7796 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1129
ID ABM28026 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1130
ID ABM06307 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1131
ID ABM03813 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1132
ID ABM35264 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1133
ID ABM26501 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1134
ID ABO48283 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1135
ID ABR93025 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      7.6%; Score 134.5; DB 6; Length 198;
```

```
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1136
ID ABO24786 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1137
ID ABM11797 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1138
ID ABM02898 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1139
ID ABM16194 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1140
ID ABO27755 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1141
ID ABM29246 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1142
ID ABM07222 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1143
ID ABM21316 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1144
ID ABM09662 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1145
ID ABO41532 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1146
ID ABO36347 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1147
ID ABO43876 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1148
ID ABM76576 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1149
ID ABM76272 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1150
ID ABM25891 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1151
ID ABM26196 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1152
ID ABO03549 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1153
ID ABO02634 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1154
ID ABR90805 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
```

Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1155
ID ABR73873 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1156
ID ABO17125 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1157
ID ABR94550 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1158
ID ABR76057 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1159
ID ABR71433 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059860-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1160
ID ABR93330 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1161
ID ABR93635 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1162
ID ABR88060 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1163
ID ABO28060 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1164
ID ABO30195 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1165
ID ABO33404 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1166
ID ABO05092 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1167
ID ABO09052 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1168
ID ABO36652 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1169
ID ABO35737 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1170
ID ABO39702 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1171
ID ABO10577 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1172
ID ABO12102 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1173
ID ABO52248 standard; protein; 198 AA.
DE Human PRO polypeptide #251.

PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1174
ID ABO52553 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1175
ID ABO23871 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1176
ID ABR97357 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1177
ID ABR87145 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1178
ID ABM1187 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1179
ID ABM28331 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1180
ID ABO32330 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1181
ID ABM15457 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1182
ID ABM06612 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1183
ID ABM04423 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1184
ID ABM22536 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1185
ID ABM07832 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1186
ID ABO40922 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1187
ID ABM35569 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1188
ID ABM33332 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1189
ID ABO52858 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1190
ID ABO50418 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1191
ID ABU99412 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;


```
RESULT 1192
ID ABO04464 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1193
ID ABM18634 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1194
ID ABR97662 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1195
ID ABR80762 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1196
ID ABM01373 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1197
ID ABR88975 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1198
ID ABM13627 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1199
ID ABM21011 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1200
ID ABO42142 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1201
ID ABO42752 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1202
ID ABM10272 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1203
ID ABO38787 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1204
ID ABM33027 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1205
ID ABM22841 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1206
ID ABM75052 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1207
ID ADA80046 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1208
ID ABR36442 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1209
ID ABM02593 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
RESULT 1210
ID ABR86535 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00029; Length 198;
```

```
RESULT 1211
ID ABR6840 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1212
ID ABR16804 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1213
ID ABR29886 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1214
ID ABO29280 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1215
ID ABR24061 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1216
ID ABR23451 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1217
ID ABR22231 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1218
ID ABR37872 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1219
ID ABR8636 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1220
ID ABR28941 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1221
ID ABR6585 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1222
ID ABR75967 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1223
ID ABR34247 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1224
ID ABR4552 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1225
ID ABO20483 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1226
ID ABO21398 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1227
ID ABO22313 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1228
ID ABR96747 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
RESULT 1229
ID ABR85925 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00029;
```

```
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1230
ID ABR99907 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1231
ID ABM00458 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1232
ID ABM00763 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1233
ID ABO29890 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1234
ID ABM23756 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1235
ID ABM29551 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1236
ID ABO38482 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1237
ID ABO45782 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1238
ID ABM20706 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1239
ID ADA01773 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1240
ID ABO16820 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1241
ID ABO18446 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1242
ID ABO22873 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1243
ID ABO23178 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1244
ID ABR92720 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1245
ID ABR81677 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1246
ID ABM78101 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1247
ID ABR98990 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1248
ID ABM26806 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
```

```
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1249
ID ABM13932 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1250
ID ABO28670 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1251
ID ABO30500 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1252
ID ABM07527 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1253
ID ABM04118 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1254
ID ABO37262 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1255
ID ABO41837 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1256
ID ABO35432 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1257
ID ABM5281 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1258
ID ABO47673 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1259
ID ABO47978 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1260
ID ABO4858 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1261
ID ABO51638 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1262
ID ABO51943 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1263
ID ABO50723 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1264
ID ABR79847 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1265
ID ABM17109 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1266
ID ABO18141 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1267
ID ABO21093 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032132-A1.
```

PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1268
ID ABR37052 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1269
ID ABM12407 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1270
ID ABM16499 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1271
ID ABM14366 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1272
ID ABM14847 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1273
ID ABM04728 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1274
ID ABM06917 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1275
ID ABM09357 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1276
ID ABO39397 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;

RESULT 1277
ID ABM75662 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1278
ID ABM25586 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1279
ID ABM20096 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1280
ID ABO47002 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1281
ID ABO47307 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1282
ID ADA63571 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1283
ID ABR71738 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1284
ID ABR72348 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1285
ID ABR98687 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1286
ID ABO07057 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040053-A1.
PD 27-FEB-2003.

```
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1287
ID ABR85010 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1288
ID ABR73568 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1289
ID ABR76662 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1290
ID ABR73263 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1291
ID ABM18329 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1292
ID ABO20788 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1293
ID ABO25531 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1294
ID ABO25836 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1295
ID ABR94245 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1296
ID ABR0152 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1297
ID ABM1492 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1298
ID ABO33099 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1299
ID ABO30805 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1300
ID ABO31110 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1301
ID ABM27416 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1302
ID ABM30161 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1303
ID ABM05697 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1304
ID ABM15762 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1305
ID ABM08747 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068759-A1.
PD 10-APR-2003.
```

PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1306
ID ABO42447 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1307
ID ABO38177 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1308
ID ABO46087 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1309
ID ABM66890 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1310
ID ADB20614 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1311
ID ABM19791 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1312
ID ABO49503 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1313
ID ABO49808 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1314
ID ADA78666 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;

Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1315
ID ABR88365 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1316
ID ABM27111 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1317
ID ABM03508 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1318
ID ABO40007 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1319
ID ABO50113 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1320
ID ABO51028 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1321
ID ABO05484 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1322
ID ABR74788 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1323
ID ABR77267 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1324
ID ABM18024 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.

PN US2003040072-A1.
ID 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1325
ID ABR96075 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1326
ID ABO22008 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1327
ID ABO20178 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1328
ID ABO24481 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1329
ID ABR86230 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1330
ID ABM10882 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1331
ID ABR6881 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1332
ID ABR9585 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1333
ID ABM12712 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;

RESULT 1334
ID ABM06002 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1335
ID ABO35127 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1336
ID ABM03203 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1337
ID ABM19181 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1338
ID ABM19486 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1339
ID ABO46697 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1340
ID ABO49198 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1341
ID ABR69241 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1342
ID ABR89280 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1343
ID ABR72653 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.


```

PN US2003036120-A1.
PD 20-FEB-2003.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1344
ID ABR74483 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1345
ID ABO18751 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1346
ID ABR80457 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1347
ID ABM01678 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1348
ID ABM02288 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1349
ID ABR87450 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1350
ID ABM13017 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1351
ID ABM10771 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1352
ID ABM24671 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1353
ID ABO29585 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1354
ID ABO31415 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1355
ID ABM14542 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1356
ID ABM0967 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1357
ID ABO39092 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1358
ID ABM34857 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1359
ID ABO51333 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1360
ID ABO04159 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1361
ID ABO10629 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
  7.6%; Score 134.5; DB 7; Length 198;
  Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1362
ID ABR77872 standard; protein; 198 AA.
```

DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1363
ID ABR79082 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1364
ID ABO24176 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1365
ID ABR93940 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1366
ID ABR01983 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1367
ID ABR78406 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1368
ID ABR90195 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1369
ID ABR27721 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1370
ID ABR13322 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1371
ID ABO32025 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1372
ID ABR14237 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1373
ID ABR08442 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1374
ID ABO40312 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1375
ID ABR74747 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1376
ID ABR33942 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1377
ID ABR20401 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1378
ID ABO4893 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1379
ID ABR72958 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1380
ID ABO15600 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1381

```
ID ABR85315 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1382  
ID ABO15295 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1383  
ID ABO17430 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1384  
ID ABM17719 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1385  
ID ABR85620 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1386  
ID ABM77186 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1387  
ID ABO28365 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1388  
ID ABM33146 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1389  
ID ABM0466 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1390  
ID ABM21926 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1391  
ID ABM21621 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1392  
ID ABM15152 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1393  
ID ABO41227 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1394  
ID ABO36957 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1395  
ID ABO37567 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1396  
ID ABM75357 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1397  
ID ABM33637 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1398  
ID ABO46392 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1399  
ID ADA82937 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00029;  
RESULT 1399  
ID ADA82937 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;
```


Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1419
ID ADG00895 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1420
ID ADG3151 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1421
ID ADH6432 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1422
ID ADH33401 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1423
ID ADJ55140 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1424
ID ADJ64911 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1425
ID ADM1807 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1426
ID ADM36854 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1427
ID ADM4659 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;

Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1428
ID ADN38267 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00029;
RESULT 1429
ID ADE6380 standard; protein; 240 AA.
DE Rat Protein p10252, SEQ ID NO 9319.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.6%; Score 134; DB 7; Length 240;
Best Local Similarity 24.6%; Pred. No. 0.00043;
RESULT 1430
ID ADV90298 standard; protein; 327 AA.
DE Protease-hydrolysed polypeptide #75.
PN WO2004113522-A1.
PD 29-DEC-2004.
PA (DIRE) DIREVO BIOTECH AG.
Query Match 7.5%; Score 133.5; DB 9; Length 327;
Best Local Similarity 22.7%; Pred. No. 0.00076;
RESULT 1431
ID AAR74221 standard; protein; 332 AA.
DE Epitope on the primary CD2 sequence.
PN US5411861-A.
PD 02-MAY-1995.
PA (GENO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 2; Length 332;
Best Local Similarity 22.7%; Pred. No. 0.00078;
RESULT 1432
ID AAY30457 standard; protein; 332 AA.
DE Predicted sequence of the mature CD2 protein.
PN US595264-A.
PD 21-SEP-1999.
PA (GENO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 2; Length 332;
Best Local Similarity 22.7%; Pred. No. 0.00078;
RESULT 1433
ID ADA25185 standard; protein; 332 AA.
DE Mature CD2 protein.
PN US6579676-B1.
PD 17-JUN-2003.
PA (GENO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 6; Length 332;
Best Local Similarity 22.7%; Pred. No. 0.00078;
RESULT 1434
ID AAR11921 standard; protein; 351 AA.
DE Human T11 sugar protein.
PN JP03035782-A.
PD 15-FEB-1991.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 24.4%; Pred. No. 0.00085;
RESULT 1435
ID AAR20803 standard; protein; 351 AA.
DE Human CD2 antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GENO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00085;
RESULT 1436
ID AAR34223 standard; protein; 351 AA.
DE Amino acid sequence of CD2.
PN WO9306852-A2.
PD 15-APR-1993.
PA (BIOC) BIOGEN INC.
Query Match 7.5%; Score 133.5; DB 2; Length 351;

```
Best Local Similarity 23.6%; Pred. No. 0.00085;
RESULT 1437
ID AAR91431 standard; protein; 351 AA.
DE Human CD2.
PN USS506126-A.
PD 09-APR-1996.
PA (GHEO ) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00085;
RESULT 1438
ID AAW80440 standard; protein; 351 AA.
DE Human CD2 antigen.
PN US5830731-A.
PD 03-NOV-1998.
PA (GHEO ) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00085;
RESULT 1439
ID AAW86188 standard; protein; 351 AA.
DE Human CD2 antigen.
PN US5849898-A.
PD 15-DEC-1998.
PA (GHEO ) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00085;
RESULT 1440
ID AAY6126 standard; protein; 351 AA.
DE Human cell surface antigen CD2.
PN US611093-A.
PD 29-AUG-2000.
PA (GHEO ) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 3; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00085;
RESULT 1441
ID AAU02435 standard; protein; 351 AA.
DE Human lymphocyte cell surface antigen CD2 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GHEO ) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 4; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00085;
RESULT 1442
ID ADD25530 standard; protein; 351 AA.
DE Binding domain-immunoglobulin fusion protein-associated protein #42.
PN US200318592-A1.
PD 26-JUN-2003.
PA (GENE-) GENECAST INC.
Query Match 7.5%; Score 133.5; DB 7; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00085;
RESULT 1443
ID ADF76723 standard; protein; 351 AA.
DE Novel human secreted and transmembrane protein Segid 398.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GHEH ) GENENTECH INC.
Query Match 7.5%; Score 133.5; DB 7; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00085;
RESULT 1444
ID ADO49339 standard; protein; 351 AA.
DE Human CD2 antigen.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALIE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFER L.
PA (OOUB/) OOUENDO C.
PA (STIM/) STIMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELEIN S.
PA (AMIO/) AMIOT M.
Query Match 7.5%; Score 133.5; DB 8; Length 351;

Best Local Similarity 22.7%; Pred. No. 0.00085;
RESULT 1445
ID ADQ18464 standard; protein; 351 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1283.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.5%; Score 133.5; DB 8; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00085;
RESULT 1446
ID ADP56034 standard; protein; 351 AA.
DE Human PRO protein sequence SEQ ID NO:2010.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.5%; Score 133.5; DB 8; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00085;
RESULT 1447
ID ADY19602 standard; protein; 351 AA.
DE PRO polypeptide SEQ ID NO 5408.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH ) GENENTECH INC.
Query Match 7.5%; Score 133.5; DB 9; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00085;
RESULT 1448
ID ADY15634 standard; protein; 351 AA.
DE PRO polypeptide SEQ ID NO 1440.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH ) GENENTECH INC.
Query Match 7.5%; Score 133.5; DB 9; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00085;
RESULT 1449
ID AAP1178 standard; protein; 360 AA.
DE Sequence of human T11 sheep erythrocyte glycoprotein (T11) cDNA deduced from FBI.
PN EP260880-A.
PD 23-MAR-1988.
PA (DAND ) DNA FARRER CANCER INST INC.
Query Match 7.5%; Score 133.5; DB 1; Length 360;
Best Local Similarity 23.9%; Pred. No. 0.00088;
RESULT 1450
ID AAB4368 standard; protein; 737 AA.
DE Human cancer associated protein sequence SEQ ID NO:1133.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.5%; Score 133.5; DB 3; Length 737;
Best Local Similarity 22.3%; Pred. No. 0.0025;
RESULT 1451
ID ABU04810 standard; protein; 737 AA.
DE Human expressed protein tag (EPT) #1476.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOOS INC.
Query Match 7.5%; Score 133.5; DB 6; Length 737;
Best Local Similarity 22.3%; Pred. No. 0.0025;
RESULT 1452
ID AAR28366 standard; protein; 225 AA.
DE Sheep LFA-3 protein.
PN EP517174-A2.
PD 09-DEC-1992.
PA (KANP ) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.4%; Score 131; DB 2; Length 225;
Best Local Similarity 25.0%; Pred. No. 0.00077;
RESULT 1453
ID AAR43473 standard; protein; 351 AA.
DE Sequence encoded by a naturally occurring human CD2.
PN WO9306866-A2.
PD 15-APR-1993.
PA (BIOC ) BIOGEN INC.
Query Match 7.4%; Score 130.5; DB 2; Length 351;
```

Best Local Similarity 23.2%; Pred. No. 0.0017;
RESULT 1454
ID AAR54714 standard; protein; 526 AA.
DE Carcinoembryonic antigen CEA-(c).
PN US5274087-A.
PD 28-DEC-1993.
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.
Query Match
Best Local Similarity 7.4%; Score 130.5; DB 2; Length 526;
RESULT 1455
ID AAR60314 standard; protein; 225 AA.
DE Sheep LFA-3.
PN JP06157334-A.
PD 03-JUN-1994.
PA (KANF) KANEBUCHI KAGAKU KOGYO KK.
Query Match
Best Local Similarity 7.2%; Score 128; DB 2; Length 225;
RESULT 1456
ID AAR06434 standard; protein; 321 AA.
DE SPI-1-like protein encoded by clone h1s1.
PN WO9007937-A.
PD 26-JUL-1990.
PA (OKLA-) OKLAHOMA MED RES FO.
Query Match
Best Local Similarity 7.2%; Score 128; DB 2; Length 321;
RESULT 1457
ID ABU05236 standard; protein; 321 AA.
DE Human expressed protein tag (EPT) #1902.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
Best Local Similarity 7.2%; Score 128; DB 6; Length 321;
RESULT 1458
ID AAY43139 standard; protein; 451 AA.
DE NAIL-Fc protein sequence.
PN WO9950297-A1.
PD 07-OCT-1999.
PA (IMMV) IMMUNEX CORP.
Query Match
Best Local Similarity 7.2%; Score 128; DB 2; Length 451;
RESULT 1459
ID ADE08687 standard; protein; 697 AA.
DE Novel protein (useful for identifying genetic disorders) #842.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 7.2%; Score 128; DB 7; Length 697;
RESULT 1460
ID AAU74427 standard; protein; 240 AA.
DE Mouse protein sequence #4, related to isolation of genes within SLF-1B.
PN WO200188200-A2.
PD 22-NOV-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match
Best Local Similarity 7.1%; Score 126.5; DB 5; Length 240;
RESULT 1461
ID AAY43140 standard; protein; 243 AA.
DE NAIL-Flag-polyHis protein sequence.
PN WO9950297-A1.
PD 07-OCT-1999.
PA (IMMV) IMMUNEX CORP.
Query Match
Best Local Similarity 7.1%; Score 126.5; DB 2; Length 243;
RESULT 1462
ID AAY43141 standard; protein; 272 AA.
DE NAIL-12-polyHis protein sequence.
PN WO9950297-A1.
PD 07-OCT-1999.
PA (IMMV) IMMUNEX CORP.
Query Match
Best Local Similarity 7.1%; Score 126.5; DB 2; Length 272;
Query Match
Best Local Similarity 23.8%; Pred. No. 0.0028;

RESULT 1463
ID AAB71855 standard; protein; 427 AA.
DE Human D-SLAM extracellular domain carrying C-terminal HIS tag.
PN WO20011046-A1.
PD 15-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 7.1%; Score 126; DB 4; Length 427;
RESULT 1464
ID ABG32414 standard; protein; 427 AA.
DE D-SLAM protein with C-terminal His tag.
PN WO200262955-A2.
PD 15-AUG-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 7.1%; Score 126; DB 5; Length 427;
RESULT 1465
ID AAM82480 standard; protein; 856 AA.
DE Mammalian ZAP-70 protein #1.
PN JP10313868-A.
PD 02-DEC-1998.
PA (KAGA-) KAGAKU GIYUTSU SHINKO JIGYODAN.
Query Match
Best Local Similarity 7.1%; Score 126; DB 2; Length 856;
RESULT 1466
ID AAR22045 standard; protein; 321 AA.
DE Carcino embryonic antigen-related antigen encoded by clone W233.
PN JP04045788-A.
PD 14-FEB-1992.
PA (SUNR) SUNTORY LTD.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 2; Length 321;
RESULT 1467
ID ABU04836 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1502.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 6; Length 344;
RESULT 1468
ID ABU04804 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1470.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 6; Length 344;
RESULT 1469
ID ABU04839 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1505.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 6; Length 344;
RESULT 1470
ID AEC04936 standard; protein; 344 AA.
DE Human breast cancer marker protein SBQ ID NO 13 variant.
PN WO2005072050-A2.
PD 11-AUG-2005.
PA (COMP-) COMPUEN USA INC.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 9; Length 344;
RESULT 1471
ID AAR22318 standard; protein; 351 AA.
DE Carcino embryonic antigen-related antigen encoded by clone W239.
PN JP04045788-A.
PD 14-FEB-1992.
PA (SUNR) SUNTORY LTD.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 2; Length 351;
RESULT 1472
Query Match
Best Local Similarity 25.1%; Pred. No. 0.0051;

ID AAP93996 standard; protein; 368 AA.
DE Transmembrane-4 carcinoembryonic antigen amino acid sequence.
PN EP346710-A.
PD 20-DEC-1989.
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.
Query Match 7.1%; Score 125.5; DB 1; Length 368;
Best Local Similarity 25.1%; Pred. No. 0.0054;
RESULT 1473
ID AAR2044 standard; protein; 417 AA.
DE Carcino embryonic antigen-related antigen encoded by clone W211.
PN JP04045788-A.
PD 14-FEB-1992.
PA (SUNR) SUNTORY LTD.
Query Match 7.1%; Score 125.5; DB 2; Length 417;
Best Local Similarity 25.1%; Pred. No. 0.0065;
RESULT 1474
ID AAP93994 standard; protein; 430 AA.
DE Sequence of transmembrane (TM)-2 carcinoembryonic antigen (CEA) - (c).
PN EP346710-A.
PD 20-DEC-1989.
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.
Query Match 7.1%; Score 125.5; DB 1; Length 430;
Best Local Similarity 25.1%; Pred. No. 0.0068;
RESULT 1475
ID AEA23827 standard; protein; 430 AA.
DE Human PRO polypeptide SEQ ID NO 369.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GENH) GENENTECH INC.
Query Match 7.1%; Score 125.5; DB 9; Length 430;
Best Local Similarity 25.1%; Pred. No. 0.0068;
RESULT 1476
ID AAP93995 standard; protein; 464 AA.
DE Transmembrane-3 carcinoembryonic antigen amino acid sequence.
PN EP346710-A.
PD 20-DEC-1989.
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.
Query Match 7.1%; Score 125.5; DB 1; Length 464;
Best Local Similarity 25.1%; Pred. No. 0.0076;
RESULT 1477
ID AAR65166 standard; protein; 464 AA.
DE Biliary glycoprotein.
PN WO9506067-A1.
PD 02-MAR-1995.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Query Match 7.1%; Score 125.5; DB 2; Length 464;
Best Local Similarity 25.1%; Pred. No. 0.0076;
RESULT 1478
ID AAR77436 standard; protein; 468 AA.
DE BGP (1-314)/CEA (490-643) chimeric protein.
PN WO9506067-A1.
PD 02-MAR-1995.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Query Match 7.1%; Score 125.5; DB 2; Length 468;
Best Local Similarity 25.1%; Pred. No. 0.0077;
RESULT 1479
ID AAR77435 standard; protein; 493 AA.
DE BGP (1-314)/CEA (490-C-terminal) chimeric protein.
PN WO9506067-A1.
PD 02-MAR-1995.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Query Match 7.1%; Score 125.5; DB 2; Length 493;
Best Local Similarity 25.1%; Pred. No. 0.0083;
RESULT 1480
ID AAR77437 standard; protein; 509 AA.
DE BGP (1-314)/CEA (490-644)/BGP (391-430) chimeric protein.
PN WO9506067-A1.
PD 02-MAR-1995.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Query Match 7.1%; Score 125.5; DB 2; Length 509;
Best Local Similarity 25.1%; Pred. No. 0.0087;
RESULT 1481
ID AAR77438 standard; protein; 511 AA.

DE BGP (1-314)/CEA (490-642)/BGP (387-430) chimeric protein.
PN WO9506067-A1.
PD 02-MAR-1995.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Query Match 7.1%; Score 125.5; DB 2; Length 511;
Best Local Similarity 25.1%; Pred. No. 0.0088;
RESULT 1482
ID AAP81223 standard; protein; 526 AA.
DE FL-CEA or carcinoembryonic antigen-C.
PN EP263933-A.
PD 20-APR-1988.
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.
Query Match 7.1%; Score 125.5; DB 1; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0091;
RESULT 1483
ID AAM06873 standard; protein; 526 AA.
DE Carcinoembryonic antigen CEA-C.
PN US5571710-A.
PD 05-NOV-1996.
PA (FARB) BAYER CORP.
Query Match 7.1%; Score 125.5; DB 2; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0091;
RESULT 1484
ID AAW83138 standard; protein; 526 AA.
DE FL-CEA protein.
PN US5843761-A.
PD 01-DEC-1998.
PA (FARB) BAYER CORP FORMERLY MOLECULAR DIAGNOSTIC.
Query Match 7.1%; Score 125.5; DB 2; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0091;
RESULT 1485
ID ADL15001 standard; protein; 526 AA.
DE Human carcinoembryonic antigen BGpa protein for cancer treatment.
PN WO2003068268-A2.
PD 21-AUG-2003.
PA (BIOI) BIOINVENT INT AB.
Query Match 7.1%; Score 125.5; DB 7; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0091;
RESULT 1486
ID ADN95238 standard; protein; 526 AA.
DE Human BEC/LEC-related protein sequence SeqID160.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDM-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 7.1%; Score 125.5; DB 7; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0091;
RESULT 1487
ID ADQ17310 standard; protein; 526 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 127.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.1%; Score 125.5; DB 8; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0091;
RESULT 1488
ID ADQ17232 standard; protein; 526 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 48.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.1%; Score 125.5; DB 8; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0091;
RESULT 1489
ID ADQ29706 standard; protein; 526 AA.
DE Human colorectal cancer-associated protein #61.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 7.1%; Score 125.5; DB 8; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0091;
RESULT 1490

ID AD67261 standard; protein; 526 AA.
 DE Human bladder cancer associated amino acid sequence.
 PN WO2004076613-A2.
 PD 10-SEP-2004.
 PA (HERR/) HERR A.
 PA (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (STAU/) STAU B.
 PA (PILA/) PILARSKY C.
 PA (SPEC/) SPEC T.
 Query Match 7.1%; Score 125.5; DB 8; Length 526;
 Best Local Similarity 25.1%; Pred. No. 0.0091;
 RESULT 1491
 ID AEA04517 standard; protein; 526 AA.
 DE Human protein from gene under-expressed in cancer, CEACAM1.
 PN WO2005044990-A2.
 PD 19-MAY-2005.
 PA (FAR) BAYER HEALTHCARE LLC.
 PA (MAYO) MAYO FOUND MEDICAL EDUCATION & RES.
 Query Match 7.1%; Score 125.5; DB 9; Length 526;
 Best Local Similarity 25.1%; Pred. No. 0.0091;
 RESULT 1492
 ID AEB08040 standard; protein; 526 AA.
 DE Human CEACAM1 protein, SEQ ID NO: 2.
 PN WO2005058358-A2.
 PD 30-JUN-2005.
 PA (UTKU/) UTKU N.
 Query Match 7.1%; Score 125.5; DB 9; Length 526;
 Best Local Similarity 25.1%; Pred. No. 0.0091;
 RESULT 1493
 ID ABJ37104 standard; protein; 437 AA.
 DE Concatameric immunoadhesion human protein sequence SEQ ID NO 14.
 PN WO2003010202-A1.
 PD 06-FEB-2003.
 PA (MEDE-) MEDEXGEN CO LTD.
 Query Match 7.1%; Score 125; DB 6; Length 437;
 Best Local Similarity 23.5%; Pred. No. 0.0078;
 RESULT 1494
 ID ADQ79912 standard; protein; 437 AA.
 DE Human CD2/Ig construct.
 PN KR2004009997-A.
 PD 31-JAN-2004.
 PA (MEDE-) MEDEXGEN INC.
 Query Match 7.1%; Score 125; DB 8; Length 437;
 Best Local Similarity 23.5%; Pred. No. 0.0078;
 RESULT 1495
 ID ABJ37106 standard; protein; 617 AA.
 DE Concatameric immunoadhesion human protein sequence SEQ ID NO 18.
 PN WO2003010202-A1.
 PD 06-FEB-2003.
 PA (MEDE-) MEDEXGEN CO LTD.
 Query Match 7.1%; Score 125; DB 6; Length 617;
 Best Local Similarity 23.5%; Pred. No. 0.013;
 RESULT 1496
 ID ABJ37108 standard; protein; 617 AA.
 DE Concatameric immunoadhesion human protein sequence SEQ ID NO 22.
 PN WO2003010202-A1.
 PD 06-FEB-2003.
 PA (MEDE-) MEDEXGEN CO LTD.
 Query Match 7.1%; Score 125; DB 6; Length 617;
 Best Local Similarity 23.5%; Pred. No. 0.013;
 RESULT 1497
 ID ADQ79916 standard; protein; 617 AA.
 DE Human CD2-CD2/Ig construct.
 PN KR2004009997-A.
 PD 31-JAN-2004.
 PA (MEDE-) MEDEXGEN INC.
 Query Match 7.1%; Score 125; DB 8; Length 617;
 Best Local Similarity 23.5%; Pred. No. 0.013;
 RESULT 1498
 ID ADQ79920 standard; protein; 617 AA.
 DE Human mgCD2-CD2/Ig construct.
 PN KR2004009997-A.

PD 31-JAN-2004.
 PA (MEDE-) MEDEXGEN INC.
 Query Match 7.1%; Score 125; DB 8; Length 617;
 Best Local Similarity 23.5%; Pred. No. 0.013;
 RESULT 1499
 ID ADP14932 standard; protein; 820 AA.
 DE Human albumin therapeutic fusion protein Seqid228.
 PN WO2003060071-A2.
 PD 24-JUL-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (DEUZ-) DELTA BIOTECHNOLOGY LTD.
 PA (PRIN-) PRINCIPIA PHARM CORP.
 Query Match 7.1%; Score 125; DB 7; Length 820;
 Best Local Similarity 25.1%; Pred. No. 0.002;
 RESULT 1500
 ID AEC03856 standard; protein; 344 AA.
 DE Human breast cancer marker protein SEQ ID NO 13.
 PN WO2005072050-A2.
 PD 11-AUG-2005.
 PA (COMP-) COMPUGEN USA INC.
 Query Match 7.0%; Score 124.5; DB 9; Length 344;
 Best Local Similarity 22.4%; Pred. No. 0.0061;

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 16, 2005, 10:34:37 ; Search time 39 Seconds

(without alignments)
826,477 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 1772

Sequence: 1 MAGSPCTCLTYIIMQLTGS.....PHSLITMPDTRRLPAYENVVI 335

Scoring table: BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	343	19.4	629	2 A46500	ly-9.2 antigen - m
2	182.5	10.3	335	2 S58892	signaling lymphocy
3	144	8.1	344	2 B28967	T-cell surface gly
4	138	7.8	344	2 I49585	CD2 antigen protei
5	136.5	7.7	351	1 RWHUC2	T-cell surface gly
6	134	7.6	240	1 S01299	OX-45 membrane gly
7	130	7.3	344	1 RWHUC2	T-cell surface gly
8	126.5	7.1	240	2 J10143	antigen BCM1 precu
9	125.5	7.1	321	2 JH0395	biliary glycoprote
10	125.5	7.1	351	2 JH0396	biliary glycoprote
11	125.5	7.1	417	2 JH0394	biliary glycoprote
12	125.5	7.1	464	2 C30127	transmembrane carc
13	125.5	7.1	526	1 A32164	biliary glycoprote
14	124.5	7.0	344	2 A27681	nonspecific cross-
15	122.5	6.9	521	2 S34338	biliary glycoprote
16	119	6.7	458	2 JCI509	carcinoembryonic a
17	114.5	6.5	702	2 A36319	biliary glycoprote
18	113.5	6.4	458	1 WMM5R1	biliary glycoprote
19	113.5	6.4	521	2 JCI508	biliary glycoprote
20	109.5	6.2	432	2 S30193	T-cell surface gly
21	108.5	6.1	365	2 JCI780	coxsackie- and ade
22	107.5	6.1	398	2 I49443	gene 2B4 protein -
23	106	6.0	897	2 G84613	hypothetical prote
24	105.5	6.0	329	1 A48754	B7-2 antigen - hum
25	104	5.9	349	2 A34815	carcinoembryonic a
26	102.5	5.8	458	2 S23969	cell-adhesion mole
27	102.5	5.8	526	2 A37821	butyrophilin - bov
28	101.5	5.7	761	2 T00940	hypothetical prote
29	101	5.7	587	2 JH0464	DM-GRASP precursor

30	101	5.7	588	2 JH0506	adhesion molecule
31	100.5	5.7	259	2 A86822	hypothetical prote
32	100	5.6	392	2 B44194	poliovirus recepto
33	99	5.6	417	2 A44194	poliovirus recepto
34	99	5.6	588	2 A45254	surface glycoprote
35	98.5	5.6	1227	2 T23004	hypothetical prote
36	98	5.5	347	2 S41638	T-cell surface gly
37	98	5.5	503	2 JCI528	SHP substrate-1 pr
38	97	5.5	523	2 I50478	neurotlin - goldfis
39	97	5.5	773	1 ORRBG	secretory componen
40	96.5	5.4	402	2 A40678	T-cell adhesion re
41	96	5.4	210	2 S36297	T-cell receptor ga
42	96	5.4	526	2 S70587	butyrophilin precu
43	96	5.4	1087	2 I51552	platelet-derived g
44	96	5.4	1451	2 S42167	190K protein - hum
45	95.5	5.4	341	2 JCI512	biliary glycoprote
46	95.5	5.4	417	1 RWHUPA	poliovirus recepto
47	95.5	5.4	458	2 S68177	C-CAM2a protein is
48	95.5	5.4	519	2 A44783	ecto-ATPase precu
49	95.5	5.4	700	1 S12053	protein-tyrosine-p
50	94.5	5.3	218	2 A36198	T-cell receptor be
51	94	5.3	233	2 JH0372	42K surface glycop
52	94	5.3	1088	1 IJX1ML	neural cell adhesi
53	93.5	5.3	2409	1 A60979	versican precursor
54	93	5.2	419	2 B54312	pregnancy-specific
55	93	5.2	419	2 A36109	pregnancy-specific
56	93	5.2	419	2 JCI4123	pregnancy-specific
57	92.5	5.2	299	2 S56749	pregnancy-specific
58	92.5	5.2	330	2 I46691	junctional adhesio
59	92.5	5.2	761	2 A96810	CD86 precursor - r
60	92	5.2	822	2 T01095	probable Mutator-1
61	91.5	5.2	1079	2 T28197	hypothetical prote
62	91	5.1	417	2 A28277	probable DNA-direc
63	91	5.1	419	2 A33258	pregnancy-specific
64	91	5.1	426	2 B33258	pregnancy-specific
65	91	5.1	467	1 H1MSP3	poliovirus recepto
66	90	5.1	250	2 A28564	lymphocyte functio
67	90	5.1	395	2 D43354	pregnancy-specific
68	90	5.1	397	2 C43354	pregnancy-specific
69	90	5.1	406	2 B43354	pregnancy-specific
70	90	5.1	419	2 A31135	pregnancy-specific
71	90	5.1	426	2 A35964	pregnancy-specific
72	90	5.1	426	2 A35341	pregnancy-specific
73	90	5.1	426	2 A27658	pregnancy-specific
74	89.5	5.1	243	2 A53244	leukocyte antigen
75	89.5	5.1	349	2 B84968	outer membrane pro
76	89.5	5.1	428	2 T36655	probable penicilli
77	89	5.0	309	2 I49522	gene B7-2 protein
78	89	5.0	341	2 JCI511	biliary glycoprote
79	89	5.0	821	2 C1H0H3	calpain (BC 3.4.22
80	89	5.0	5175	1 T20992	hypothetical prote
81	89	5.0	5198	2 T43290	hemocentin precurs
82	88.5	5.0	1390	1 T7H0ME	hepatocyte growth
83	88	5.0	363	2 F70195	UDP-N-acetylglucos
84	88	5.0	422	2 A71147	hypothetical prote
85	88	5.0	530	2 A53437	poliovirus recepto
86	88	5.0	668	2 S56909	polymyxin B resist
87	88	5.0	699	2 JCI6132	protein-tyrosine-p
88	88	5.0	821	1 B34468	calpain (BC 3.4.22
89	88	5.0	1092	1 JN0635	neural cell adhesi
90	88	5.0	6669	2 S55024	nebulin, skeletal
91	87.5	4.9	265	2 A55811	carcinoembryonic a
92	87.5	4.9	275	2 S20660	31.6K hypothetical
93	87.5	4.9	392	1 RWHUDD	poliovirus recepto
94	87.5	4.9	769	1 QKR7ES	secretory componen
95	87.5	4.9	2340	2 I48310	kinase-related pro
96	87.5	4.9	4162	2 T42633	connectin/titin -
97	87	4.9	457	1 RWM5T4	T-cell surface gly
98	87	4.9	583	2 I39428	alcam - human
99	87	4.9	1666	2 A48594	skelentin - mouse
100	87	4.9	1907	2 S50893	protein-tyrosine-p
101	87	4.9	3707	2 S18252	heparan sulfate pr
102	86.5	4.9	528	2 B75364	extracellular solu

103	86	4.9	212	2	C33258	pregnancy-specific
104	86	4.9	354	1	VGBE67	glycoprotein D pre
105	86	4.9	428	2	I57486	pregnancy-specific
106	86	4.9	885	2	B86257	NBS/LRR disease re
107	86	4.9	1327	2	T09402	immunoglobulin-lik
108	85.5	4.8	324	2	G43354	pregnancy-specific
109	85.5	4.8	326	2	F43354	pregnancy-specific
110	85.5	4.8	333	2	A43354	pregnancy-specific
111	85.5	4.8	335	2	H43354	pregnancy-specific
112	85.5	4.8	941	1	TVWVMD	protein-tyrosine k
113	85.5	4.8	2588	2	T14342	NS1 protein - mou
114	85	4.8	428	2	JS0032	pregnancy-specific
115	85	4.8	731	2	T16524	hypothetical prote
116	85	4.8	757	1	S48841	secretory componen
117	84.5	4.8	656	2	A96724	hypothetical prote
118	84	4.7	275	2	JC7604	CD86 spliced varia
119	84	4.7	851	2	D90216	hypothetical prote
120	84	4.7	1379	1	S01254	hepatocyte growth
121	84	4.7	1499	2	I50212	protein-tyrosine-p
122	84	4.7	3034	2	T14119	seven-pass transme
123	83.5	4.7	315	2	H71009	probable prolifera
124	83.5	4.7	392	2	T33444	hypothetical prote
125	83.5	4.7	656	2	B49423	semaphorin I - fru
126	83.5	4.7	775	2	T21436	hypothetical prote
127	83.5	4.7	1501	2	I58148	protein-tyrosine-p
128	83.5	4.7	1863	2	S46217	pregnancy-specific
129	83	4.7	335	2	A33514	pregnancy-specific
130	83	4.7	757	2	I45956	polymeric immunogl
131	83	4.7	757	1	A49729	VDL receptor prec
132	83	4.7	925	2	T37475	lipoprotein recept
133	83	4.7	1106	2	T29496	hypothetical prote
134	83	4.7	2489	2	S59782	probable membrane
135	82.5	4.7	393	2	B96780	hypothetical prote
136	82.5	4.7	826	2	B36203	iron-responsive el
137	82.5	4.7	1004	2	A71617	SSEA antigen/papai
138	82.5	4.7	26926	1	T18344	retin, cardiac mus
139	82	4.6	386	2	B69666	Na+ ABC transporte
140	82	4.6	609	2	S43009	hemagglutinin - ri
141	82	4.6	880	2	B53743	protein-tyrosine k
142	82	4.6	3562	2	A47171	chondroitin sulfat
143	82	4.6	278	1	TDRTOX	Ox-2 membrane glyc
144	81.5	4.6	352	2	I77374	pregnancy-specific
145	81.5	4.6	355	2	T06122	cysteine proteinas
146	81.5	4.6	378	2	S00842	leukostallin precu
147	81.5	4.6	497	2	D97264	galactose-1-phosph
148	81.5	4.6	524	2	S44982	flagellin - Shigel
149	81.5	4.6	708	2	T48022	hypothetical prote
150	81	4.6	335	2	B33251	nonspecific cross-
151	81	4.6	338	2	UC4776	limbic-system-asso
152	81	4.6	374	2	S57750	naringenin 3-dioxy
153	81	4.6	760	2	S19374	probable membrane
154	81	4.6	769	2	B97092	glycosyltransferas
155	81	4.6	829	1	IYHUCP	cadherin 3 precurs
156	81	4.6	1898	2	S46216	leukocyte antigen-
157	81	4.6	1941	2	T30554	ubiquitin-protein
158	80.5	4.5	346	2	S46993	elk ligand - human
159	80.5	4.5	376	2	B85435	cysteine proteinas
160	80.5	4.5	462	2	H97292	UDP-N-acetylmuramo
161	80.5	4.5	473	2	AG0612	probable transport
162	80.5	4.5	475	2	I76668	pregnancy-specific
163	80.5	4.5	540	2	B64829	membrane protein b
164	80.5	4.5	540	2	H90751	probable transport
165	80.5	4.5	540	2	B85615	probable transport
166	80.5	4.5	721	2	T09631	probable acylamino
167	80.5	4.5	823	2	T08092	plus fringe glycop
168	80.5	4.5	823	2	S44887	ZK12.7 protein -
169	80.5	4.5	6642	1	T29757	protein UNC-89 - C
170	80	4.5	307	1	RMWSBC	T-cell receptor as
171	80	4.5	341	2	I61725	natural killer as
172	80	4.5	343	2	G90680	probable periplasm
173	80	4.5	343	2	C85531	periplasmic ferric
174	80	4.5	454	2	A46532	Ig mu chain C regi
175	80	4.5	482	2	JH0110	arginine/ornithine
176	80	4.5	1040	2	A49356	transient axonal g
177	80	4.5	1170	2	A40558	thrombospondin 1 p
178	79.5	4.5	134	2	I46627	rearranged T-cell
179	79.5	4.5	244	2	JC8019	CD58 protein - pig
180	79.5	4.5	249	1	A61087	myelin po glycopro
181	79.5	4.5	273	2	B28928	pregnancy-specific
182	79.5	4.5	275	2	A28928	pregnancy-specific
183	79.5	4.5	282	2	C28928	pregnancy-specific
184	79.5	4.5	289	2	G90314	oxidoreductase (im
185	79.5	4.5	328	2	Q01121	cysteine proteinas
186	79.5	4.5	400	2	A10104	probable galactosi
187	79.5	4.5	430	2	T28143	tapasin 1 homolog,
188	79.5	4.5	446	2	T34782	probable signal pe
189	79.5	4.5	490	2	I41293	EcO5 type I restrit
190	79.5	4.5	769	2	S16236	fibroblast growth
191	79.5	4.5	822	2	A45081	fibroblast growth
192	79.5	4.5	822	2	A41794	keratinocyte growt
193	79.5	4.5	873	1	I48952	VDL receptor prec
194	79.5	4.5	980	1	TVCTMD	macrophage colony-
195	79.5	4.5	1465	1	S43529	165k protein, skel
196	79.5	4.5	2491	1	A28332	insulin-like growt
197	79	4.5	210	2	C87256	hypothetical prote
198	79	4.5	244	2	AC1765	B. subtilis TagA p
199	79	4.5	438	2	G64513	hypothetical prote
200	79	4.5	479	2	C84039	carboxy-terminal p
201	79	4.5	584	2	T08678	hypothetical prote
202	79	4.5	657	2	S77543	short-chain alchoh
203	79	4.5	903	2	T20804	hypothetical prote
204	79	4.5	1228	2	G96751	hypothetical prote
205	79	4.5	1361	2	T30984	neural specific DN
206	78.5	4.4	235	2	S25750	Ig lambda chain -
207	78.5	4.4	429	1	EHRT	Ig epsilon chain C
208	78.5	4.4	497	2	C91225	probable oxidoredu
209	78.5	4.4	497	2	A86072	probable oxidoredu
210	78.5	4.4	539	2	T01513	Cmp synthase (EC 6
211	78.5	4.4	588	2	I37202	B-CAM protein - hu
212	78.5	4.4	628	2	I38000	Lutheran blood gro
213	78.5	4.4	638	2	T51383	receptor protein k
214	78.5	4.4	831	2	S39835	hypothetical prote
215	78.5	4.4	847	2	JH0371	B-cell adhesion pr
216	78.5	4.4	1036	2	S22383	axomin 1 precursor
217	78.5	4.4	1038	2	AG2187	hypothetical prote
218	78.5	4.4	1468	2	T05672	hypothetical prote
219	78	4.4	257	2	A97121	undecaprenyl pyrop
220	78	4.4	272	2	I48268	bilialy glycoprote
221	78	4.4	286	2	A28333	carcinoembryonic a
222	78	4.4	335	2	C54312	pregnancy-specific
223	78	4.4	402	2	T09062	probable advanced
224	78	4.4	490	2	T43184	DEAD box ATP-depen
225	78	4.4	604	2	T41249	DEAD box ATP-depen
226	78	4.4	608	2	AB3562	gcp-binding protei
227	78	4.4	609	1	HMNZKA	hemagglutinin - ri
228	78	4.4	761	1	IYHUNG	neural cell adhesi
229	78	4.4	836	2	T42323	hypothetical prote
230	78	4.4	905	2	S43064	cadherin - African
231	78	4.4	905	2	T38314	probable vacuolar
232	77.5	4.4	172	2	T34227	hypothetical prote
233	77.5	4.4	214	2	C89833	hypothetical prote
234	77.5	4.4	236	2	T41012	conserved hypotnet
235	77.5	4.4	239	2	I46082	C88 alpha-chain -
236	77.5	4.4	448	2	H98007	exodeoxyribonuclea
237	77.5	4.4	509	2	JC5288	SNP substrate-1 pr
238	77.5	4.4	513	2	JC5289	SNP substrate-1 pr
239	77.5	4.4	539	2	G86465	fl2G12.2 protein -
240	77.5	4.4	591	2	H83362	glucuronate dehydrog
241	77.5	4.4	717	2	AD3037	ferritinobactin-
242	77.5	4.4	717	2	B98189	ferritinobactin-
243	77.5	4.4	739	2	A41288	vascular cell adhe
244	77.5	4.4	757	1	S64742	dynamn-related pr
245	77.5	4.4	863	2	S06017	neuraxin - rat
246	77.5	4.4	881	2	S03068	eny protein - huma
247	77.5	4.4	968	2	T25667	hypothetical prote
248	77.5	4.4	991	2	T48631	polynucleotide pho

249	77.5	4.4	1015	2	T32186	hypothetical prote
250	77.5	4.4	1099	2	T18713	hypothetical prote
251	77.5	4.4	1205	2	T13959	limeless protein r
252	77.5	4.4	1262	1	B48758	protein-tyrosine-p
253	77.5	4.4	1496	1	A48758	protein-tyrosine-p
254	77.5	4.4	1894	2	C54689	protein-tyrosine-p
255	77.5	4.4	1912	2	A56178	protein-tyrosine-p
256	77.5	4.4	1950	2	S12332	ubiquitin-protein
257	77	4.3	327	2	S06611	Ig gamma-2 chain c
258	77	4.3	328	2	I47158	Ig gamma 1 chain c
259	77	4.3	338	2	JC5519	50K glycoprotein p
260	77	4.3	398	2	B86353	protein P2E2.6 (im
261	77	4.3	439	2	S51378	probable membrane
262	77	4.3	491	2	SE0276	voltage-gated pota
263	77	4.3	502	2	S61935	SKS1 protein - yea
264	77	4.3	523	2	T05946	cytochrome P450 78
265	77	4.3	796	2	JC7966	xylian 1,4-beta-xy1
266	77	4.3	873	1	ORRBD	VLDL receptor prec
267	77	4.3	1021	2	I39207	leukocyte surface
268	77	4.3	1029	2	D83120	probable RND efflu
269	77	4.3	1041	2	S55862	probable membrane
270	77	4.3	1897	1	TDBULK	leukocyte antigen-
271	77	4.3	2167	2	AP1489	cell wall-associat
272	77	4.3	4836	2	T14346	hcr2 protein - mo
273	76.5	4.3	177	1	C40428	nonspecific cross-
274	76.5	4.3	191	2	E75132	molybdopterin-guan
275	76.5	4.3	238	2	T24314	hypothetical prote
276	76.5	4.3	251	2	S75312	hypothetical prote
277	76.5	4.3	296	2	G82131	conserved hypotnet
278	76.5	4.3	390	2	D86291	hypothetical prote
279	76.5	4.3	394	2	S20905	hypothetical prote
280	76.5	4.3	402	2	A54312	pregnancy-specific
281	76.5	4.3	423	2	AB1142	N-carbamyl-L-amino
282	76.5	4.3	426	2	C55181	pregnancy-specific
283	76.5	4.3	426	2	S09016	pregnancy-specific
284	76.5	4.3	426	2	B35334	pregnancy-specific
285	76.5	4.3	436	2	B55181	pregnancy-specific
286	76.5	4.3	495	2	A55181	pregnancy-specific
287	76.5	4.3	497	2	D65189	WicG protein - Bac
288	76.5	4.3	582	2	A71906	DNA polymerase III
289	76.5	4.3	727	2	T21585	hypothetical prote
290	76.5	4.3	788	2	S17906	hypothetical prote
291	76.5	4.3	839	2	B96538	hypothetical prote
292	76.5	4.3	876	2	D85350	hypothetical prote
293	76.5	4.3	876	2	S71277	serine/threonine-s
294	76.5	4.3	1005	2	T18537	Ig heavy chain - c
295	76.5	4.3	1043	2	T19734	hypothetical prote
296	76.5	4.3	1071	2	T18307	suppressor protein
297	76.5	4.3	1089	1	PFHUGA	platelet-derived g
298	76.5	4.3	1124	2	JX0293	zinc finger protei
299	76.5	4.3	1154	2	A56242	E-box-binding repr
300	76.5	4.3	1328	2	S62467	ATP-dependent DNA
301	76.5	4.3	1461	2	B70588	probable polyketid
302	76.5	4.3	1802	2	S69703	HKX1 protein precu
303	76.5	4.3	2039	2	T15347	anxyrin-related un
304	76.5	4.3	138	2	S16199	phocovsytam I prot
305	76	4.3	144	2	AM1172	mannose-specific p
306	76	4.3	230	2	S49449	Ig lambda chain -
307	76	4.3	239	2	T23147	hypothetical prote
308	76	4.3	262	2	A64882	probable carboxype
309	76	4.3	262	2	H85751	probable carboxype
310	76	4.3	262	2	A99867	probable carboxype
311	76	4.3	286	2	B97010	prephenate dehydro
312	76	4.3	305	2	H69759	conserved hypotnet
313	76	4.3	333	2	A31923	amalgam protein pr
314	76	4.3	378	2	I46268	brevican precursor
315	76	4.3	487	1	S55194	DNA-directed DNA p
316	76	4.3	507	2	T47021	hypothetical prote
317	76	4.3	508	2	AD0236	L-asparagine perme
318	76	4.3	550	2	G90497	hypothetical prote
319	76	4.3	758	2	T15577	hypothetical prote
320	76	4.3	841	2	T01011	hypothetical prote
321	76	4.3	964	2	T15746	hypothetical prote
322	76	4.3	978	2	S16385	macrophage colony-
323	76	4.3	1018	2	JC4211	neural adhesion pr
324	76	4.3	1099	2	T51503	valine-tRNA ligase
325	76	4.3	2029	1	TDFFLK	protein-tyrosine-p
326	75.5	4.3	246	2	A47712	myelin/oligodentro
327	75.5	4.3	326	2	JC4124	pregnancy-specific
328	75.5	4.3	419	2	S42989	T48 protein - frui
329	75.5	4.3	421	2	T40614	G beta repeat prot
330	75.5	4.3	432	2	T30130	hypothetical prote
331	75.5	4.3	446	2	A95140	exodeoxyribonuclea
332	75.5	4.3	462	2	A84689	chloroplast membra
333	75.5	4.3	485	2	T28076	hypothetical prote
334	75.5	4.3	819	2	T05744	hypothetical prote
335	75.5	4.3	933	2	S05944	neuronal cell surf
336	75.5	4.3	1020	2	S05944	aggreacan precursor
337	75.5	4.3	2109	1	I50421	hypothetical prote
338	75	4.2	150	2	D95131	probable anthranil
339	75	4.2	208	2	D71529	probable beta-keto
340	75	4.2	466	2	D84906	glucose-6-phosphat
341	75	4.2	491	2	AC2650	glucose-6-phosphat
342	75	4.2	503	2	B97432	glutamate/aspartat
343	75	4.2	543	2	S26609	Ig Y heavy chain (
344	75	4.2	572	2	B46529	Ig mu chain precu
345	75	4.2	573	2	S12838	hypothetical prote
346	75	4.2	622	2	B96751	hypothetical prote
347	75	4.2	686	2	A55665	microtubule-associ
348	75	4.2	747	1	ORBCPE	ferrichrome-iron r
349	75	4.2	747	2	B85499	outer membrane rec
350	75	4.2	747	2	B90648	outer membrane rec
351	75	4.2	821	1	TVMSBK	fibroblast growth
352	75	4.2	976	1	TVMSKD	macrophage colony-
353	75	4.2	1091	1	IUCHNL	neural cell adhesi
354	75	4.2	1256	2	T03096	CD0 protein - rat
355	75	4.2	1338	2	T02206	hypothetical prote
356	75	4.2	7962	2	I38346	elastic titin - hu
357	74.5	4.2	232	1	DXCH	ovalbumin-related
358	74.5	4.2	278	2	A39037	carcinoembryonic a
359	74.5	4.2	309	2	T31908	hypothetical prote
360	74.5	4.2	321	2	S10006	hypothetical prote
361	74.5	4.2	379	2	D91078	probable lipoprote
362	74.5	4.2	379	2	B85923	lipoprotein (lipor
363	74.5	4.2	379	2	B55522	lipoprotein D prec
364	74.5	4.2	463	2	T14884	hypothetical prote
365	74.5	4.2	518	2	D69539	conserved hypotnet
366	74.5	4.2	544	2	I51593	protein-tyrosine k
367	74.5	4.2	688	2	A47705	triacylglycerol li
368	74.5	4.2	705	2	S51635	fibroblast growth
369	74.5	4.2	741	2	B90739	probable transport
370	74.5	4.2	741	2	H85589	probable transport
371	74.5	4.2	764	2	A49448	irregular chlaem C
372	74.5	4.2	771	2	T34376	hypothetical prote
373	74.5	4.2	786	2	H64817	probable membrane
374	74.5	4.2	795	2	T20609	hypothetical prote
375	74.5	4.2	889	1	VCLJ05	env polyprotein -
376	74.5	4.2	984	2	T00326	hypothetical prote
377	74.5	4.2	1003	2	T19638	hypothetical prote
378	74.5	4.2	1007	2	PM0156	glutamate receptor
379	74.5	4.2	1008	2	S28858	glutamate receptor
380	74.5	4.2	1021	2	A57112	contactin precurs
381	74.5	4.2	1178	2	B87145	[beta] subunit of
382	74.5	4.2	1179	2	S31145	DNA-directed RNA p
383	74.5	4.2	1522	2	T00028	brain-specific ang
384	74.5	4.2	1523	2	S58860	receptor DEC-205 -
385	74.5	4.2	1896	2	T08851	Down syndrome cell
386	74.5	4.2	2256	2	AD1018	large repetitive p
387	74.5	4.2	2266	2	A56577	microtubule-associ
388	74.5	4.2	2364	2	T34416	hypothetical prote
389	74.5	4.2	2783	2	S36291	T-cell receptor ga
390	74	4.2	203	2	S01320	ig kappa chain pre
391	74	4.2	278	2	JC1506	biliary glycoprote
392	74	4.2	333	2	PS0018	Ig gamma-2b chain
393	74	4.2	334	2	T19637	hypothetical prote
394	74	4.2	349	2	S68092	protein-glutamine

395	74	4.2	384	2	H64161	hypothetical prote
396	74	4.2	403	2	I52550	m33-B isoform - mo
397	74	4.2	424	2	T43498	hypothetical prote
398	74	4.2	463	2	CE6997	probable prolina t
399	74	4.2	468	2	S70297	SP22 protein homol
400	74	4.2	502	2	T40792	hypothetical prote
401	74	4.2	548	2	M44302	protein-glutamine
402	74	4.2	586	2	T15259	hypothetical prote
403	74	4.2	611	2	F82442	probable peptidase A
404	74	4.2	645	2	T39614	kinase-binding pro
405	74	4.2	673	2	T48701	hypothetical prote
406	74	4.2	860	2	JC5702	ErbB kinase activa
407	74	4.2	862	2	T49583	differentiation an
408	74	4.2	876	2	B96693	probable receptor
409	74	4.2	900	2	G96617	probable disease r
410	74	4.2	1063	2	A33830	cation efflux syst
411	74	4.2	1063	2	JC4700	cadmium, zinc, cob
412	74	4.2	1130	2	T23104	hypothetical prote
413	74	4.2	1133	2	T23103	hypothetical prote
414	74	4.2	1165	1	S45879	chitin synthase (E
415	74	4.2	1237	2	E86457	probable RNA helic
416	74	4.2	1367	2	T33819	hypothetical prote
417	74	4.2	1582	2	T15308	hypothetical prote
418	74	4.2	4344	1	A53489	dysnein heavy chain
419	74	4.2	5232	2	M45086	HC-toxin synthetas
420	74	4.2	6658	2	T13931	protectin - fruit
421	73.5	4.1	325	2	S49451	cysteine proteinas
422	73.5	4.1	364	2	A30521	amyloid cell surf
423	73.5	4.1	428	2	B83967	dhidroocotolase pyr
424	73.5	4.1	647	2	T33773	hypothetical prote
425	73.5	4.1	740	2	M06000	probable membrane
426	73.5	4.1	797	2	T27518	hypothetical prote
427	73.5	4.1	880	1	JC5700	ErbB kinase activa
428	73.5	4.1	850	1	VCLJ52	env polypeptide pr
429	73.5	4.1	923	2	F84732	probable ligand-ga
430	73.5	4.1	925	2	D83868	glucan 1,4-beta-gl
431	73.5	4.1	957	2	CE9463	type I restriction
432	73.5	4.1	1166	2	S37692	probable tumor sup
433	73.5	4.1	1225	2	T48251	ubiquitin-protein
434	73.5	4.1	1240	2	T03097	CDO protein - huma
435	73.5	4.1	2013	2	AD1129	probable peptidogl
436	73.5	4.1	2301	1	T18399	variant-specific s
437	73.5	4.1	2355	1	G81702	genome polypeptid
438	73.5	4.1	3255	1	S02392	adherence factor T
439	73.5	4.1	4544	1	T34265	alpha-2-macroglobu
440	73	4.1	147	2	T34265	hypothetical prote
441	73	4.1	220	1	G69047	conserved hypothet
442	73	4.1	235	2	S14675	Ig lambda chain -
443	73	4.1	250	2	S27544	hypothetical prote
444	73	4.1	293	2	H96906	hypothetical prote
445	73	4.1	322	2	H84095	hypothetical prote
446	73	4.1	354	2	T27712	hypothetical prote
447	73	4.1	389	2	T46722	conserved hypothet
448	73	4.1	397	2	E86304	R611.9 protein - A
449	73	4.1	413	2	S65948	hemolin - cecropia
450	73	4.1	413	2	A37778	hemolin precursor
451	73	4.1	432	1	RMWQ74	T-cell surface gly
452	73	4.1	476	2	H84524	probable fatty aci
453	73	4.1	519	2	S38921	interleukin 1 prece
454	73	4.1	590	2	I56526	hypothetical prote
455	73	4.1	666	1	A36026	kinasin-related pr
456	73	4.1	730	2	S64998	hypothetical prote
457	73	4.1	735	2	T00850	probable receptor-
458	73	4.1	853	1	IJBONC	neural cell adhesi
459	73	4.1	864	2	JH0438	penicillin-binding
460	73	4.1	901	1	P2XR17	core protein VP3 -
461	73	4.1	1014	2	T13476	hypothetical prote
462	73	4.1	1072	2	A38457	integrin alpha-6 c
463	73	4.1	1171	2	T31635	hypothetical prote
464	73	4.1	1179	2	T05673	hypothetical prote
465	73	4.1	1515	1	S51863	cadmium resistance
466	73	4.1	1737	2	A59235	unconventional myo
467	73	4.1	1806	2	T23298	hypothetical prote
468	73	4.1	3788	2	T30851	lysosomal traffick
469	72.5	4.1	202	2	S36293	T-cell receptor ga
470	72.5	4.1	221	2	T31620	hypothetical prote
471	72.5	4.1	334	2	G01650	malate dehydrogena
472	72.5	4.1	336	2	C27658	pregnancy-specific
473	72.5	4.1	342	2	AG1729	protein gp19 (Bact
474	72.5	4.1	351	2	B34595	pregnancy-specific
475	72.5	4.1	363	2	I39726	manopine biosynth
476	72.5	4.1	371	2	T40287	hypothetical prote
477	72.5	4.1	399	2	B90437	hypothetical prote
478	72.5	4.1	424	2	A34595	surface protein (p
479	72.5	4.1	435	2	D33258	pregnancy-specific
480	72.5	4.1	435	2	SE2885	pregnancy-specific
481	72.5	4.1	440	2	SE2885	TYA protein - yea
482	72.5	4.1	443	2	AE3294	tolB protein (lipo
483	72.5	4.1	478	2	A49228	tryptan-like prote
484	72.5	4.1	487	2	A11146	hypothetical cell
485	72.5	4.1	491	2	T22844	hypothetical prote
486	72.5	4.1	527	2	D75127	hypothetical prote
487	72.5	4.1	666	2	A39610	slit1 protein - yea
488	72.5	4.1	682	2	A35969	heparin-binding gr
489	72.5	4.1	687	2	T39838	hypothetical prote
490	72.5	4.1	768	2	JC7352	glucose-regulated
491	72.5	4.1	769	2	T45854	hypothetical prote
492	72.5	4.1	842	2	E96641	hypothetical prote
493	72.5	4.1	851	2	S44880	ncl-1 ZK112.2 prot
494	72.5	4.1	876	2	A49508	protein-tyrosine k
495	72.5	4.1	895	2	T11979	receptor tyrosine
496	72.5	4.1	913	2	A48280	probable membrane
497	72.5	4.1	1057	2	S45801	exodeoxyribonuclea
498	72.5	4.1	1123	2	AB0125	membrane nuclease
499	72.5	4.1	1138	2	A82939	neurotactin - chic
500	72.5	4.1	1272	2	S26180	transmembrane prot
501	72.5	4.1	1434	2	T30172	lysobactin synthet
502	72.5	4.1	1575	2	T18545	dynein heavy chain
503	72.5	4.1	4367	1	B54802	probable peptidase
504	72.5	4.1	4924	2	TM50176	hypothetical prote
505	72.5	4.1	4936	2	AH2515	purine nucleoside
506	72	4.1	265	2	H72233	searcrow-like pro
507	72	4.1	320	2	C89867	hypothetical prote
508	72	4.1	378	2	T51237	hypothetical prote
509	72	4.1	423	2	T29549	hypothetical prote
510	72	4.1	437	2	AP3613	hypothetical prote
511	72	4.1	442	2	E71553	hypothetical prote
512	72	4.1	446	2	B89922	conserved hypothet
513	72	4.1	469	2	C69628	gamma-aminobutyrat
514	72	4.1	505	2	F69867	two-component sens
515	72	4.1	510	2	A84707	probable pseudouri
516	72	4.1	521	2	E82377	ABC transporter, p
517	72	4.1	543	2	S38353	glutamate transpor
518	72	4.1	549	2	T33517	hypothetical prote
519	72	4.1	558	2	T01343	hypothetical prote
520	72	4.1	565	2	C82280	sensor kinase cItA
521	72	4.1	585	2	S48929	hypothetical prote
522	72	4.1	599	2	T16774	hypothetical prote
523	72	4.1	617	2	T23197	hypothetical prote
524	72	4.1	646	2	I38049	cell surface glyco
525	72	4.1	783	2	T45899	receptor protein X
526	72	4.1	808	2	F81180	conserved hypothet
527	72	4.1	868	2	JC5701	ErbB kinase activa
528	72	4.1	873	2	H96503	protein P9C16.17 (
529	72	4.1	885	2	D86151	P22M8.8 protein -
530	72	4.1	900	2	T04839	core protein p3 -
531	72	4.1	901	2	S07419	androgen receptor
532	72	4.1	911	2	B34721	hypothetical prote
533	72	4.1	1038	2	H90053	hypothetical prote
534	72	4.1	1186	2	T19334	Smad interacting p
535	72	4.1	1214	2	JC7259	hypothetical prote
536	72	4.1	1216	2	H85023	sax-3 protein - Ca
537	72	4.1	1273	2	T42405	vascular endotheli
538	72	4.1	1348	2	S51656	myosin-light-chain
539	72	4.1	1906	1	S68235	probable membrane
540	72	4.1	2383	2	D64962	

541	72	4.1	4872	2	S27272	614	71	4.0	1217	2	T22672	hypothetical prote
542	71.5	4.0	145	2	S25743	615	71	4.0	1251	2	T21389	hypothetical prote
543	71.5	4.0	229	1	B43685	616	71	4.0	1338	2	S09982	protein-tyrosine k
544	71.5	4.0	238	2	A49613	617	71	4.0	4391	2	A38096	perlecan precursor
545	71.5	4.0	299	2	S50803	618	71	4.0	5107	2	T29144	partial GDS - Caen
546	71.5	4.0	312	2	A64461	619	70.5	4.0	203	2	E93381	flagellin (flaB1-1
547	71.5	4.0	338	2	A64303	620	70.5	4.0	223	2	A81068	hypothetical prote
548	71.5	4.0	339	2	S08981	621	70.5	4.0	238	2	D86302	hypothetical prote
549	71.5	4.0	362	2	T05167	622	70.5	4.0	246	2	B82764	hypothetical prote
550	71.5	4.0	443	2	T14916	623	70.5	4.0	332	2	T45770	hypothetical prote
551	71.5	4.0	498	2	G90067	624	70.5	4.0	338	1	DSRTM	malate dehydrogena
552	71.5	4.0	500	2	T11946	625	70.5	4.0	358	1	B95588	protein R09P10.8 l
553	71.5	4.0	542	2	AP2587	626	70.5	4.0	429	1	B41902	arsenical pump mem
554	71.5	4.0	542	2	F97369	627	70.5	4.0	455	2	G01923	KIR (c1-5) NK rece
555	71.5	4.0	589	2	T50385	628	70.5	4.0	502	2	T19108	hypothetical prote
556	71.5	4.0	603	2	H64442	629	70.5	4.0	505	2	T15159	hypothetical prote
557	71.5	4.0	669	2	T48466	630	70.5	4.0	522	2	T26319	hypothetical prote
558	71.5	4.0	707	2	A38429	631	70.5	4.0	526	1	TVFV60	protein-tyrosine k
559	71.5	4.0	707	2	A54846	632	70.5	4.0	533	1	TVCHS	protein-tyrosine k
560	71.5	4.0	764	1	QRHUGS	633	70.5	4.0	537	1	A45501	protein-tyrosine k
561	71.5	4.0	822	2	B54846	634	70.5	4.0	545	2	S52313	protein-tyrosine k
562	71.5	4.0	919	2	S33942	635	70.5	4.0	546	2	S52314	protein-tyrosine k
563	71.5	4.0	921	2	F71486	636	70.5	4.0	557	1	TVFVS2	protein-tyrosine k
564	71.5	4.0	1032	2	H64100	637	70.5	4.0	558	1	MMXKRT	RNA 10 protein - r
565	71.5	4.0	1089	1	S33727	638	70.5	4.0	568	1	TVFVS1	protein-tyrosine k
566	71.5	4.0	1180	2	B86719	639	70.5	4.0	569	2	A45624	trephozoite cystei
567	71.5	4.0	1348	2	S27812	640	70.5	4.0	587	1	TVFVPR	protein-tyrosine k
568	71.5	4.0	1348	2	A43917	641	70.5	4.0	627	2	S14683	Ig mu chain precu
569	71.5	4.0	1374	2	S62524	642	70.5	4.0	627	2	A59663	DNA mismatch repai
570	71.5	4.0	1374	2	C70148	643	70.5	4.0	630	2	A39344	tumor-associated m
571	71.5	4.0	1413	2	D84481	644	70.5	4.0	646	2	T48644	negative regulator
572	71.5	4.0	1462	2	T11648	645	70.5	4.0	656	2	H84206	acetyl-CoA synthet
573	71.5	4.0	2397	1	A55535	646	70.5	4.0	663	1	TVMVR	protein-tyrosine k
574	71	4.0	61	2	C82536	647	70.5	4.0	669	2	T13640	probable minor str
575	71	4.0	142	2	S38392	648	70.5	4.0	743	2	F71062	hypothetical prote
576	71	4.0	189	2	G64496	649	70.5	4.0	787	2	T41974	replidation origin
577	71	4.0	207	2	T50206	650	70.5	4.0	793	2	T41703	diethylidyl amino
578	71	4.0	221	2	T21117	651	70.5	4.0	844	2	S05988	transactin elonga
579	71	4.0	224	2	H81568	652	70.5	4.0	877	1	IUBOEN	N-cadherin precurs
580	71	4.0	231	2	B86520	653	70.5	4.0	878	2	S11842	hypothetical prote
581	71	4.0	231	2	G72102	654	70.5	4.0	895	2	A55413	triglyceride trans
582	71	4.0	258	2	S73803	655	70.5	4.0	906	1	IUMSCN	N-cadherin precurs
583	71	4.0	329	1	DEDFLM	656	70.5	4.0	928	2	G81591	polymorphic membra
584	71	4.0	333	2	AP0407	657	70.5	4.0	928	2	G81591	polymorphic membra
585	71	4.0	343	2	A10358	658	70.5	4.0	938	2	H85458	polymorphic oute
586	71	4.0	344	2	I56551	659	70.5	4.0	938	2	H72074	polymorphic membra
587	71	4.0	345	2	I48780	660	70.5	4.0	1088	2	B56715	calcium receptor (
588	71	4.0	346	2	AP1820	661	70.5	4.0	1200	2	T17404	hyalin - sea urchi
589	71	4.0	387	2	B71611	662	70.5	4.0	1356	2	UC1402	protein-tyrosine k
590	71	4.0	389	2	S68155	663	70.5	4.0	1402	2	F84480	probable retrolem
591	71	4.0	390	2	T27033	664	70.5	4.0	1427	2	I51669	tumor suppressor -
592	71	4.0	407	2	T34442	665	70.5	4.0	1694	2	S50065	staiodhesin - mou
593	71	4.0	423	1	EHMS	666	70.5	4.0	2051	2	T30938	receptor tyrosine
594	71	4.0	455	2	S50391	667	70.5	4.0	2303	1	GNNYPR	genome polypotein
595	71	4.0	462	2	JN0719	668	70.5	4.0	2303	2	S13554	genome polypotein
596	71	4.0	463	2	AH1758	669	70.5	4.0	2464	1	ORMSP1	microbulbule-associ
597	71	4.0	509	1	MMVZMX	670	70.5	4.0	6831	2	A88852	protein unc-22 lim
598	71	4.0	570	2	T11647	671	70.5	4.0	6839	2	S57242	twitclin [similari
599	71	4.0	609	2	H82039	672	70.5	4.0	7160	2	T27935	hypothetical prote
600	71	4.0	615	2	B38575	673	70	4.0	115	1	KVMSU6	Ig kappa chain pre
601	71	4.0	682	2	T22064	674	70	4.0	203	2	S23043	T-cell receptor ga
602	71	4.0	687	2	A49636	675	70	4.0	224	2	I37243	CRMP-35 antigen -
603	71	4.0	690	2	A24545	676	70	4.0	236	2	S25746	Ig lambda chain -
604	71	4.0	691	2	B83797	677	70	4.0	283	2	AB0105	probable maltodext
605	71	4.0	765	2	E36558	678	70	4.0	292	2	T44230	hypothetical prote
606	71	4.0	821	1	TVHUF2	679	70	4.0	299	2	DB3010	probable binding p
607	71	4.0	876	2	T51507	680	70	4.0	304	2	G71624	rtifin PFB0025C - m
608	71	4.0	902	1	S54495	681	70	4.0	347	2	T29415	hypothetical prote
609	71	4.0	940	2	T41992	682	70	4.0	356	2	G82938	hematin transport
610	71	4.0	956	2	G70327	683	70	4.0	374	2	A46352	ORP1 protein - Chl
611	71	4.0	1018	2	A54744	684	70	4.0	403	2	B36151	tryptophan synthas
612	71	4.0	1027	2	B85089	685	70	4.0	410	2	I50434	serine proteinase
613	71	4.0	1082	2	S64903	686	70	4.0	469	2	T46929	hypothetical prote

687	70	4.0	491	2	T27661	hypothetical prote	760	69.5	3.9	1045	2	G69167	cobalamin biosynth
688	70	4.0	517	2	T00980	hypothetical prote	761	69.5	3.9	1102	2	T28666	protein kinase C- γ
689	70	4.0	516	2	T37544	hypothetical serin	762	69.5	3.9	1102	2	F70535	probable rpoB prot
690	70	4.0	548	2	B71549	hypothetical prote	763	69.5	3.9	1199	2	C71150	probable swi/snf h
691	70	4.0	550	2	T03714	5-epi-aristolochan	764	69.5	3.9	1260	1	S05479	neuronal cell adhesi
692	70	4.0	576	2	A32604	interleukin-1 rece	765	69.5	3.9	1463	2	T30290	AAS surface proteol
693	70	4.0	599	2	T48450	hypothetical prote	766	69.5	3.9	1832	2	AC2594	glutamate synthase
694	70	4.0	609	2	AE2062	gamma-glutamylL-tran	767	69.5	3.9	1858	2	D97376	hypothetical prote
695	70	4.0	611	1	W1WLEP	B1 protein - Europ	768	69	3.9	115	2	C90907	hypothetical prote
696	70	4.0	611	1	H70938	probable fadex pro	769	69	3.9	139	2	AH1847	photosystem I reac
697	70	4.0	648	2	T08856	hypothetical prote	770	69	3.9	222	2	A69458	conserved hypothet
698	70	4.0	687	1	A39045	protein-glutamine	771	69	3.9	279	2	S04693	T-cell receptor de
699	70	4.0	790	2	T01537	S-receptor kinase	772	69	3.9	289	2	T18048	hypothetical prote
700	70	4.0	805	2	S68441	leptin receptor, s	773	69	3.9	291	2	A87153	carbohydrate degra
701	70	4.0	810	1	S57196	calpain (EC 3.4.22	774	69	3.9	306	2	T75625	hypothetical prote
702	70	4.0	818	2	T32154	hypothetical prote	775	69	3.9	330	2	AD1533	hypothetical prote
703	70	4.0	828	2	AD2004	hypothetical prote	776	69	3.9	348	2	D96815	probable gamma-glu
704	70	4.0	837	2	A34898	granulocyte colony	777	69	3.9	363	2	AG0675	probable secreted
705	70	4.0	838	2	AC1064	outer membrane fil	778	69	3.9	390	2	F72863	AcroF-109 protein
706	70	4.0	849	2	T22306	hypothetical prote	779	69	3.9	391	2	T41849	ACMNPV orf109 - Bo
707	70	4.0	892	2	S68439	leptin receptor, s	780	69	3.9	396	2	T76678	probable septum bi
708	70	4.0	894	2	S68437	leptin receptor, s	781	69	3.9	418	2	T35753	probable periplasm
709	70	4.0	900	2	S68440	leptin receptor, s	782	69	3.9	428	2	S09134	gene ND4L introm 1
710	70	4.0	933	2	H90247	ATP-dependent heli	783	69	3.9	461	2	F83772	hypothetical prote
711	70	4.0	990	2	T16554	hypothetical prote	784	69	3.9	465	2	B85358	SRRIN CARBOXYPEPT
712	70	4.0	1040	2	A34695	axonal glycoprotei	785	69	3.9	469	2	T46930	hypothetical prote
713	70	4.0	1086	2	T40354	hypothetical prote	786	69	3.9	490	2	B28516	cytochrome P450 2C
714	70	4.0	1092	2	T30214	fibrinogen-binding	787	69	3.9	493	2	E71008	hypothetical prote
715	70	4.0	1152	2	S68438	leptin receptor, s	788	69	3.9	501	1	PWLB2	hypothetical prote
716	70	4.0	1190	2	T00842	probable histidine	789	69	3.9	505	1	PWYCA	H ⁺ -transporting tw
717	70	4.0	1317	2	B41950	retrovirus-related	790	69	3.9	542	2	T20457	hypothetical prote
718	70	4.0	1456	1	WMGVP	RNA-directed RNA p	791	69	3.9	584	1	ABBY	alpha-glucosidase
719	70	4.0	1456	2	UQ2294	hypothetical 165.1	792	69	3.9	615	2	UB0358	ra1b binding prote
720	70	4.0	2003	2	AC0314	coagulable membrane	793	69	3.9	633	2	D82527	proteinase IV XR26
721	70	4.0	2183	2	T42764	hypothetical prote	794	69	3.9	644	2	A25684	hypothetical prote
722	70	4.0	2193	2	S76412	hypothetical prote	795	69	3.9	653	2	A54366	sodium/phosphate c
723	70	3.9	219	2	S74483	hypothetical prote	796	69	3.9	657	2	S25194	cap1 protein - Cor
724	69.5	3.9	285	1	I85488	alcohol sulfoxtrans	797	69	3.9	715	2	T45832	scinderin - bovine
725	69.5	3.9	332	1	E71105	hypothetical prote	798	69	3.9	733	2	T10049	adeverin - mouse
726	69.5	3.9	338	1	DEM5WM	malate dehydrogena	799	69	3.9	773	2	T46283	hypothetical prote
727	69.5	3.9	346	2	T49148	nitrilase (EC 3.5.	800	69	3.9	824	2	T51057	related to tol pro
728	69.5	3.9	366	2	E97304	iron-regulated ABC	801	69	3.9	919	2	C86578	type III secretion
729	69.5	3.9	407	2	T08732	hypothetical prote	802	69	3.9	919	2	F72045	vacuolar carboxype
730	69.5	3.9	427	2	C23703	ribulose-bisphosph	803	69	3.9	1049	2	S67613	ribonuclease E VC2
731	69.5	3.9	437	2	D70353	adenylosuccinate 1	804	69	3.9	1052	2	A82127	hypothetical prote
732	69.5	3.9	442	2	H86144	hypothetical prote	805	69	3.9	1244	2	T19615	hypothetical serin
733	69.5	3.9	444	2	E97750	tolb protein precu	806	69	3.9	1283	2	T39174	hypothetical serin
734	69.5	3.9	447	2	B81519	UDP-N-acetylmutam	807	69	3.9	1357	2	S61187	probable membrane
735	69.5	3.9	447	2	A86603	mutamoyl-DAP ligas	808	69	3.9	1360	2	T732833	hypothetical prote
736	69.5	3.9	447	2	F72021	mutamoyl-dap ligas	809	69	3.9	1442	2	T18538	patched protein -
737	69.5	3.9	453	2	B88040	protein 11n-42 [im	810	69	3.9	1656	2	S54520	probable membrane
738	69.5	3.9	461	2	T47782	hypothetical prote	811	69	3.9	1802	2	S52611	Y8 protein - yeas
739	69.5	3.9	503	2	S63257	probable membrane	812	69	3.9	2132	1	A55182	aggregran precursor
740	69.5	3.9	506	2	T05272	fatty acid elongas	813	69	3.9	2437	2	T18482	hypothetical prote
741	69.5	3.9	523	1	TVFVMT	protein-tyrosine K	814	69	3.9	4563	1	LPHUB	apolipoprotein B-1
742	69.5	3.9	548	2	A26511	amds protein - Eme	815	69	3.9	5188	2	B85547	probable RTX fami
743	69.5	3.9	548	2	S27958	transcription fact	816	69	3.9	5291	2	F90696	hypothetical prote
744	69.5	3.9	568	2	T39840	conserved hypothet	817	69	3.9	10797	2	T30192	probable peptidase
745	69.5	3.9	585	2	A39395	delayed rectifier	818	68.5	3.9	134	2	S11245	Ig kappa chain pre
746	69.5	3.9	616	2	D64569	conserved hypothet	819	68.5	3.9	135	2	J00472	T-cell receptor be
747	69.5	3.9	633	2	S19352	amino acid transpo	820	68.5	3.9	145	2	S36324	T-cell receptor de
748	69.5	3.9	640	2	T43724	dhak-type molecula	821	68.5	3.9	227	2	T133766	hypothetical prote
749	69.5	3.9	682	2	D90946	hypothetical prote	822	68.5	3.9	228	2	AB2200	two-component resp
750	69.5	3.9	682	2	H85794	hypothetical prote	823	68.5	3.9	234	2	S25757	Ig lambda chain -
751	69.5	3.9	682	2	A41798	carboxy-terminal p	824	68.5	3.9	234	2	S14237	Ig kappa chain pre
752	69.5	3.9	710	1	I51283	hepatocyte growth	825	68.5	3.9	240	2	A39016	T-cell surface gly
753	69.5	3.9	736	2	T40904	pombe specific hyp	826	68.5	3.9	267	2	G90579	hypothetical prote
754	69.5	3.9	757	2	T24266	hypothetical prote	827	68.5	3.9	268	2	S48942	hypothetical prote
755	69.5	3.9	776	2	A41704	genome polypotein	828	68.5	3.9	292	2	C64699	proteinase IV (BC
756	69.5	3.9	776	2	F81289	probable sugar tra	829	68.5	3.9	296	2	G65002	hypothetical prote
757	69.5	3.9	846	2	T04533	hypothetical prote	830	68.5	3.9	299	2	T32094	hypothetical prote
758	69.5	3.9	849	1	UTPVAD	noncapsid protein	831	68.5	3.9	310	2	A41776	syndecan 1 precurs
759	69.5	3.9	1034	2	H86399	protein F17i21.26	832	68.5	3.9	327	2	AB1192	replication protei

833	68.5	3.9	328	2	147161	Ig gamma 3 chain c	906	68	3.8	401	2	B89863	argininosuccinate
834	68.5	3.9	329	2	T19872	hypothetical prote	907	68	3.8	402	1	PAWTF	fructose-bisphosph
835	68.5	3.9	366	2	A70852	hypothetical prote	908	68	3.8	412	1	T35664	probable prokaryot
836	68.5	3.9	375	2	B96567	hypothetical prote	909	68	3.8	431	2	F64072	multidrug oxidoredu
837	68.5	3.9	393	2	B48965	subtilin biosynthe	910	68	3.8	444	2	D87296	hypothetical prote
838	68.5	3.9	423	2	AG0451	maltopectin (import	911	68	3.8	459	2	T76138	hypothetical prote
839	68.5	3.9	448	1	G69960	exodeoxyribonuclea	912	68	3.8	459	2	T21105	hypothetical prote
840	68.5	3.9	458	1	RWHUT4	T-cell surface gly	913	68	3.8	466	2	T46054	hypothetical prote
841	68.5	3.9	463	1	T19343	ribulose-bisphosph	914	68	3.8	471	1	A81680	conserved hypotnet
842	68.5	3.9	464	2	T06176	DNA damage inducib	915	68	3.8	479	1	S22542	transcription fact
843	68.5	3.9	493	2	T41397	glycoprotein B pre	916	68	3.8	525	1	P5XR10	outer capsid prote
844	68.5	3.9	498	2	J02353	flagella-related p	917	68	3.8	528	2	T38027	hypothetical prote
845	68.5	3.9	513	2	H90401	SRP1 protein - yea	918	68	3.8	541	2	E96789	protein T2318.10
846	68.5	3.9	522	2	S30884	dihydroxyacid dehy	919	68	3.8	584	2	S46183	alpha-glucosidase
847	68.5	3.9	555	2	P70372	probable membrane	920	68	3.8	602	2	D90557	hypothetical prote
848	68.5	3.9	561	2	SE3388	protein-tyrosine k	921	68	3.8	632	2	T37810	RNA-binding post-t
849	68.5	3.9	581	2	A59182	aldehyde-ferredoxi	922	68	3.8	637	2	D82816	fibrinectin-bindin
850	68.5	3.9	589	2	C71078	phosphoribosylamin	923	68	3.8	638	2	SS4418	DNA topoisomerase
851	68.5	3.9	592	2	T40252	hypothetical prote	924	68	3.8	640	2	S35734	probable receptor
852	68.5	3.9	592	2	SS4489	DNA mismatch repair	925	68	3.8	645	2	B96631	cellulase (EC 3.2.
853	68.5	3.9	601	2	AD1250	GMP-binding tyrosi	926	68	3.8	649	1	CZCLDM	hypothetical prote
854	68.5	3.9	606	2	AP2903	hypothetical prote	927	68	3.8	656	2	F71675	proteinase II (EC
855	68.5	3.9	606	2	H97678	hypothetical prote	928	68	3.8	690	2	JC4185	GedR family prote
856	68.5	3.9	630	2	S77346	hypothetical prote	929	68	3.8	710	2	R82492	hypothetical prote
857	68.5	3.9	636	2	A86248	protein T23J18.9 l	930	68	3.8	721	2	T27570	androgen-regulated
858	68.5	3.9	654	2	A69656	methy1-accepting c	931	68	3.8	789	2	S28259	cadherin 8 - human
859	68.5	3.9	672	2	D81746	type III secretion	932	68	3.8	793	2	D38992	hypothetical prote
860	68.5	3.9	689	2	S70661	transferrin-bindin	933	68	3.8	795	2	T21487	catomer complex b
861	68.5	3.9	772	1	T05753	S-receptor kinase	934	68	3.8	796	2	T39962	limbalral outer mem
862	68.5	3.9	776	1	B41704	genome polyprotein	935	68	3.8	814	1	C40618	ferriochrome-iron r
863	68.5	3.9	789	2	SE2172	SHB4 protein - yea	936	68	3.8	878	2	AH2075	probable DNA-direc
864	68.5	3.9	818	2	B83537	hypothetical prote	937	68	3.8	896	2	S26984	core protein VP3 -
865	68.5	3.9	827	2	A37849	S-layer protein -	938	68	3.8	901	2	JBO062	N-cadherin 2 precu
866	68.5	3.9	831	2	U01655	prolactin receptor	939	68	3.8	905	1	T1XLC2	brevian precursor
867	68.5	3.9	906	1	I0HUCN	cadherin 2 precurs	940	68	3.8	912	2	A54423	internalin protein
868	68.5	3.9	950	1	T51134	ionotropic glutama	941	68	3.8	940	2	AB1744	carboxymethylcellu
869	68.5	3.9	972	1	TVHUMD	macrophage colony-	942	68	3.8	962	2	S03818	iron-responsive el
870	68.5	3.9	976	2	A42465	alpha-amyliase (EC	943	68	3.8	963	2	A57238	protein F40H6.2 li
871	68.5	3.9	1043	2	A56037	DNA-binding protei	944	68	3.8	997	2	D88473	tyrosine kinase re
872	68.5	3.9	1074	2	F72217	conserved hypotet	945	68	3.8	1019	2	T13039	methionine S-methy
873	68.5	3.9	1086	2	T18294	Ca2+-transporting	946	68	3.8	1071	2	T52306	serine/threonine-s
874	68.5	3.9	1134	2	S53955	hypothetical prote	947	68	3.8	1147	2	S64930	protein-tyrosine-p
875	68.5	3.9	1257	1	A41060	neural cell adhesi	948	68	3.8	1174	2	T18140	protein ZK250.10 l
876	68.5	3.9	1269	2	A90267	proteinase related	949	68	3.8	1192	2	F88062	chitin synthase (B
877	68.5	3.9	1466	2	A35426	SP2 protein - yea	950	68	3.8	1195	2	S61886	p-glycoprotein iso
878	68.5	3.9	1520	2	AB1731	polymorphic memba	951	68	3.8	1281	2	T48123	microbial collagen
879	68.5	3.9	1767	2	T20766	hypothetical prote	952	68	3.8	1282	2	UC4393	hypothetical prote
880	68.5	3.9	2013	2	A11489	probable peptidogl	953	68	3.8	1291	2	T21694	reverse transcript
881	68.5	3.9	2288	2	T30568	acetyl-CoA carboxy	954	68	3.8	1295	2	T30528	hypothetical prote
882	68.5	3.9	3229	2	S27852	probable cell-surf	955	68	3.8	1318	2	T05745	adult-specific bru
883	68.5	3.9	4116	2	T13719	calo protein - fru	956	68	3.8	1458	2	A45665	hypothetical prote
884	68	3.8	1442	2	S36307	T-cell receptor de	957	68	3.8	1466	2	T32422	conserved hypotet
885	68	3.8	144	2	A11529	mannose-specific p	958	68	3.8	1664	2	H82601	hypothetical prote
886	68	3.8	155	2	I64130	PAI cross-reacting	959	68	3.8	1707	2	T18951	probable exclucule
887	68	3.8	157	2	T09659	pathogenesis-relat	960	68	3.8	1786	1	H1527	hypothetical prote
888	68	3.8	180	2	A71634	hypothetical prote	961	68	3.8	1946	2	AB1449	proteoglycan core
889	68	3.8	221	2	S73349	adhesin p1 precurs	962	68	3.8	2124	1	A28452	genome polyprotein
890	68	3.8	338	2	C83653	oligopeptide ABC t	963	68	3.8	3341	1	A42996	cytochrome b5 - w1
891	68	3.8	338	2	B96027	probable aliphatic	964	67.5	3.8	134	2	T14454	hypothetical prote
892	68	3.8	266	2	G69483	NAPC membrane prot	965	67.5	3.8	177	2	H90493	stem bromelain (EC
893	68	3.8	275	2	S03967	intercellular adhe	966	67.5	3.8	212	2	S03964	hypothetical prote
894	68	3.8	276	2	D82169	conserved hypotet	967	67.5	3.8	221	1	B42521	hypokappa chain pre
895	68	3.8	286	2	A82159	hypothetical prote	968	67.5	3.8	229	2	A20969	hypokappa chain pre
896	68	3.8	311	2	AH3197	transmembrane sens	969	67.5	3.8	261	2	S55139	hypokappa chain pre
897	68	3.8	326	2	T51811	protein farnesyltr	970	67.5	3.8	267	2	I72882	pc gamma receptor
898	68	3.8	330	2	B96027	probable aliphatic	971	67.5	3.8	277	2	B97703	hypothetical prote
899	68	3.8	338	2	C83653	oligopeptide ABC t	972	67.5	3.8	278	2	JC1507	biliary glycoprote
900	68	3.8	340	2	T49006	farnesyltransferas	973	67.5	3.8	299	2	R82975	hypothetical prote
901	68	3.8	341	2	AE1824	permease protein o	974	67.5	3.8	315	2	G69785	mannose-6-phosphat
902	68	3.8	355	2	SS8401	synaptotagmin VII	975	67.5	3.8	327	2	T22407	hypothetical prote
903	68	3.8	371	2	A71378	probable DNA polym	976	67.5	3.8	329	1	G2GP	Ig gamma-2 chain C
904	68	3.8	378	2	E84806	probable elongatio	977	67.5	3.8	345	2	I58406	outer membrane pro
905	68	3.8	385	2	T27626	hypothetical prote	978	67.5	3.8	348	1	MMNHBP	

979	67.5	3.8	348	2	B70743	hypothetical prote	1052	67	3.8	127	2	S52447	Ig kappa chain V r
980	67.5	3.8	357	2	T34012	hypothetical prote	1053	67	3.8	128	2	S31468	Ig kappa chain pre
981	67.5	3.8	360	2	T27022	hypothetical prote	1054	67	3.8	131	2	S30552	T-cell activation
982	67.5	3.8	361	2	D83798	phosphoserine amin	1055	67	3.8	135	2	S49200	cytochrome b5 - co
983	67.5	3.8	362	2	A81397	conserved hypotet	1056	67	3.8	137	2	B70221	rev protein (rev)
984	67.5	3.8	364	2	T46630	cysteine proteinas	1057	67	3.8	182	2	T23259	hypothetical prote
985	67.5	3.8	364	2	T12039	hypothetical prote	1058	67	3.8	214	2	B71159	probable flagellin
986	67.5	3.8	367	2	AP2494	aggreccan - pig (fr	1059	67	3.8	239	2	AC2042	hypothetical prote
987	67.5	3.8	370	2	S29139	aggreccan - pig (fr	1060	67	3.8	255	2	B69962	amino acid ABC tra
988	67.5	3.8	402	2	T25732	hypothetical prote	1061	67	3.8	282	2	B84984	geranyltransferasi
989	67.5	3.8	426	2	T36948	Ig epsilon-chain -	1062	67	3.8	300	2	HE4050	glucose kinase hom
990	67.5	3.8	443	2	T19512	hypothetical prote	1063	67	3.8	302	2	AC1387	phosphate ABC tran
991	67.5	3.8	450	2	H71135	probable adenylosu	1064	67	3.8	302	2	AE1752	phosphate ABC tran
992	67.5	3.8	451	2	T06090	hypothetical prote	1065	67	3.8	311	2	C86638	glycosyl transfera
993	67.5	3.8	458	2	A83095	UDP-N-acetylmuramo	1066	67	3.8	358	1	G64461	biotin synthase (E
994	67.5	3.8	466	2	A11894	two-component sens	1067	67	3.8	373	1	PDBYB	RBP1 protein - yea
995	67.5	3.8	487	2	S65133	butyrophilin - mou	1068	67	3.8	430	2	T14420	S-lucos-specific g
996	67.5	3.8	510	2	A87482	conserved hypotet	1069	67	3.8	441	2	F71425	hypothetical prote
997	67.5	3.8	511	2	A46020	potassium channel	1070	67	3.8	450	2	S38424	S-lucos-specific g
998	67.5	3.8	511	2	S07095	59k antigen - Chla	1071	67	3.8	461	2	T09933	probable phosphodi
999	67.5	3.8	525	2	J00642	hypothetical prote	1072	67	3.8	474	2	I50830	Ig mu chain - Lep1
1000	67.5	3.8	527	2	G85760	hypothetical prote	1073	67	3.8	477	2	G86833	6-phospho-beta-glu
1001	67.5	3.8	527	2	H90858	hypothetical prote	1074	67	3.8	495	1	A26396	T-cell surface gly
1002	67.5	3.8	541	1	A43610	protein-tyrosine k	1075	67	3.8	518	2	JC4024	poliovirus recepto
1003	67.5	3.8	542	1	TVHUSC	protein-tyrosine k	1076	67	3.8	524	2	G64243	hypothetical prote
1004	67.5	3.8	547	2	B45808	B-lymphocyte antig	1077	67	3.8	532	2	C97228	probable peptide A
1005	67.5	3.8	547	2	T27253	hypothetical prote	1078	67	3.8	542	2	T41650	importin alpha sub
1006	67.5	3.8	567	2	S29498	lymphocyte antigen	1079	67	3.8	544	2	S41626	spike protein chai
1007	67.5	3.8	570	2	A181828	flavoprotein [limpo	1080	67	3.8	569	2	S64957	aspergillopepsin I
1008	67.5	3.8	572	2	S55982	asparagine synthas	1081	67	3.8	599	2	S55363	maltase-like prote
1009	67.5	3.8	584	2	S48327	hypothetical prote	1082	67	3.8	619	2	S67067	probable membrane
1010	67.5	3.8	591	2	S73708	MG321 homolog H08	1083	67	3.8	622	2	HE4447	hypothetical prote
1011	67.5	3.8	619	2	A13336	potassium/proton a	1084	67	3.8	623	1	S64774	yahu protein - Bsc
1012	67.5	3.8	621	2	A72091	metalloproteinase	1085	67	3.8	625	1	S52485	glucokinase regula
1013	67.5	3.8	621	2	D81578	zinc proteinase CP	1086	67	3.8	661	1	G71063	probable ferrous i
1014	67.5	3.8	627	2	D96956	ntic family transc	1087	67	3.8	690	2	H71237	hypothetical prote
1015	67.5	3.8	651	2	T49986	lectin-like protei	1088	67	3.8	717	2	T25431	hypothetical prote
1016	67.5	3.8	651	2	E95196	neuraminidase B [i	1089	67	3.8	721	2	A12447	transport protein
1017	67.5	3.8	697	2	AC50837	Tomb-dependent out	1090	67	3.8	746	2	A75018	hypothetical prote
1018	67.5	3.8	732	1	JU0132	acylaminoacyl-pept	1091	67	3.8	747	2	T23607	hypothetical prote
1019	67.5	3.8	748	2	I48744	semaphorin A - mou	1092	67	3.8	750	2	T19080	cell surface glyco
1020	67.5	3.8	759	2	S67164	probable membrane	1093	67	3.8	836	2	B84417	hypothetical trans
1021	67.5	3.8	776	2	S67053	cadherin-14 - huma	1094	67	3.8	850	2	AE3484	cell surface glyco
1022	67.5	3.8	790	2	G02678	protein-tyrosine k	1095	67	3.8	852	2	A28459	DNA topoisomerase
1023	67.5	3.8	832	2	A01096	internalin protein	1096	67	3.8	871	2	D72038	HIR2 protein - yea
1024	67.5	3.8	832	2	AD0196	protein K07E3.2 [i	1097	67	3.8	875	2	S62177	protein-tyrosine k
1025	67.5	3.8	837	2	B89583	hypothetical prote	1098	67	3.8	896	2	T49452	hypothetical prote
1026	67.5	3.8	855	2	T10685	serine/threonine-s	1100	67	3.8	898	2	UC7313	aryl hydrocarbon r
1027	67.5	3.8	866	2	T10587	hypothetical prote	1101	67	3.8	920	2	AE2275	hypothetical prote
1028	67.5	3.8	879	2	S73757	hypothetical prote	1102	67	3.8	939	2	B86613	zinc metalloprotei
1029	67.5	3.8	906	2	AG1957	hypothetical prote	1103	67	3.8	974	2	T29545	hypothetical prote
1030	67.5	3.8	926	2	D86897	hypothetical prote	1104	67	3.8	976	2	T29583	hypothetical prote
1031	67.5	3.8	933	2	AD3309	hypothetical membr	1105	67	3.8	980	2	I57936	glutamate receptor
1032	67.5	3.8	944	2	T47246	chitin synthase (E	1106	67	3.8	981	2	T18234	beta transducin ho
1033	67.5	3.8	956	2	JH0826	glutamate ionotro	1107	67	3.8	982	2	DB1379	transmembrane effi
1034	67.5	3.8	992	2	JQ1165	Env protein - Maed	1108	67	3.8	1040	2	HE4459	hypothetical prote
1035	67.5	3.8	1036	2	A29832	HPI layer surface	1109	67	3.8	1048	2	JC4593	protein-tyrosine k
1036	67.5	3.8	1042	2	E85968	evolved beta-D-gal	1110	67	3.8	1070	2	JC4593	neural cell adhe
1037	67.5	3.8	1042	2	P91123	conserved hypotet	1111	67	3.8	1115	1	T04587	hypothetical prote
1038	67.5	3.8	1061	2	D98008	hypothetical prote	1112	67	3.8	1134	2	T04587	probable peptidogl
1039	67.5	3.8	1118	2	T27865	probable pyrolys	1113	67	3.8	1151	1	AG1717	chromospondin 1 p
1040	67.5	3.8	1155	2	H71456	chitinase A [impor	1114	67	3.8	1170	1	S41603	type V adenylyl cy
1041	67.5	3.8	1215	2	T43916	P-glycoprotein-lik	1115	67	3.8	1264	2	BVBYP9	RAD9 protein - yea
1042	67.5	3.8	1229	2	D85023	P-glycoprotein-lik	1116	67	3.8	1309	1	T23007	hypothetical prote
1043	67.5	3.8	1229	2	TS2319	protein-tyrosine k	1117	67	3.8	1328	2	T45031	hypothetical prote
1044	67.5	3.8	1260	1	TVRTNU	embryonic receptor	1118	67	3.8	1365	2	S62419	hypothetical prote
1045	67.5	3.8	1263	2	T13465	myosin-2 isoform -	1119	67	3.8	1428	2	T13717	CRAG protein - fru
1046	67.5	3.8	1330	2	S49010	beta-galactosidase	1120	67	3.8	1441	1	A48148	protein-tyrosine-p
1047	67.5	3.8	1471	2	T40117	kinase-related pro	1121	67	3.8	1533	2	F71274	hypothetical prote
1048	67.5	3.8	1928	2	J50610	variant surface pr	1122	67	3.8	1589	2	T22668	hypothetical prote
1049	67.5	3.8	2338	2	T73957	gp330 protein prec	1123	67	3.8	1680	2	T41628	probable transcript
1050	67.5	3.8	3026	2	T28431		1124	67	3.8				
1051	67.5	3.8	4660	2	T42737								

1125	67	3.8	1723	2	H86557	polymorphic membra
1126	67	3.8	1723	2	E72067	polymorphic membra
1127	67	3.8	1732	2	C81601	polymorphic membra
1128	67	3.8	1742	2	S24600	prolectin - fruit
1129	67	3.8	1790	1	S27772	vitellogenin precu
1130	67	3.8	1813	2	T30564	resistance protein
1131	67	3.8	2095	2	S29529	genome polypotein
1132	67	3.8	2380	2	T29551	hypothetical prote
1133	67	3.8	2626	2	T31059	mosin-RhoGAP prot
1134	66.5	3.8	136	2	C72524	hypothetical prote
1135	66.5	3.8	147	2	JC7237	receptor-activity-
1136	66.5	3.8	181	2	AC0686	hypothetical prote
1137	66.5	3.8	191	2	AH0196	probable lipoprote
1138	66.5	3.8	218	2	D72494	probable thiosulfa
1139	66.5	3.8	228	2	AG2107	hypothetical prote
1140	66.5	3.8	245	2	T12334	L-ascorbate peroxi
1141	66.5	3.8	245	2	H71429	hypothetical prote
1142	66.5	3.8	250	2	S64849	hypothetical prote
1143	66.5	3.8	285	2	T12156	nodulin, isoform N
1144	66.5	3.8	301	2	S57531	transcription regu
1145	66.5	3.8	318	2	S61840	porin class PIB -
1146	66.5	3.8	328	2	D69452	conserved hypothet
1147	66.5	3.8	335	2	A53434	cell surface glyco
1148	66.5	3.8	344	2	I51330	androgen receptor
1149	66.5	3.8	352	2	T09760	chymopapain (EC 3.
1150	66.5	3.8	358	2	G70026	conserved hypothet
1151	66.5	3.8	362	2	T41842	ACNPNV orf101 - Bo
1152	66.5	3.8	367	2	T06529	cysteine proteinas
1153	66.5	3.8	382	2	C86321	hypothetical prote
1154	66.5	3.8	384	2	F84675	hypothetical prote
1155	66.5	3.8	394	2	AC3364	glutaryl-CoA dehyd
1156	66.5	3.8	397	2	T34441	hypothetical prote
1157	66.5	3.8	404	1	I61596	advanced glycosyla
1158	66.5	3.8	413	2	H82270	hypothetical prote
1159	66.5	3.8	417	2	A27775	phosphoglycerate k
1160	66.5	3.8	422	1	BVBXMS	Msl1 protein - yea
1161	66.5	3.8	438	2	A97595	hypothetical prote
1162	66.5	3.8	438	2	AH2811	Arpase, AAA family
1163	66.5	3.8	438	2	A82262	conserved hypothet
1164	66.5	3.8	442	2	B55211	chorismate lyase u
1165	66.5	3.8	453	2	A89873	hypothetical prote
1166	66.5	3.8	461	2	D96835	probable cyclin, 4
1167	66.5	3.8	463	2	T26655	hypothetical prote
1168	66.5	3.8	475	2	A54879	pregnancy-specific
1169	66.5	3.8	491	2	D91217	ketol-acid reducto
1170	66.5	3.8	491	2	B86063	ketol-acid reducto
1171	66.5	3.8	497	2	JB0275	voltage-gated pola
1172	66.5	3.8	532	2	T15354	hypothetical prote
1173	66.5	3.8	542	2	A49114	protein-tyrosine k
1174	66.5	3.8	549	2	H64992	hypothetical prote
1175	66.5	3.8	553	2	T15220	hypothetical prote
1176	66.5	3.8	557	2	S21596	extracellular prote
1177	66.5	3.8	592	2	S25705	Ig mu chain - shae
1178	66.5	3.8	616	2	G64160	GTP-binding protei
1179	66.5	3.8	636	2	H87789	protein C34G6.1 [i
1180	66.5	3.8	656	1	S59631	endo-1,4-beta-xyla
1181	66.5	3.8	679	2	C71007	probable format'd
1182	66.5	3.8	697	2	B98063	exo-alpha-stalida
1183	66.5	3.8	709	2	A53364	carcinoembryonic a
1184	66.5	3.8	718	1	VCPVIM	coat protein VP1 -
1185	66.5	3.8	773	2	S46011	probable pre-mRNA-
1186	66.5	3.8	848	2	C70203	DNA topoisomerase
1187	66.5	3.8	862	2	B36786	hypothetical prote
1188	66.5	3.8	917	2	I48950	telencephalin prec
1189	66.5	3.8	921	2	T51136	ionotropic glutama
1190	66.5	3.8	923	2	T41350	meiotic recombina
1191	66.5	3.8	969	2	C86394	protein T24P3.14
1192	66.5	3.8	1005	2	S73711	probable lipoprote
1193	66.5	3.8	1009	2	JH0266	glutamate receptor
1194	66.5	3.8	1044	2	T10050	integrin alpha-v c
1195	66.5	3.8	1061	2	JC7116	xeal-3 protein - A
1196	66.5	3.8	1080	2	A35088	phycobilisome link
1197	66.5	3.8	1097	2	T45622	hypothetical prote
1198	66.5	3.8	1117	2	JC4934	delta-crystallin/B
1199	66.5	3.8	1160	2	T39898	carbamoyl-phosphat
1200	66.5	3.8	1181	2	T20386	hypothetical prote
1201	66.5	3.8	1182	2	S59951	DNA-directed RNA p
1202	66.5	3.8	1183	2	H89821	RNA polymerase bet
1203	66.5	3.8	1184	2	A42904	adenyllylcyclase ty
1204	66.5	3.8	1344	2	T14316	rig-I protein - mo
1205	66.5	3.8	1376	2	F83711	exopolysaccharona
1206	66.5	3.8	1447	2	A54100	tumor suppressor p
1207	66.5	3.8	1462	2	T06819	DNA topoisomerase
1208	66.5	3.8	1471	2	F86218	protein F22013.8 [
1209	66.5	3.8	1484	2	T42632	breast cancer tumo
1210	66.5	3.8	1545	2	T26589	hypothetical prote
1211	66.5	3.8	1565	2	T01060	hypothetical prote
1212	66.5	3.8	1616	2	T00713	helicase homolog F
1213	66.5	3.8	1643	2	T14274	versican precursor
1214	66.5	3.8	2089	2	C85426	ATM-like protein [
1215	66.5	3.8	2303	1	GNNYTM	genome polypotein
1216	66.5	3.8	2470	2	I50726	peptide independent
1217	66.5	3.8	2588	2	A12136	hypothetical prote
1218	66.5	3.8	3262	2	AH2137	apoliophorin prec
1219	66.5	3.8	3305	2	T18358	versican precursor
1220	66.5	3.8	3381	2	T42389	hypothetical prote
1221	66.5	3.8	3798	2	T05501	dynein heavy chain
1222	66.5	3.8	4092	1	S38128	hypothetical prote
1223	66.5	3.8	4436	2	E71086	polyketide synthas
1224	66.5	3.8	4447	2	A69679	cadherin-related p
1225	66.5	3.8	5147	1	IJFFPM	Ig lambda chain pr
1226	66	3.7	118	2	S12627	T-cell receptor ga
1227	66	3.7	132	1	RMSI12	cyclochrome B5 [imp
1228	66	3.7	134	2	T52469	Ig light chain - r
1229	66	3.7	167	2	S29579	pregnancy-specific
1230	66	3.7	182	2	A34647	T-cell receptor CD
1231	66	3.7	189	2	A31348	hypothetical prote
1232	66	3.7	192	2	B75144	Ig lambda chain (D
1233	66	3.7	216	2	S69130	hypothetical prote
1234	66	3.7	226	2	T38234	probable 4-nitroph
1235	66	3.7	255	2	H72539	hypothetical prote
1236	66	3.7	261	2	G87608	replication protei
1237	66	3.7	272	2	T10116	hypothetical prote
1238	66	3.7	281	2	G71095	hypothetical prote
1239	66	3.7	307	2	A71602	klfin PFB0955w - m
1240	66	3.7	324	2	S56435	hypothetical 35.5-
1241	66	3.7	362	2	T04079	ferredoxin-NADP re
1242	66	3.7	376	2	T19186	hypothetical prote
1243	66	3.7	381	2	AE2197	ABC transport prot
1244	66	3.7	400	2	T24830	hypothetical prote
1245	66	3.7	406	2	H64793	yeDn protein - Bsc
1246	66	3.7	406	2	A99709	hypothetical prote
1247	66	3.7	406	2	B85559	hypothetical prote
1248	66	3.7	417	1	S22784	acetyl-CoA C-acylt
1249	66	3.7	428	2	T14529	s-locus-specific g
1250	66	3.7	432	2	T05236	hypothetical prote
1251	66	3.7	448	2	G83818	hypothetical prote
1252	66	3.7	451	2	T30603	perlecan homolog 2
1253	66	3.7	457	2	D69059	glycylamide ribonu
1254	66	3.7	469	2	T08594	probable sulfate a
1255	66	3.7	466	2	T27120	hypothetical prote
1256	66	3.7	469	2	E70076	arabian endo-1,5-
1257	66	3.7	471	2	S14165	cyclin B1 - yeast
1258	66	3.7	489	1	VGBETA	glycylproteolisin A - t
1259	66	3.7	495	2	C71679	UDP-n-acetylmurama
1260	66	3.7	525	2	S55099	GMP synthase (glut
1261	66	3.7	532	1	B34104	protein-tyrosine k
1262	66	3.7	538	1	A34104	protein-tyrosine k
1263	66	3.7	545	2	JC2457	vascular cell adhe
1264	66	3.7	545	2	D81973	probable integrin
1265	66	3.7	550	2	I37579	Digeorge syndrome
1266	66	3.7	553	2	T48486	hypothetical prote
1267	66	3.7	580	2	H72270	ABC transporter. A
1268	66	3.7	589	2	B90605	hypothetical prote
1269	66	3.7	592	2	E70455	sulfur oxidatlon p
1270	66	3.7	603	2	S03020	dopamine beta-mono

1271	66	3.7	624	2	D84986	1344	65.5	3.7	237	2	G87286	conserved hypotet
1272	66	3.7	631	2	I52257	1345	65.5	3.7	254	1	VCCV7Y	coat protein - tob
1273	66	3.7	640	2	B96784	1346	65.5	3.7	276	1	A69077	conserved hypotet
1274	66	3.7	662	2	T23271	1347	65.5	3.7	283	2	H90409	hypothetical prote
1275	66	3.7	687	2	G81970	1348	65.5	3.7	289	2	B82534	heat shock protei
1276	66	3.7	719	2	S44237	1349	65.5	3.7	290	2	A75497	UDP-N-acetyleno
1277	66	3.7	738	2	A40096	1350	65.5	3.7	290	2	A34439	concanavalin A pr
1278	66	3.7	747	2	S66959	1351	65.5	3.7	290	2	G71623	rifin PRP0065w - m
1279	66	3.7	750	2	T04010	1352	65.5	3.7	309	2	A29812	sputatation protei
1280	66	3.7	751	2	T01449	1353	65.5	3.7	311	2	F69820	conserved hypotet
1281	66	3.7	754	2	JC4898	1354	65.5	3.7	312	2	G71864	probable chemoctaxi
1282	66	3.7	808	2	D81924	1355	65.5	3.7	323	2	F71130	probable oligopept
1283	66	3.7	810	2	A81965	1356	65.5	3.7	321	2	AD2134	iron(III) dicitrat
1284	66	3.7	815	2	T35970	1357	65.5	3.7	336	2	S42632	probable binding p
1285	66	3.7	833	2	T49782	1358	65.5	3.7	344	2	F83620	formate dehydrogen
1286	66	3.7	839	2	T16753	1359	65.5	3.7	379	2	B64300	hypothetical 39.2K
1287	66	3.7	851	2	T47495	1360	65.5	3.7	383	2	S47711	hypothetical prote
1288	66	3.7	863	2	A80525	1361	65.5	3.7	383	2	C86020	hypothetical prote
1289	66	3.7	864	2	H85335	1362	65.5	3.7	386	2	C91174	hypothetical prote
1290	66	3.7	864	2	T04518	1363	65.5	3.7	386	2	T25755	hypothetical prote
1291	66	3.7	901	2	A80519	1364	65.5	3.7	393	2	D83589	glutaryl-CoA dehyd
1292	66	3.7	902	2	A60560	1365	65.5	3.7	398	1	G3MSM	ig gamma-3 chain C
1293	66	3.7	912	1	LYCHCN	1366	65.5	3.7	399	2	B24698	formate dehydrogen
1294	66	3.7	920	2	B84640	1367	65.5	3.7	405	2	D82542	two-component syst
1295	66	3.7	961	2	G90053	1368	65.5	3.7	407	2	A71613	hypothetical prote
1296	66	3.7	974	2	A72012	1369	65.5	3.7	409	2	T14611	alanine transamina
1297	66	3.7	977	2	I45877	1370	65.5	3.7	410	1	C69585	antipeptidase amp
1298	66	3.7	979	2	JH0589	1371	65.5	3.7	410	1	B83930	antipeptidase BH2
1299	66	3.7	979	2	JH0592	1372	65.5	3.7	411	1	QOCV2P	PI polypeptide - m
1300	66	3.7	1006	2	AD2195	1373	65.5	3.7	411	2	F64224	hypothetical prote
1301	66	3.7	1043	2	T15191	1374	65.5	3.7	414	2	E90572	hypothetical prote
1302	66	3.7	1053	2	S72194	1375	65.5	3.7	429	2	S27793	hypothetical prote
1303	66	3.7	1065	2	H95321	1376	65.5	3.7	430	2	G89962	hypothetical prote
1304	66	3.7	1100	2	A35007	1377	65.5	3.7	440	2	S45737	TYA protein - yeas
1305	66	3.7	1105	2	S21173	1378	65.5	3.7	440	2	S49765	TYA protein - yeas
1306	66	3.7	1112	2	T30202	1379	65.5	3.7	447	2	T28207	hypothetical prote
1307	66	3.7	1118	2	S44641	1380	65.5	3.7	452	2	T39751	probable respirato
1308	66	3.7	1139	2	T22811	1381	65.5	3.7	486	2	D70439	conserved hypotet
1309	66	3.7	1207	2	T52459	1382	65.5	3.7	487	2	A11505	hypothetical cell
1310	66	3.7	1223	2	S29717	1383	65.5	3.7	489	2	D71420	EcoA system protei
1311	66	3.7	1232	2	T343027	1384	65.5	3.7	506	2	A47601	hypothetical prote
1312	66	3.7	1242	2	T39453	1385	65.5	3.7	527	2	S37899	hypothetical prote
1313	66	3.7	1248	2	C89874	1386	65.5	3.7	545	2	B88479	protein P47D12.9 [
1314	66	3.7	1335	2	T30211	1387	65.5	3.7	555	2	A30902	inositol-3-phospha
1315	66	3.7	1335	2	T26301	1388	65.5	3.7	561	2	S35637	high mobility grou
1316	66	3.7	1363	2	S44241	1389	65.5	3.7	564	2	A89956	hypothetical prote
1317	66	3.7	1367	2	A41228	1390	65.5	3.7	566	2	F84903	probable ubiquitin
1318	66	3.7	1549	2	D86338	1391	65.5	3.7	575	2	S46692	hypothetical prote
1319	66	3.7	1601	2	T18800	1392	65.5	3.7	582	2	H97326	methyl-accepting c
1320	66	3.7	1750	2	G84649	1393	65.5	3.7	588	1	B83218	hypothetical prote
1321	66	3.7	1792	2	T08878	1394	65.5	3.7	608	1	RD20K1	dihydrofolate redu
1322	66	3.7	1822	2	T14106	1395	65.5	3.7	615	2	T29223	hypothetical prote
1323	66	3.7	1828	2	T14455	1396	65.5	3.7	621	2	T20863	hypothetical prote
1324	66	3.7	1828	2	T14455	1397	65.5	3.7	623	2	AD2295	hypothetical prote
1325	66	3.7	1993	2	T30902	1398	65.5	3.7	638	2	AH0340	putative autotransp
1326	66	3.7	2035	2	AC0233	1399	65.5	3.7	647	1	HRXL70	dnak-type molecula
1327	66	3.7	2041	2	T17439	1400	65.5	3.7	659	2	T05630	hypothetical prote
1328	66	3.7	2186	2	H89960	1401	65.5	3.7	666	2	B86289	probable serine/th
1329	66	3.7	2347	1	T30201	1402	65.5	3.7	672	2	S75001	hypothetical prote
1330	66	3.7	2352	2	T30201	1402	65.5	3.7	683	2	D82674	hypothetical prote
1331	66	3.7	2352	2	T30201	1402	65.5	3.7	683	2	D82674	hypothetical prote
1332	66	3.7	2352	2	T30201	1402	65.5	3.7	683	2	D82674	hypothetical prote
1333	66	3.7	2352	2	T30201	1402	65.5	3.7	683	2	D82674	hypothetical prote
1334	66	3.7	2352	2	T30201	1402	65.5	3.7	683	2	D82674	hypothetical prote
1335	66	3.7	2352	2	T30201	1402	65.5	3.7	683	2	D82674	hypothetical prote
1336	66	3.7	2352	2	T30201	1402	65.5	3.7	683	2	D82674	hypothetical prote
1337	66	3.7	2352	2	T30201	1402	65.5	3.7	683	2	D82674	hypothetical prote
1338	66	3.7	2352	2	T30201	1402	65.5	3.7	683	2	D82674	hypothetical prote
1339	66	3.7	2352	2	T30201	1402	65.5	3.7	683	2	D82674	hypothetical prote
1340	66	3.7	2352	2	T30201	1402	65.5	3.7	683	2	D82674	hypothetical prote
1341	66	3.7	2352	2	T30201	1402	65.5	3.7	683	2	D82674	hypothetical prote
1342	66	3.7	2352	2	T30201	1402	65.5	3.7	683	2	D82674	hypothetical prote
1343	66	3.7	2352	2	T30201	1402	65.5	3.7	683	2	D82674	hypothetical prote

1417 65.5 3.7 921 2 S49965
1418 65.5 3.7 946 1 A47299
1419 65.5 3.7 948 1 C75265
1420 65.5 3.7 953 2 B64732
1421 65.5 3.7 956 2 B64732
1422 65.5 3.7 956 2 J50685
1423 65.5 3.7 1051 2 G84316
1424 65.5 3.7 1052 2 B49120
1425 65.5 3.7 1054 2 D70425
1426 65.5 3.7 1066 2 A81228
1427 65.5 3.7 1066 2 A81581
1428 65.5 3.7 1068 1 U01329
1429 65.5 3.7 1084 2 B64088
1430 65.5 3.7 1091 2 A58532
1431 65.5 3.7 1100 1 D8BYD1
1432 65.5 3.7 1125 2 H87644
1433 65.5 3.7 1132 2 A01809
1434 65.5 3.7 1174 2 A40853
1435 65.5 3.7 1259 2 S36126
1436 65.5 3.7 1270 2 T51227
1437 65.5 3.7 1464 2 JCS144
1438 65.5 3.7 1476 2 JCS143
1439 65.5 3.7 1487 2 A62560
1440 65.5 3.7 1657 2 T15838
1441 65.5 3.7 1744 2 JH0720
1442 65.5 3.7 1755 2 S45736
1443 65.5 3.7 1871 2 S27938
1444 65.5 3.7 2062 2 G96602
1445 65.5 3.7 2311 1 TWCHSR
1446 65.5 3.7 2336 2 T39911
1447 65.5 3.7 2335 2 A48584
1448 65.5 3.7 3147 2 T21328
1449 65.5 3.7 4302 2 A38972
1450 65 3.7 61 2 F26420
1451 65 3.7 115 1 KWSM2
1452 65 3.7 128 1 KVMST1
1453 65 3.7 140 2 I46638
1454 65 3.7 158 2 D83809
1455 65 3.7 216 2 J80245
1456 65 3.7 219 2 T02114
1457 65 3.7 231 1 A29459
1458 65 3.7 235 2 S25758
1459 65 3.7 244 2 I62393
1460 65 3.7 255 1 I62389
1461 65 3.7 273 2 S48146
1462 65 3.7 273 2 T42928
1463 65 3.7 308 2 C84072
1464 65 3.7 313 2 B63588
1465 65 3.7 322 2 P50019
1466 65 3.7 331 2 G91133
1467 65 3.7 331 2 B65979
1468 65 3.7 345 2 B65106
1469 65 3.7 350 2 A46052
1470 65 3.7 359 1 A28658
1471 65 3.7 354 2 D84923
1472 65 3.7 355 2 S21057
1473 65 3.7 358 2 G70601
1474 65 3.7 363 2 B65057
1475 65 3.7 373 1 VB5ETC
1476 65 3.7 388 1 EHMS
1477 65 3.7 392 2 S04205
1478 65 3.7 394 2 B70411
1479 65 3.7 397 2 T31803
1480 65 3.7 404 2 F86517
1481 65 3.7 404 2 G72106
1482 65 3.7 412 2 B65146
1483 65 3.7 414 2 S43340
1484 65 3.7 414 2 A81500
1485 65 3.7 416 1 A42879
1486 65 3.7 425 2 D70436
1487 65 3.7 432 1 RWC2T4
1488 65 3.7 443 1 B64667
1489 65 3.7 443 2 T17970

probable membrane
ror-related recept
hexagonally packe
probable ligand-ga
glutamate receptor
ribonucleoside red
protein-tyrosine k
conserved hypotet
transporter, (to B
sucrose-phosphate
hemoglobin-binding
glial cell membran
RAD1 protein - Yea
TonB-dependent rec
phycobiosome core
potassium channel
neural cell adhesi
related to verruco
murinoglobulin pre
alpha-macroglobuli
hypothetical prote
hypothetical prote
tanabin - African
Tyb protein - yeas
hypothetical prote
probable receptor
kinase-related pro
rad3 checkpoint pr
transmission block
hypothetical prote
polycystic kidney
T-cell receptor ga
Ig kappa chain pre
rearranged T-cell
transcription elon
Ig lambda chain NI
hypothetical prote
orotate phosphori
Ig lambda chain -
outer membrane pro
mucin 1 precursor,
immediate-early pr
UDP-glucose 4-epim
L-arabinose transp
Ig gamma-2a chain
probable collagena
probable proteinas
vacuolar cell adhe
nitriase (EC 3.5.
probable exonuclea
conserved hypotet
reep protein - Sal
hypothetical prote
glycoprotein A - t
Ig epsilon chain C
protein-tyrosine k
fibribial assembly
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical 47.4
glycerol-dehyde-3-p
N-carbamyl-L-amino
advanced glycosyla
DNA mismatch repai
T-cell surface gly
multidrug-efflux t
hypothetical prote

1490 65 3.7 444 1 DYB02
1491 65 3.7 444 2 PC4436
1492 65 3.7 449 2 A69643
1493 65 3.7 451 2 T33763
1494 65 3.7 452 2 G95306
1495 65 3.7 468 2 T49682
1496 65 3.7 469 2 S50584
1497 65 3.7 487 2 A12692
1498 65 3.7 487 2 B97474
1499 65 3.7 493 2 T01206
1500 65 3.7 494 2 A35551

ALIGNMENTS

RESULT 1
A46500
Ly-9.2 antigen - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A46500
R:Sandrin, M.S.; Gunley, T.P.; Henning, M.M.; Vaughan, H.A.; Genez, L.J.; Trapani, J.A.;
J. Immunol. 149, 1636-1641, 1992
A:Title: Isolation and characterization of cDNA clones for mouse Ly-9.
A:Reference number: A46500; MUID:92373005; PMID:1506686
A:Accession: A46500
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-629 <584>
A:Cross-references: UNIPARC:UP10000047632; GB:M64412; NID:G198931; PIDN:AAA39468.1; PID:
A:Experimental source: C57BL/6
A>Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIPI:111654)
C:Keywords: transmembrane protein

Query Match 19.4%; Score 343; DB 2; Length 629;
Best Local Similarity 29.3%; Pred. No. 2.7e-20;
Matches 105; Conservative 58; Mismatches 143; Indels 52; Gaps 14;

QY 14 LMOU-TGSA-----ASGPVKELVSGAVTPPLKSK-VKQVDSIVTPTNTPTLYTIQPEG 67
DB 217 IWQCTGASRRKTAG--KTVVGILGEPVTLPLEFRATRAKVVWVWLNTS--VISQERR 272
QY 68 GTIIVTQNR-----NREVRDPDGGYSLSKSLKKNDSIGYVGVYSSLSQGPSTOEVYL 122
DB 273 GAATADSRKPKSGEERRVRTSDQDQSLKSLQKMBDGPYHAAYVCSASNDPSVRHTL 332
QY 123 HVEHLSKPKVTWGLQSNKNGTCVTNLTCCMEHEGEEDVITYTKALGQANSHNGSILPI 182
DB 333 LVYRLEKPSVTKSPVHMNGICEVVLTCSDVGGNNVTYTMPLQNKAVMSQGSHTLV 392
QY 183 SWRNGESDMFTICVARNPVSRNRPSPILARLCEGAADDPDSSNVLLCLLVPLLSLFFV 242
DB 393 SWEGEHLPNFTCAHNPVS--NSSSOPSSGTCISG---PERNKRFWLLLLVLLMLI 447
QY 243 LGLFLMLKRRQREYIEBK-KRVDICRETPNICPHSG-----ENTB 283
DB 448 GGYFT--LKKKKQSSSLATRRQAEPAELPE--PPTGQGFVSLSQRYEKLDSAKTR 503
QY 284 Y-----DTIPHTRTLLKEPDNPATVYSTEVI PKKMNPHSLTMPPTPLFAVENYV 335
DB 504 HQPIPTDTSSESSATTBEDDEKTRMSTANSRNLQ---YDLVTHQDIAMLAALVAGGV 558

RESULT 2
S58892
signaling lymphocytic activation molecule - human
C:Species: Homo sapiens (man)
C>Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: S58892
R:Cocks, B.G.; Chang, C.C.; Carballido, J.M.; Vessel, H.; de Vries, J.E.; Aversa, G.
Nature 376, 260-263, 1995
A:Title: A novel receptor involved in T-cell activation.


```

Db      163 PCKNMSYQWNTNLSAPFKCAINPVSKESKTEVV-----NCEPKGSPFYTVGVGAG 213
QY      232 -LLVPLLSLTVFLGFLWFLMKRROEYIEBKRVDCRSTNICHSGENTGYDTIIPPT 290
Db      214 GLLLVLLVLAFLT---FCICRRKRRRRRRROBELEIYASTS-----TYERGKPKHS 261
QY      291 NRTILKEDPANTVYSTEIPIKMEPHSLLTWPDTP 326
Db      262 T-----PAAAGNSVALQAAPPPEHHIQTGPHRP 290

RESULT 5
RHMUC2
T-cell surface glycoprotein CD2 precursor - human
N.Alternate names: E rosette receptor; erythrocyte receptor; erythrocyte-binding protein
C.Species: Homo sapiens (man)
C.Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C.Accession: A28967; A26486; B26486; A28416; A28023; S02292; A30430; S00829; A29874
R.Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988
A.Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)
A.Reference number: A28967; PMID:88144486; PMID:2894031
A.Accession: A28967
A.Molecule type: DNA
A.Cross-references: UNIPROT:P06729; UNIPARC:UPI0000062209; GB:M19806; GB:J03622; GB:J036
R.Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 8718-8722, 1986
A.Title: Molecular cloning of the human T-lymphocyte surface CD2 (T11) antigen.
A.Reference number: A26486; PMID:87041523; PMID:3490670
A.Accession: A26486
A.Molecule type: mRNA
A.Residues: 1-338, 'W', 340, 'QOKTGPCPLPIKDRKCLFQ' <SE1>
A.Cross-references: UNIPARC:UPI000004D168
A.Accession: B26486
A.Molecule type: protein
A.Residues: 25-46 'X', 50 <SE2>
A.Cross-references: UNIPARC:UPI000004D168
R.Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 7256, 1987
A.Reference number: A28416
A.Contents: revision
A.Accession: A28416
A.Molecule type: mRNA
A.Residues: 333-351 <SE3>
A.Cross-references: UNIPARC:UPI0000173764
R.Seed, B.; Aruffo, A.
Proc. Natl. Acad. Sci. U.S.A. 84, 3365-3369, 1987
A.Title: Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a RAP
A.Reference number: A28023; PMID:87204137; PMID:2437578
A.Accession: A28023
A.Molecule type: mRNA
A.Residues: 1-265, 'Q', 267-351 <SE>
A.Cross-references: UNIPARC:UPI0000127347; GB:M16445; NID:G178668; PIND:AAA51738.1; PID:
R.Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; C
Proc. Natl. Acad. Sci. U.S.A. 84, 2941-2945, 1987
A.Title: Molecular cloning and expression of T11 cDNAs reveal a receptor-like structure
A.Reference number: S02292; PMID:87204243; PMID:2883656
A.Accession: S02292
A.Molecule type: mRNA
A.Residues: 1-338, 'W', 340, 'QOKTGPCPLPIKDRKCLFQ' <SA1>
A.Cross-references: UNIPARC:UPI000004D168; GB:M16336; NID:G180093; PIND:AAA51946.1; PID:
A.Accession: A30430
A.Molecule type: protein
A.Residues: 25-43, 152-163 <SA2>
A.Cross-references: UNIPARC:UPI0000173765
R.Liang, G.; Morton, D.; Owen, M.J.; Sewell, W.A.; Brown, M.H.; Mason, D.Y.; Crumpton, M.
EMBO J. 7, 1675-1682, 1988
A.Title: The structure of the human CD2 gene and its expression in transgenic mice.
A.Reference number: S00829; PMID:89005055; PMID:2901953
A.Accession: S00829
A.Molecule type: DNA

```

```

A.Residues: 1-351 <LAN>
A.Cross-references: UNIPARC:UPI0000062209; EMBL:X07871
C.Comment: CD2 is a surface antigen expressed on all peripheral blood T-cells. It appear
or is closely associated with, the erythrocyte receptor.
C.Genetics:
A.Gene: GDB:CD2
A.Cross-references: GDB:118735, OMTM:186990
A.Map position: 1p13.1-1p13.1
A.Introns: 21/1, 128/1, 205/1, 246/1
C.Superfamily: T-cell surface glycoprotein CD2
C.Keywords: glycoprotein; T-cell; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-351/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F:25-206/Domain: extracellular #status predicted <EXT>
F:210-234/Domain: transmembrane #status predicted <TM>
F:237-351/Domain: intracellular #status predicted <INT>
F:89,141,150/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match
Best Local Similarity 7.6%; Score 134; DB 1; Length 351;
Matches 71; Conservative 44; Mismatches 11; Indels 71; Gaps 15;

QY      28 ELVSGVGAATVPPLKS--KRVQVDSIW--TNTPTPLTIOPEGTTIVTQNRNRVD 83
Db      32 ERTGALGQDINDIDPSFGMSDDIDIDIKWEKTSDDKKIKQFRKEKPTF--KSDYTKL-F 87
QY      84 PDGGVSLKSLKLRKNDGSIYVGIYSSLSQGSTOEVYLVHVEHLSKPKVTGLQSNKNG 143
Db      86 KNG--TLKIKHLKTDODIYKVSITDTGKAVLKLFLDKIERSKPKISM----- 137
QY      144 TCV-TNLTCMEHGEVDIYTWKALQAANESHNSILPISNR-----WGSS-DMTFICV 196
Db      138 TCINTTLTCEVNVNGTDPDL-----NLQDGHKLKSGRVTHKWTSLSAFKCT 187
QY      197 ANNPVSKNPS-SPT-----LARKLCBAADDPSSMWLLCLLVPLLSLFLVGL 245
Db      188 AGNKVSKSVSPVSCPEKGLDIYLLIGCGGS-----LLMFVALL 230
QY      246 FLMFLKREROEYIEBKRVDCRSTNICHSGENTGYDTIIPHTNRTILKEDPANT 302
Db      231 VYITRKQKQ-----RSRRNDELETR--AHRVATBERGRKPHQIPASTPQNPATS 279

RESULT 6
S01299
OX-45 membrane glycoprotein precursor - rat
N.Alternate names: MRC OX-45 antigen
C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C.Accession: S01299
R.Killien, N.; Moesner, R.; Arvieux, J.; Willis, A.; Williams, A.F.
EMBO J. 7, 3087-3091, 1988
A.Title: The MRC OX-45 antigen of rat leukocytes and endothelium is in a subset of the i
A.Reference number: S01299; PMID:89030603; PMID:3181129
A.Accession: S01299
A.Molecule type: mRNA
A.Residues: 1-240 <LI>
A.Cross-references: UNIPROT:P10252; UNIPARC:UPI0000127370; EMBL:X13016; NID:G56804; PIND:
C.Superfamily: B-cell surface glycoprotein blast-1
C.Keywords: glycoprotein; membrane protein; surface antigen
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-240/Product: OX-45 membrane glycoprotein #status predicted <MAT>
F:38,97,140,186,203/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match
Best Local Similarity 7.6%; Score 134; DB 2; Length 240;
Matches 48; Conservative 33; Mismatches 104; Indels 10; Gaps 4;

QY      13 ILMOLTGSAAAGPVKELVGSV-----GGAATFP-LNSKVVQVDSIYFWNTPTLTIOPEG 67
Db      11 ILESLLSLVTFQDQSVFNVAITGSNVTLLTLKHPLASIYRLTWLHTTNQKILEFPN 70
QY      68 GTIIVTQNRNRVDPPDGVSLKSLKLRKNDGSIYVGIYSSLSQGSTOEVYLVHVEH 127

```

```
Db      71 GKRTVPESEFKORVDIDKTNGLARITVNSKEDGDIYMMHLHETDQ---WKITMEVYL 127
Qy      128 LSKPKVTWGLQSNKNGTCVTNLTCCEHGEEDVITYWKALGQANESHNGSILPIWMRG 187
Db      128 VSKPAIKIEKTNLUDSCHLRLSCKVE--DQGVDTYTWYEDSGPFPQRNRYVLEIITTH 185
Qy      188 ESDMTFCVARNPV 202
Db      186 NKSTFYTCCVSNPV 200

RESULT 7
NRRTC2
T-cell surface glycoprotein CD2 precursor - rat
N.Alternate names: CD2 antigen; OX-34 antigen
C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text_change 25-Oct-1996
C.Accession: A33071; B27560; A27560; A33346
R.Barclay, A.N.; Williams, A.P.
submitted to the EMBL Data Library, May 1987
A.Reference number: A33071
A.Accession: A33071
A.Molecule type: mRNA
A.Residues: 1-344 <BAR>
A.Cross-references: UNIPARC:UPI0000173766
R.Williams, A.F.; Barclay, A.N.; Clark, S.J.; Paterson, D.J.; Willis, A.C.
J. Exp. Med. 165, 368-380, 1987
A.Title: Similarities in sequences and cellular expression between rat CD2 and CD4 antigen
A.Reference number: A27560; MUID:87139793; PMID:3102667
A.Accession: B27560
A.Molecule type: protein
A.Residues: 'X',24-52,'X',54-55,'X',57-62,93-109,119-150,238-245 <W1>
A.Cross-references: UNIPARC:UPI0000173767; UNIPARC:UPI0000173768; UNIPARC:UPI0000173769;
A.Accession: A27560
A.Molecule type: mRNA
A.Residues: 44-344 <W12>
A.Cross-references: UNIPARC:UPI0000173767; UNIPARC:UPI0000173768; UNIPARC:UPI0000173769;
A.Note: 112-Asn was also found
R.He, Q.; Beyers, A.D.; Barclay, A.N.; Williams, A.F.
Cell 54, 979-984, 1988
A.Title: A role in transmembrane signaling for the cytoplasmic domain of the CD2 T lymph
A.Reference number: A33346; MUID:88327862; PMID:2501293
A.Accession: A33346
A.Molecule type: mRNA
A.Residues: 1-33,'H',35-41 <H1>
A.Cross-references: UNIPARC:UPI000017376C; GB:X05111
C.Keywords: T-cell surface glycoprotein CD2
C.Keywords: glycoprotein; T-cell; transmembrane protein
F.1-22/Domain: signal sequence #status predicted <Sig>
F.23-344/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F.23-199/Domain: extracellular #status predicted <EXT>
F.200-222/Domain: transmembrane #status predicted <TM>
F.229-344/Domain: intracellular #status predicted <INT>
F.99,106,134/Binding site: carbohydrate (Aan) (covalent) #status experimental

Query Match      7.3%; Score 130; DB 1; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.0047;
Matches 65; Conservative 51; Mismatches 112; Indels 62; Gaps 13;

Qy      12 YILMOLVTSAA---SGPYKELVSGVAVTPELKSQVDSIVTFTPTPLVITIQPG 67
Db      10 PLLFSLSSKGDORDBGTWVGALGR-GIMLNIPNFQMTDDIDBVRW-----BR 56
Qy      68 GTIITYONRRERVDPPDGY-----SLKSLKKNDSGIYVGYSSLDQPSIQEV 121
Db      57 GSTLVAEPFRKKPKPLKSGAFETILANGDKIKNLITDDSDGTYNVITYSTNGRIILDKAD 116
Qy      122 LHVYHLTSKPKVTWGLQSNKNGTCV---TNLTCCHEGEEDVITYWKALGQANESHNG 177
Db      117 LRIILEVNSPMTYMEC-SNAITLTCEVLTBGTDEALKIYQKEHL-----RSIRQKT----- 165
Qy      178 SILPIPSRWGESDMTFCVARNPVSRNFSPIILARLCEGAADDPDSSMVLCLLVLPL- 236
```

```
Db      166 ---MSYQWNLNADPKCAVNRVSQSEMEV-----NCPKGIPLTLYIGVSG 212
Qy      237 -LHSHFVLGLFLMFL-----KRERQETYEER-KRVDICRETPNICPS 278
Db      213 GILLVFPFGALFIFCIQKRRKRRRRKGELEIKARMSVVERGPK--PMS 260

RESULT 8
JL0143
antigen BCM1 precursor - mouse
N.Alternate names: CD48 antigen homolog gsp-60; OX45 antigen, Blast-1 antigen
C.Species: Mus musculus (house mouse)
C.Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C.Accession: JL0143; S21319; B47469; B47469
R.Wong, Y.W.; Williams, A.F.; Kingmore, S.F.; Seidlin, M.F.
J. Exp. Med. 171, 2115-2130, 1990
A.Title: Structure, expression, and genetic linkage of the mouse BCM1 (OX45 or Blast-1)
region on mouse chromosome 3.
A.Reference number: JL0143; MUID:90278362; PMID:1693656
A.Accession: JL0143
A.Molecule type: mRNA
A.Residues: 1-240 <NON>
A.Cross-references: UNIPROT:P18181; UNIPARC:UPI0000003BBF; EMBL:X17501; NID:950134; PIDN
R.Wong, Y.W.; Williams, A.F.; Kingmore, S.F.; Seidlin, M.F.
submitted to the EMBL Data Library, June 1990
A.Description: Structure, expression and genetic linkage of the mouse BCM1 (OX45 or Blas
3 region on mouse chromosome 3.
A.Reference number: S21319
A.Accession: S21319
A.Molecule type: protein
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-240 <WON2>
A.Cross-references: UNIPARC:UPI0000003BBF; EMBL:X53526; NID:950138; PIDN:CAA37604.1; PID
R.Cabrero, J.G.; Freeman, G.J.; Lane, W.S.; Reiser, H.
Proc. Natl. Acad. Sci. U.S.A. 90, 3418-3422, 1993
A.Title: Identification, by protein sequencing and gene transfection, of gsp-60 as the m
A.Reference number: A47469; MUID:93234508; PMID:8475091
A.Accession: A47469
A.Molecule type: protein
A.Residues: 74-80 <CAB>
A.Cross-references: UNIPARC:UPI0000176785
A.Experimental source: EL-4 lymphoma cells
A.Note: sequence extracted from NCBI backbone (NCBIP:129658)
A.Accession: B47469
A.Molecule type: protein
A.Residues: 84-98 <CA2>
A.Cross-references: UNIPARC:UPI0000176786
A.Experimental source: EL-4 lymphoma cells
A.Note: sequence extracted from NCBI backbone (NCBIP:129660)
C.Comment: This antigen is widely expressed on leukocytes and is likely to be anchored t
C.Keywords: B-cell surface glycoprotein blast-1
C.Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
F.1-22/Domain: signal sequence #status predicted <Sig>
F.23-217/Product: antigen BCM1 #status predicted <MAT>
F.218-240/Domain: carboxyl-terminal propeptide #status predicted <CPT>
F.32,38,70,136,186,203/Binding site: carbohydrate (Aan) (covalent) #status predicted
F.217/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query Match      7.1%; Score 126.5; DB 2; Length 240;
Best Local Similarity 21.4%; Pred. No. 0.0058;
Matches 52; Conservative 45; Mismatches 125; Indels 21; Gaps 8;

Qy      7 CLTIYIIMOLVGSAAASGPYKELVSGVAVTPEL-KSKVKQVDSIVTFTPTPLVITIQ 65
Db      9 CLVLELLLPDGTGQGHISIPDINATTSNVTLKHKDPLGKYKAITMLATKQKILEYN 68
Qy      66 EGGTIIVTONRRERVDPPDGYSLKSLKKNDSGIYVGYSSLDQPSIQ-EXVLAV 124
Db      69 YNSTITPESERKGVYLEENNNGALHISVNRKEDGTYTMRV---LRTEHMLKITLEV 124
Qy      125 YHLSKPKVTWGLQSNKNGTCVTNLTCCEHGEEDVITYWKALGQANESHNGSILPISW 184
```


Db 125 FDPVPKSEIEINKREASTDSCHLRISC--EYKDQHVDTWTYESSGPPPKSPGYVLDLIY 182
Qy 185 RWGSDMTFICVARNPVSARN-----FSSPI-LARK-LCEGAADPDSSWVLLCLLAVPL 236
Db 183 TPQNSTFYTCQVSNPVSXKDDTYFTLPCLDARSSGCMWA-----TWLVVTLIIHRI 237
Qy 237 LLS 239
Db 238 LLT 240

RESULT 9

JH0395
biliary glycoprotein h precursor - human
C|Species: Homo sapiens (man)
C|Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C|Accession: JH0395
R|Kuraki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A|Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A|Reference number: JH0394; MUID:91222218; PMID:2025273
A|Accession: JH0395
A|Molecule type: mRNA
A|Residues: 1-321 <KUR>
A|Cross-references: UNIPROT:P13688; UNIPARC:UPI000002A625; GB:M69176; NID:G179434; PIDN:
A|Experimental source: leukocyte
C|Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C|Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C|Keywords: glycoprotein; transmembrane protein
F|1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F|1-34/Domain: signal sequence #status predicted <SIG>
F|35-321/Product: biliary glycoprotein h #status predicted <MAT>
F|160-217/Domain: immunoglobulin homology <IMM1>
F|252-301/Domain: immunoglobulin homology <IMM2>

Query Match 7.1%; Score 125.5; DB 2; Length 321;
Best Local Similarity 25.1%; Pred. No. 0.01;
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

Qy 68 GTIIVTQ-----NRNRERDPDGYSLSKLKKNDSGIYVGYSSSL-QQPSFOE 119
Db 81 GYALGTQDATGPANSGEETI-YRNA--SLIQNVTDNDTFYTLQVYKSLDVNEBATGQ 137
Qy 120 YVLHVEHLSPKRYTMGLQSNKNGTCVTNLTCCMEHGBEDVIYTWKALGQANESHNGSI 179
Db 138 F--HYVPELPKPSISNNNSNPVEDKDAVAFTC--EPETQDTTYLMMI-----NNQS 184
Qy 180 LPISMRW-----GESDMTFICVARN-----NPVSRNFPSSPIARKLCEG-----A 218
Db 185 LPVSPRLQLSNGNRITLLSVTRNDTGPYECIEIQNPVSANRSDPV-TLNVYGGDPDPTIS 243
Qy 219 ADD-----PDSSWVLLCLLL--VPLLSLFLVGLFLMFLKREGRQBYIEKKRVDCRPT 272
Db 244 PSDTYRFGANLSISCYAASNPPAQSWSLINTGF-----QQSTQELFLI-----P 287
Qy 273 NI-CPHSGENTY--DTIPHTNRITLK 296
Db 288 NITVNNSSSYTCHANNSTVGCNRTTVK 314

RESULT 10

JH0396
biliary glycoprotein i precursor - human
C|Species: Homo sapiens (man)
C|Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C|Accession: JH0396
R|Kuraki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A|Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A|Reference number: JH0394; MUID:91222218; PMID:2025273
A|Accession: JH0396
A|Molecule type: mRNA
A|Residues: 1-351 <KUR>

A|Cross-references: UNIPROT:P13688; UNIPARC:UPI000002A626; GB:M72238; NID:G179436; PIDN:
A|Experimental source: leukocyte
C|Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C|Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C|Keywords: glycoprotein; transmembrane protein
F|1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F|1-34/Domain: signal sequence #status predicted <SIG>
F|35-351/Product: biliary glycoprotein i #status predicted <MAT>
F|160-217/Domain: immunoglobulin homology <IMM1>
F|252-301/Domain: immunoglobulin homology <IMM2>

Query Match 7.1%; Score 125.5; DB 2; Length 351;
Best Local Similarity 25.1%; Pred. No. 0.011;
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

Qy 68 GTIIVTQ-----NRNRERDPDGYSLSKLKKNDSGIYVGYSSSL-QQPSFOE 119
Db 81 GYALGTQDATGPANSGEETI-YRNA--SLIQNVTDNDTFYTLQVYKSLDVNEBATGQ 137
Qy 120 YVLHVEHLSPKRYTMGLQSNKNGTCVTNLTCCMEHGBEDVIYTWKALGQANESHNGSI 179
Db 138 F--HYVPELPKPSISNNNSNPVEDKDAVAFTC--EPETQDTTYLMMI-----NNQS 184
Qy 180 LPISMRW-----GESDMTFICVARN-----NPVSRNFPSSPIARKLCEG-----A 218
Db 185 LPVSPRLQLSNGNRITLLSVTRNDTGPYECIEIQNPVSANRSDPV-TLNVYGGDPDPTIS 243
Qy 219 ADD-----PDSSWVLLCLLL--VPLLSLFLVGLFLMFLKREGRQBYIEKKRVDCRPT 272
Db 244 PSDTYRFGANLSISCYAASNPPAQSWSLINTGF-----QQSTQELFLI-----P 287
Qy 273 NI-CPHSGENTY--DTIPHTNRITLK 296
Db 288 NITVNNSSSYTCHANNSTVGCNRTTVK 314

RESULT 11

JH0394
biliary glycoprotein g precursor - human
C|Species: Homo sapiens (man)
C|Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C|Accession: JH0394
R|Kuraki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A|Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A|Reference number: JH0394; MUID:91222218; PMID:2025273
A|Accession: JH0394
A|Molecule type: mRNA
A|Residues: 1-417 <KUR>
A|Cross-references: UNIPROT:P13688; UNIPARC:UPI000002A624; GB:M72238; NID:G179436; PIDN:
A|Experimental source: leukocyte
C|Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C|Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C|Keywords: glycoprotein; transmembrane protein
F|1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F|1-34/Domain: signal sequence #status predicted <SIG>
F|35-383/Product: biliary glycoprotein g #status predicted <MAT>
F|160-217/Domain: immunoglobulin homology <IMM1>
F|252-301/Domain: immunoglobulin homology <IMM2>
F|341-398/Domain: immunoglobulin homology <IMM3>

Query Match 7.1%; Score 125.5; DB 2; Length 417;
Best Local Similarity 25.1%; Pred. No. 0.014;
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

Qy 68 GTIIVTQ-----NRNRERDPDGYSLSKLKKNDSGIYVGYSSSL-QQPSFOE 119
Db 81 GYALGTQDATGPANSGEETI-YRNA--SLIQNVTDNDTFYTLQVYKSLDVNEBATGQ 137
Qy 120 YVLHVEHLSPKRYTMGLQSNKNGTCVTNLTCCMEHGBEDVIYTWKALGQANESHNGSI 179
Db 138 F--HYVPELPKPSISNNNSNPVEDKDAVAFTC--EPETQDTTYLMMI-----NNQS 184

Qy 180 LPIBMRW---GESDMPTICVAR-----NPSERNSSPILAKLCEG-----A 218
 Db 185 LPVSPRLQLSNGNRLTLTLLSTRNDTGPCEGCIQNPVANSNDPV-TLNVVYGPPTPTIS 243
 Qy 219 ADD-----PDSSMWLLCLLL--VPLLLSLFVLGLFLMFLKREGEYIEKKRVDCRTRP 272
 Db 244 PSDTYRRGANVLISCYAASNPAPYSLWLNIGTF---QOSTQELFI-----P 287
 Qy 273 NI-CPHSGENTREY--DTIPHTNRITLK 296
 Db 288 NITVNNSSGYTCNANNSTYGCNRTTVK 314

RESULT 12

C30127
 transmembrane carcinoembryonic antigen 3 precursor - human
 N:Alternate names: CD66 splice form BGPC
 C:Species: Homo sapiens (man)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C:Accession: C30127; 152597
 J:Barnett, T.R.; Kreischer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; K
 J. Cell Biol. 108, 267-276, 1989
 A:Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs
 A:Reference number: A92752; MUID:89139550; PMID:2537311
 A:Accession: C30127
 A:Molecule type: mRNA
 A:Residues: 1-464 <BAR>
 A:Cross-references: UNIPROT:Q16170; UNIPARC:UPI0000072309; EMBL:X16356; EMBL:X14784
 R:Watt, S.M.; Fawcett, J.; Murdoch, S.J.; Teixeira, A.M.; Geschelssner, S.E.; Hajibagher
 Blood 84, 200-210, 1994
 A:Title: CD66 identifies the biliary glycoprotein (BGP) adhesion molecule: cloning, expr
 A:Reference number: 152597; MUID:94289702; PMID:8018919
 A:Accession: 152597
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-464 <RES>
 A:Cross-references: UNIPARC:UPI0000072309; GB:S71326; NID:9550030; PIDN:AAB31183.1; PID:
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
 C:Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein
 F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-464/Product: transmembrane carcinoembryonic antigen 3 #status predicted <MAT>
 F:160-217/Domain: immunoglobulin homology <IMM1>
 F:252-301/Domain: immunoglobulin homology <IMM2>
 F:341-398/Domain: immunoglobulin homology <IMM3>
 F:424-455/Domain: transmembrane #status predicted <TM>
 F:104, 111, 115, 152, 182, 197, 208, 224, 232, 254, 274, 288, 292, 302, 309, 345, 351, 363, 378, 405/Bindin

Query Match 7.1%; Score 125.5; DB 2; Length 464;
 Best Local Similarity 25.1%; Pred. No. 0.016;
 Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;
 Qy 68 GTTIVTQ-----NRNRRDPFDGYSILKSKKNDSGIYGYSSSL-QQPSIQE 119
 Db 81 GYAIGTQATGPGPANSGRETI-YFNA--SLIONTQNDTGYTYLQVKSIDLVNEEAQO 137
 Qy 120 YLVHYEHLSPKPYTMGLQSNNGGTCVNTLTCMEHGEEDVYTKALGQANESHNSI 179
 Db 138 F-HVPEPLPKPSSISNNSNPVEDKDAVAFTC--EPETODTYLWMT-----NNOS 184
 Qy 180 LPIBMRW---GESDMPTICVAR-----NPSERNSSPILAKLCEG-----A 218
 Db 185 LPVSPRLQLSNGNRLTLTLLSTRNDTGPCEGCIQNPVANSNDPV-TLNVVYGPPTPTIS 243
 Qy 219 ADD-----PDSSMWLLCLLL--VPLLLSLFVLGLFLMFLKREGEYIEKKRVDCRTRP 272
 Db 244 PSDTYRRGANVLISCYAASNPAPYSLWLNIGTF---QOSTQELFI-----P 287
 Qy 273 NI-CPHSGENTREY--DTIPHTNRITLK 296
 Db 288 NITVNNSSGYTCNANNSTYGCNRTTVK 314

RESULT 13

A32164
 biliary glycoprotein 1 precursor, splice form a - human
 N:Alternate names: transmembrane carcinoembryonic antigen 1 (TM1-CEA); transmembrane car
 N:Contents: biliary glycoprotein 1, splice form b; biliary glycoprotein 1, splice form x
 C:Species: Homo sapiens (man)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C:Accession: A32164; B30127; A48078; S45664; S65939; A30847; G44476
 R:Hindoda, Y.; Neumaier, M.; Hefsta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefsta,
 Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989
 A:Reference number: A32164
 A:Contents: erratum
 A:Accession: A32164
 A:Molecule type: mRNA
 A:Residues: 1-526 <HIN>
 A:Cross-references: UNIPROT:P13688; UNIPARC:UPI0000127483; GB:J03858; NID:9179439; PIDN:
 R:Hindoda, Y.; Neumaier, M.; Hefsta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefsta,
 Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988
 A:Title: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure of
 A:Reference number: A94206; MUID:88320555; PMID:2457922
 A:Contents: annotation
 A:Note: the sequence shown in this reference has been completely corrected in reference
 R:Barnett, T.R.; Kreischer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; K
 U. Cell Biol. 108, 267-276, 1989
 A:Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs
 A:Reference number: A92752; MUID:89139550; PMID:2537311
 A:Accession: A30127
 A:Molecule type: mRNA
 A:Residues: 1-526 <BAR1>
 A:Cross-references: UNIPARC:UPI0000127483; EMBL:X16354; NID:937197; PIDN:CAA34404.1; PID
 A:Experimental source: splice form a
 A:Accession: B30127
 A:Molecule type: mRNA
 A:Residues: 1-319, 'D', 417-526 <BAR2>
 A:Cross-references: UNIPARC:UPI000079D2E; EMBL:X14831; NID:937199; PIDN:CAA32940.1; PID
 A:Experimental source: splice form b
 R:Barnett, T.R.; Drake, L.; Pickle II, W.
 Mol. Cell. Biol. 13, 1273-1282, 1993
 A:Title: Human biliary glycoprotein gene: characterization of a family of novel alternat
 A:Reference number: A48078; MUID:93140765; PMID:8423792
 A:Accession: A48078
 A:Molecule type: mRNA
 A:Residues: 124-141, 'H', 417-526 <BAR3>
 A:Cross-references: UNIPARC:UPI0000173868; GB:M76742; NID:9179480; PIDN:AA57142.1; PID:
 A:Experimental source: splice form x
 A:Note: sequence extracted from NCBI backbone (NCBI:123602, NCBI:P.123606)
 A:Note: neither the complete nucleic acid sequence nor the complete translation are show
 R:Hauck, W.; Nedellec, P.; Turbide, C.; Scanniers, C.P.; Barnett, T.R.; Beauchemin, N.
 Eur. J. Biochem. 223, 529-541, 1994
 A:Title: Transcriptional control of the human biliary glycoprotein gene, a CEA gene fami
 A:Reference number: S45664; MUID:94333343; PMID:8055923
 A:Accession: S45664
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-21 <HNU>
 A:Cross-references: UNIPARC:UPI00006B9AC; EMBL:X67277; NID:929447; PIDN:CAA47694.1; PID
 R:Nedellec, P.; Turbide, C.; Beauchemin, N.
 Eur. J. Biochem. 231, 104-114, 1995
 A:Title: Characterization and transcriptional activity of the mouse biliary glycoprotein
 A:Reference number: S65939; MUID:95354678; PMID:7628460
 A:Accession: S65939
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-21 <NED>
 A:Cross-references: UNIPARC:UPI00006B9AC; EMBL:X67277; NID:929447; PIDN:CAA47694.1; PID
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
 R:Khan, W.N.; Fraenkel, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
 Genomics 14, 384-390, 1992
 A:Title: Identification of three new genes and estimation of the size of the carcinoemb
 A:Reference number: A44476; MUID:93052339; PMID:1427854
 A:Contents: annotation; alignment of related sequences

A:Gene: GDB:BCP
 A:Cross-references: GDB:127992; OMIM:109770
 A:Map position: 19q13.2-19q13.2
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal
 C:Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein
 F:1-138/Domain: signal sequence #status predicted <SIG>
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-526/Domain: extracellular #status predicted <EXT>
 F:35-319,'V',417-526/Product: biliary glycoprotein 1, splice form a #status predicted <MAT>
 F:35-141,'H',417-526/Product: biliary glycoprotein 1, splice form b #status predicted <M>
 F:160-217/Domain: immunoglobulin homology <IMM1>
 F:252-301/Domain: immunoglobulin homology <IMM2>
 F:341-398/Domain: immunoglobulin homology <IMM3>
 F:425-454/Domain: transmembrane #status predicted <TM>
 F:455-526/Domain: intracellular #status predicted <INT>
 F:104,111,115,152,182,197,208,224,232,254,274,286,292,302,309,345,351,363,378,405,475/BI

Query Match 7.1%; Score 125.5; DB 1; Length 526;
 Best Local Similarity 25.1%; Pred. No. 0.018;
 Matches 67; Conservative 36; Mismatches 99; Indels 71; Gaps 17;

Qy 68 GTTIVTQ-----NRNRVDFPDGYSLSKSKKNDGGIYVGIYSSSL-QQPSFOE 119
 Db 81 GYALGTQCATPGPANSGRETT-YFNA--SLAIQNTQNDTGFYTLQVTKSDLVNKEATGQ 137
 Qy 120 YLVHYEHLSKPKYTMGLQSNKNGCVNLTCCMHGSEDDVITYMKALGQANESHNSI 179
 Db 138 F--HYPELPKPSISSSNSNPVEDKAVAFTC--BPETQDTTYLWMT-----NNQS 184
 Qy 180 LPISMRW-----GESDMEFICVAR-----NPVSRNFPILARKLCEG-----A 218
 Db 185 LPVSPRLQLSNGNRITLTILSTRNDTGYECEIQNPVANSNDPV-TLNTVYGGPDTPTIS 243
 Qy 219 ADD---PDSSWVLLCLLL--VPLLISLFLVGLFWLKRROEYIEKKRVDCRETP 272
 Db 244 PSDTYRREGANILSLSCVAASNPAPQYSLWINGTF---QOSTQELFI-----P 287
 Qy 273 NI-CPHSGENTFY--DTIPHNRTILK 296
 Db 288 NITVNSGTYTCHANNSTYGCNRTTVK 314

RESULT 14
 A27681
 nonspecific cross-reacting antigen precursor - human
 N:Alternate names: NCA; TEX/NCA
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1989 #sequence revision 16-Sep-1992 #text change 09-Jul-2004
 C:Accession: A26902; A29875; A27681; B31037; A29918; A27709; A36271; C26414; E44476; F44
 R:Okawa, S.; Kosaki, G.; Nakazato, H.
 Biochem. Biophys. Res. Commun. 146, 464-469, 1987
 A:Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gene
 A:Reference number: A26902; MUID:87298464; PMID:3618991
 A:Accession: A26902
 A:Molecule type: DNA
 A:Residues: 1-141 <OK>
 A:Cross-references: UNIPROT:Q13774; UNIPARC:UPI000072416; GB:M17082; NID:G180230; PIDN:
 R:Thompson, J.A.; Pandey, H.; Paxton, R.J.; Shively, L.; Padma, A.; Stimmer, R.L.; Todd, C
 Proc. Natl. Acad. Sci. U.S.A. 84, 2965-2969, 1987
 A:Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene faml
 A:Reference number: A29875; MUID:87204248; PMID:3033672
 A:Accession: A29875
 A:Molecule type: DNA
 A:Residues: 23-141 <THO>
 A:Cross-references: UNIPARC:UPI0000177070; GB:M16337
 A:Note: the authors translated the codon ACT for residue 64 as Tyr
 R:Kawaguchi, Y.; Okawa, S.; Matsumoto, Y.; Kosaki, G.; Nakazato, H.
 Biochem. Biophys. Res. Commun. 150, 89-96, 1988
 A:Title: Primary structure of nonspecific cross-reacting antigen (NCA), a member of carc
 A:Reference number: A27681; MUID:8810638; PMID:3337731
 A:Accession: A27681
 A:Molecule type: mRNA

A:Residues: 1-238,'V',240-344 <RAW>
 A:Cross-references: UNIPARC:UPI000012748C; GB:M18728; NID:G189084; PIDN:AAA5907.1; PID:
 R:Barrett, T.; Goebel, S.J.; Nothdurft, M.A.; Eiting, J.J.
 Genome 3, 59-66, 1988
 A:Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and C
 A:Reference number: A31037; MUID:89122014; PMID:3220478
 A:Accession: B31037
 A:Molecule type: mRNA
 A:Residues: 1-137,'L',139-344 <BAR>
 A:Cross-references: UNIPARC:UPI000016ADC6; GB:M29541; NID:G189103; PIDN:AAA59915.1; PID:
 A:Note: the authors translated the codon TTG for residue 138 as Phe
 R:Neumaier, M.; Zimmermann, W.; Shively, L.; Hinoda, Y.; Rieger, A.D.; Shively, J.E.
 J. Biol. Chem. 263, 3202-3207, 1988
 A:Title: Characterization of a cDNA clone for the nonspecific cross-reacting antigen (NC
 A:Reference number: A29918; MUID:88139389; PMID:2830274
 A:Accession: A29918
 A:Molecule type: mRNA
 A:Residues: 1-344 <NEU>
 A:Cross-references: UNIPARC:UPI000006DF42; GB:M18216; GB:U03550; NID:G178690; PIDN:AAA51
 R:Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwaiblmair, H.; von Kleist, S.
 Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988
 A:Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and ind
 A:Reference number: A27709; MUID:88268882; PMID:3390172
 A:Accession: A27709
 A:Molecule type: protein
 A:Residues: 35-95;99-120,123-138;149-151,'X',153-162;166,'X',168-172,'X',174-193;231-235
 A:Cross-references: UNIPARC:UPI0000177071; UNIPARC:UPI0000177072; UNIPARC:UPI0000177073;
 078; UNIPARC:UPI0000177079; UNIPARC:UPI000017707A
 R:Hefta, S.A.; Paxton, R.J.; Shively, J.E.
 J. Biol. Chem. 265, 8618-8626, 1990
 A:Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspeci
 A:Reference number: A36271; MUID:90256782; PMID:2341397
 A:Accession: A36271
 A:Molecule type: protein
 A:Residues: 35-42;44-53;55-80;83-134;139-160;166-172;174-180;191-194,204-224;233-308;310
 A:Cross-references: UNIPARC:UPI000017707B; UNIPARC:UPI000017707C; UNIPARC:UPI000017707D;
 082; UNIPARC:UPI0000177083; UNIPARC:UPI0000177084
 R:Paxton, R.J.; Mosser, G.; Pandey, H.; Lee, T.D.; Shively, J.E.
 Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
 A:Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation
 A:Reference number: A26414; MUID:87147209; PMID:3469650
 A:Accession: C26414
 A:Molecule type: protein
 A:Residues: 35-69 <PAX>
 A:Cross-references: UNIPARC:UPI0000177085
 R:Khan, W.N.; Fraengely, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarettoem, S.
 Genome 14, 384-390, 1992
 A:Title: Identification of three new genes and estimation of the size of the carcinoemb
 A:Reference number: A44476; MUID:93052339; PMID:1427854
 A:Accession: B44476
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 35-141 <KHA>
 A:Cross-references: UNIPARC:UPI0000177086
 A:Accession: P44476
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 35-137,'L',139-141 <KH2>
 A:Cross-references: UNIPARC:UPI0000177086
 C:Comment: This protein appears to be processed at the carboxyl terminus and anchored th
 C:Genetics:
 A:Gene: GDB:NCA
 A:Cross-references: GDB:120221; OMIM:163980
 A:Map position: 19q13.2-19q13.2
 A:Introns: 22/1
 A:Note: the list of introns may be incomplete
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
 C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphati
 F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>
 F:160-217/Domain: immunoglobulin homology <IMM1>
 F:252-301/Domain: immunoglobulin homology <IMM2>

F:321-344/Domains: carboxyl-terminal propeptide #status predicted <CP>
 F:104,111,115,152,173,197,224,256,274,288,292/Binding site: carboxylate (Asn) (covalent)
 F:309/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form)

Query Match	7.0%;	Score 124.5;	DB 2;	Length 344;
Best Local Similarity	22.4%;	Pred. No. 0.013;		
Matches 75;	Conservative 35;	Mismatches 118;	Indels 107;	Gaps 16;

```

Oy      53 WTENTPLATVIO-----PEGGTII-----VTONR-----ANERVD-----      82
Db      28 MNPPPTAKTITESTEPNNAEGKEVILLANHLPNRIGYMYKKEKRDGNSLIYGIQTQ      87
Oy      83 --FPDGGY-----SLKSLKLNKDSGIYVIGYSSSL--QOESTOEYVLAVYEHLIS      129
Db      88 QATPBPASAGRETIYPNMSLLIQNVTONGTFTLLQVITSDLVINEEATGTF--HYVPELP      145
Oy      130 KPRTVMGLQSNKNGTCVTNLTCMEHGEEDVITYMKALQOANESHNGSLTPISWEN--      186
Db      146 KPSISSNNSNPVEDKDAVAFTC--BPEVQNTYTLMMV-----NGQSLPVPSPRLQLS      194
Oy      187 -GESMTPT-----CYARNVSNRSPSPILARKLC-----EGAADPPDS      225
Db      195 NGNMNTLTLLSVKRNDAGSYECHIQNPASANRSPPTLNLVYGPDGPTISPSKANYRGEN      254
Oy      226 WVLTLCLL--VPLLLSLFVLGLFLMWLKKEROREBEYIEKKRVDCRETPI-----      274
Db      255 IMLSLCHAASNPPAQYSWPFTNGTF---QOSTQELFI-----PNTIVNNSGSYM      298
Oy      275 CPHSGENTEYDPTIPTNRTILKEDPANTVYSYVEI      309
Db      299 COAHNSATGARTTYTMTIVSGAPVLSAVATYGI      333

```

RESULT 15

S34338
biliary glycoprotein F - mouse
N:Alternate names: mouse hepatitis virus (MHV) receptor glycoprotein
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
A:Accession: S34338, JCI510, A41093
R:Huang, D.C.; Huang, X.F.; Novel, M.; Novel, G.
Submitted to the EMBL Data Library, July 1992
A:Description: A Clp-family gene present on the lactose-protease plasmid of *Lactococcus*
A:Reference numbers: S34338
A:Accession: S34338
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-521 <HND>
R:Cross-references: UNIPROT:O61352; UNIPARC:UPI00000283F8; EMBL:X67281; NID:g312585; PIRCE:g312585; R:McNally, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A:Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprotein
A:Reference number: JCI505, MUID:93273228; PMID:8500759
A:Accession: JCI510
A:Molecule type: mRNA
A:Residues: 1-81, 'O', '83-141', 'P', '143-521' <MCG>
R:Cross-references: UNIPARC:UPI0000177068; GB:X67281
R:Williams, R.K.; Jiang, G.S.; Holmes, K.V.
Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991
A:Title: Receptor for mouse hepatitis virus is a member of the carcinoembryonic antigen
A:Reference number: A41093; MUID:91288498; PMID:1648219
A:Accession: A41093
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 35-59 <WIL>
R:Cross-references: UNIPARC:UPI0000177069
C:Comment: This protein is expressed at the cell surface and plays a determinant role in
C:Genetics:
A:Gene: Bgpf
A:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal
F11-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F:160-219/Domain: immunoglobulin homology <IMM1>
F:254-303/Domain: immunoglobulin homology <IMM2>
F:339-396/Domain: immunoglobulin homology <IMM3>
F:87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (C

Query Match	6.9%;	Score 122.5;	DB 2;	Length 521;
Best Local Similarity	22.4%;	Pred. No. 0.032;		
Matches	47;	Conservative	32;	Mismatches 70;
				Indels 61;
				Gaps 8;

[illegible]

Search completed: December 16, 2005, 10:45:35
Job time : 55 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rnp**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 10:34:22 ; Search time 229 Seconds
(without alignments)
1032.105 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 1772
Sequence: 1 MAGSPCTCLTIYIMQLTGS.....PHSLTMPDPRLPAYENVIT 335

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 1500 summaries

Database : UniProt_05.80:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1772	100.0	335	1 SLAF7_HUMAN	Q9nq25 homo sapien
2	815	46.0	333	1 SLAF7_MOUSE	Q8bhk6 mus musculu
3	362.5	20.5	328	2 015430_HUMAN	Q91430 homo sapien
4	362.5	20.5	329	2 Q92178_MOUSE	Q92178 mus musculu
5	359	20.3	339	2 Q8W18_HUMAN	Q8W18 homo sapien
6	358.5	20.2	345	2 Q6N2B6_MOUSE	Q6N2B6 mus musculu
7	358	20.2	345	2 Q9V1B8_HUMAN	Q9V1B8 homo sapien
8	354.5	20.0	328	2 Q6FHA8_HUMAN	Q6FHA8 homo sapien
9	354.5	20.0	649	2 Q7TMP7_MOUSE	Q7TMP7 mus musculu
10	354.5	20.0	654	1 L19_MOUSE	Q01965 mus musculu
11	353.5	19.9	544	2 Q8C2D4_MOUSE	Q8C2D4 mus musculu
12	353.5	19.9	654	2 Q4VBG4_MOUSE	Q4VBG4 mus musculu
13	330.5	18.7	289	2 Q96A28_HUMAN	Q96A28 homo sapien
14	329	18.6	538	2 Q8C9E4_MOUSE	Q8C9E4 mus musculu
15	328.5	18.5	289	2 Q5TRR0_HUMAN	Q5TRR0 homo sapien
16	318	17.9	655	1 L19_HUMAN	Q9hdg7 homo sapien
17	315.5	17.8	331	2 Q5TAT3_HUMAN	Q5TAT3 homo sapien
18	311	17.6	285	2 Q8BTK0_MOUSE	Q8BTK0 mus musculu
19	311	17.6	332	1 SLAF6_HUMAN	Q96d33 homo sapien
20	311	17.6	20	2 Q5TAS4_MOUSE	Q5TAS4 mus musculu
21	311	17.6	602	2 Q5VYH7_HUMAN	Q5VYH7 homo sapien
22	308.5	17.4	285	2 Q8VE93_MOUSE	Q8VE93 mus musculu
23	308	17.4	280	2 Q95660_HUMAN	Q95660 homo sapien
24	307.5	17.4	285	2 Q9D780_MOUSE	Q9D780 mus musculu
25	304	17.2	272	2 Q9U1B7_HUMAN	Q9U1B7 homo sapien
26	290.5	16.4	241	2 Q9U1B6_HUMAN	Q9U1B6 homo sapien
27	283.5	15.9	526	2 Q5VYH9_HUMAN	Q5VYH9 homo sapien
28	281	15.9	197	2 Q9UIT7_HUMAN	Q9UIT7 homo sapien
29	260	14.7	197	2 Q5BKU7_HUMAN	Q5BKU7 homo sapien
30	250.5	14.1	214	2 Q5H9R1_HUMAN	Q5H9R1 homo sapien
31	238.5	13.5	424	2 Q5VYH8_HUMAN	Q5VYH8 homo sapien

32	225.5	12.7	351	1 SLAF6_MOUSE	Q9et39 mus musculu
33	214	12.1	167	2 Q5RB10_PONPY	Q5RB10 pongo pygma
34	213.5	12.0	270	2 Q5VY11_HUMAN	Q5VY11 homo sapien
35	204.5	11.5	338	2 Q55MM6_BOVIN	Q55MM6 bos taurus
36	199.5	11.3	221	2 Q5TAS6_HUMAN	Q5TAS6 homo sapien
37	187.5	10.6	336	2 Q9GJ73_SAGOR	Q9GJ73 saginus oe
38	186	10.5	343	1 SLAF1_MOUSE	Q9nq24 mus musculu
39	186	10.5	343	2 Q544K1_MOUSE	Q544K1 mus musculu
40	183.5	10.4	335	2 Q96QR3_HUMAN	Q96QR3 homo sapien
41	183	10.3	266	2 Q9UC08_MOUSE	Q9UC08 mus musculu
42	182.5	10.3	335	1 SLAF1_HUMAN	Q13291 homo sapien
43	182.5	10.3	335	2 Q5M172_HUMAN	Q5M172 homo sapien
44	178	10.0	278	1 SLAF8_MOUSE	Q9d392 mus musculu
45	177	9.7	329	2 Q5VY15_HUMAN	Q5VY15 homo sapien
46	170	9.6	365	2 Q5VY12_HUMAN	Q5VY12 homo sapien
47	167.5	9.5	342	1 SLAF1_CANIFA	Q95mm9 canis fam11
48	163.5	9.2	370	1 CD244_HUMAN	Q92298 homo sapien
49	163.5	9.2	370	2 Q5VY17_HUMAN	Q5VY17 homo sapien
50	160.5	9.1	338	2 Q5MB93_BOVIN	Q5mb93 bos taurus
51	159.5	9.0	329	2 Q5W7A8_XENLA	Q5w7a8 xenopus lae
52	158.5	8.9	326	2 Q8CAU4_MOUSE	Q8CAU4 mus musculu
53	150.5	8.5	285	1 SLAF8_HUMAN	Q9P0V8 homo sapien
54	145.5	8.2	416	2 Q8N7J3_HUMAN	Q8N7J3 homo sapien
55	145.5	8.2	416	2 Q67IP8_HUMAN	Q67IP8 homo sapien
56	145	8.2	211	2 Q6ZRL7_HUMAN	Q6ZRL7 homo sapien
57	144	8.1	344	1 CD2_MOUSE	Q8ZT17 mus musculu
58	144	8.1	344	2 Q9R201_MOUSE	Q9R201 mus musculu
59	144	8.1	344	2 Q5SRG1_MOUSE	Q5SRG1 mus musculu
60	142	8.0	207	2 Q9HBR9_HUMAN	Q9hbr9 homo sapien
61	142	8.0	367	2 Q6ZRL4_HUMAN	Q6ZRL4 homo sapien
62	141	8.0	291	2 Q5BKQ7_XENTR	Q5BKQ7 xenopus tro
63	139	7.8	347	2 Q4SQQ1_TETNG	Q4sqq1 tetradon n
64	138.5	7.8	340	2 Q764N3_PIG	Q764n3 sus scrofa
65	138.5	7.8	413	2 Q64OR3_MOUSE	Q64OR3 mus musculu
66	137.5	7.8	345	2 Q6SZG3_PANTR	Q6szg3 pan troglod
67	136.5	7.7	351	2 Q53F96_HUMAN	Q53f96 homo sapien
68	135.5	7.6	289	2 Q6QX36_MOUSE	Q6qx36 mus musculu
69	135	7.6	302	2 Q4SOP0_TETNG	Q4sop0 tetradon n
70	134.5	7.6	198	2 Q6UWQ1_HUMAN	Q6Uwq1 homo sapien
71	134	7.6	240	1 CD48_RAT	P10252 rattus norv
72	133.5	7.5	351	2 CD2_HUMAN	P06729 homo sapien
73	133.5	7.5	394	2 Q9E0K9_RAT	Q9e0k9 rattus norv
74	133	7.5	422	2 Q502A9_BRARE	Q502a9 brachydanio
75	132.5	7.5	198	2 Q5JRO9_HUMAN	Q5jro9 homo sapien
76	132.5	7.5	372	1 QCAR_BRARE	Q9ly50 brachydanio
77	131	7.4	344	2 Q510M6_RAT	Q510m6 rattus norv
78	131	7.4	525	2 Q5R9N6_PONPY	Q5r9n6 pongo pygma
79	130	7.3	249	2 Q5BD99_BOVIN	Q5bd99 bos taurus
80	130	7.3	344	1 CD2_RAT	P08921 rattus norv
81	128.5	7.2	253	2 Q28753_9CETA	Q28753 ovis sp. 1f
82	128	7.2	193	2 Q6P2J4_HUMAN	Q6p2j4 homo sapien
83	126.5	7.1	240	1 CD48_MOUSE	P18181 mus musculu
84	126.5	7.1	240	2 Q545F2_MOUSE	Q545f2 mus musculu
85	126.5	7.1	240	2 Q6P905_MOUSE	Q6p905 mus musculu
86	126	7.1	318	2 Q4T2U2_TETNG	Q4t2u2 tetradon n
87	125.5	7.1	368	2 Q5UB49_HUMAN	Q5ub49 homo sapien
88	125.5	7.1	464	2 Q16170_HUMAN	Q16170 homo sapien
89	125.5	7.1	468	2 Q96CA7_HUMAN	Q96ca7 homo sapien
90	125.5	7.1	526	1 Q5AM1_HUMAN	P13688 homo sapien
91	125	7.1	344	2 Q6S262_PAPAN	Q6s262 papio ambl
92	125	7.1	373	2 Q7KPY5_HUMAN	Q7kpy5 homo sapien
93	124.5	7.0	344	1 Q53X77_HUMAN	P40109 homo sapien
94	124.5	7.0	344	2 Q53X77_HUMAN	Q53x77 homo sapien
95	124.5	7.0	344	2 Q13854_HUMAN	Q13854 homo sapien
96	124.5	7.0	461	2 Q13854_HUMAN	Q13854 homo sapien
97	124	7.0	345	2 Q6S258_MACAS	Q6s258 macaca assea
98	123.5	7.0	227	2 Q28754_9CETA	Q28754 ovis sp. 1f
99	123	6.9	140	2 Q8BFV0_MOUSE	Q8bfv0 m mus muscu
100	123	6.9	311	1 CD244_RAT	Q911m2 rattus norv
101	123.5	6.9	458	2 Q61351_MOUSE	Q61351 mus musculu
102	122.5	6.9	521	2 Q61352_MOUSE	Q61352 mus musculu
103	122	6.9	326	2 Q9N16_PAPHA	Q9n16 papio hamad
104	122	6.9	334	2 Q6S256_MACNE	Q6s256 macaca nemoe

105	122	6.9	341	2	Q6SZ57_MACAR	Q6Z57 macaca arct	178	101	5.7	432	2	Q6DD57_XENIA	Q6dde7 xenopus lae
106	121.5	6.9	377	2	Q80V04_MOUSE	Q80v04 mus musculu	179	101	5.7	436	2	Q6VAN6_BOVIN	Q6van6 bos taurus
107	121.5	6.9	536	2	Q8BjE2_MOUSE	Q8bje2 mus musculu	180	101	5.7	436	2	Q6VAN6_BOVIN	Q6van6 bos taurus
108	121	6.8	351	1	CD2_MACFA	Q6Z57 macaca fasc	181	101	5.7	1637	2	Q6LOY1_PICTO	P42292 gallus gall
109	119.5	6.7	332	2	Q91B08_SPERC	Q91b08 spheeroides	182	100.5	5.7	259	2	Q9CF44_LACLA	Q6LOY1 pictophilus
110	119.5	6.7	365	1	Q6XAR_HUMAN	P78310 homo sapien	183	100.5	5.7	280	2	Q8UW12_ICTPU	Q9CF44 lactococcus
111	119.5	6.7	365	1	Q6XAR_PONY	Q57764 pongo pygma	184	100.5	5.7	323	2	Q9BDM2_CBRAR	Q8uwl2 ictalurus p
112	118.5	6.7	520	2	Q925P2_MOUSE	Q925p2 mus musculu	185	100.5	5.7	340	2	Q9BDM2_CBRAR	Q9bmd2 ceropithec
113	118	6.7	347	2	Q5XG4_XENIR	Q5Xg4 xenopus tro	186	100.5	5.7	555	2	CD16_CARAU	Q9304 carabius a
114	116.5	6.6	319	1	Q6PA3_HUMAN	Q9795 homo sapien	187	100	5.6	324	2	Q6UHT1_ASF	Q6ht1 african swi
115	116.5	6.6	319	2	Q5VZP6_HUMAN	Q5vzp6 homo sapien	188	99.5	5.6	318	2	Q5SNP8_BRAR	Q5snp8 brachydano
116	116.5	6.6	350	2	Q6SZ59_CERTO	Q6sz59 cercocebus	189	99.5	5.6	323	2	Q9BDM9_MACNE	Q9bdm9 macaca neme
117	115	6.5	351	2	Q6SZ60_MACMU	Q6sz60 macaca mula	190	99.5	5.6	335	2	Q9YGV5_CHICK	Q9ygv5 gallus gall
118	115	6.5	357	2	Q90ZL5_ANAPL	Q90z15 anas platyr	191	99.5	5.6	658	2	Q75UX6_DICDI	Q75ux6 dictyosteli
119	114.5	6.5	430	2	Q8N4F1_HUMAN	Q8n4f1 homo sapien	192	99.5	5.6	693	2	Q559P5_DICDI	Q559p5 dictyosteli
120	114.5	6.5	702	1	Q6ZAM5_HUMAN	P06731 homo sapien	193	99.5	5.6	3493	2	Q4RJ20_TETNG	Q4rj20 tetradon n
121	114.5	6.5	702	2	Q53G30_HUMAN	Q53g30 homo sapien	194	99	5.6	417	1	PVR_CERAR	P32506 ceropithec
122	114.5	6.5	702	2	Q8N4D0_HUMAN	Q8n4d0 homo sapien	195	98.5	5.6	229	2	Q8BNV8_MOUSE	Q8bnv8 mus musculu
123	114	6.4	239	2	Q4SPD7_TETNG	Q4spd7 tetradon n	196	98.5	5.6	348	2	Q965T1_HUMAN	Q96st1 homo sapien
124	113.5	6.4	454	2	Q91W54_MOUSE	Q91w54 mus musculu	197	98.5	5.6	404	2	Q9GZZ9_HUMAN	Q9gzz9 homo sapien
125	113.5	6.4	521	1	Q6ZAM1_MOUSE	P31809 mus musculu	198	98.5	5.6	526	1	Q6ZAM1_MOUSE	Q9gzz9 homo sapien
126	113.5	6.4	521	2	Q925P3_MOUSE	Q925p3 mus musculu	199	98.5	5.6	733	2	Q8S0B3_TRIVU	P18892 bos taurus
127	113	6.4	373	2	Q9H6B4_HUMAN	Q9h6b4 homo sapien	200	98.5	5.6	1227	2	Q21038_CAEEL	Q8ag83 trichoburus
128	113	6.4	621	2	Q811T7_MOUSE	Q811t7 mus musculu	201	98.5	5.6	16215	2	Q9NFS3_DROME	Q21038 caenorhabdi
129	112.5	6.3	328	1	Q5IG2_MOUSE	Q94109 mus musculu	202	98	5.5	347	1	CD2_HORSE	Q9nfs3 drosophila
130	111.5	6.3	431	2	Q5DX21_HUMAN	Q5dx21 homo sapien	203	98	5.5	484	2	Q6BEO0_XENIA	P78324 h tyrosine
131	111	6.3	372	2	Q8K1G0_RAT	P33705 canis famli	204	98	5.5	503	1	Q4SFC6_TETNG	Q4sf6 tetradon n
132	110.5	6.2	463	1	CD4_CANPA	Q4wct2 xenopus sp.	205	98	5.5	1209	2	Q4SFS8_TETNG	Q4sf8 tetradon n
133	110.5	6.2	466	2	Q4WCT2_9PIPI	Q8hxg6 sus scrofa	206	98	5.5	581	2	Q4SFS8_TETNG	P51202 rattus norv
134	110	6.2	539	2	Q8HXOC_PIG	Q8lbd1 canis famli	207	98	5.5	428	2	Q5U2P2_RAT	Q5u2p2 rattus norv
135	109.5	6.2	432	2	Q61BR1_CANPA	Q8mv3 bos taurus	208	97.5	5.5	474	2	Q7Q815_ANOGA	Q7q815 anopheles g
136	109	6.2	316	2	Q8V98_MOUSE	Q8mv3 bos taurus	209	97.5	5.5	562	2	Q6NPO4_DROME	Q6npo4 drosophila
137	108.5	6.1	316	2	Q7TPB4_RAT	Q7tpb4 rattus norv	210	97.5	5.5	591	2	Q9VA4_DROME	Q9va4 drosophila
138	108	6.1	349	2	Q7QUG1_ANOGA	Q7q1g1 anopheles g	211	97.5	5.5	2772	2	Q9VA4_DROME	Q9va4 drosophila
139	107	6.0	399	2	Q9ESSE_MOUSE	Q9esse mus musculu	212	97.5	5.5	2776	2	Q869A0_DROME	Q869a0 drosophila
140	107	6.0	752	2	Q9YX64_HYDAT	Q9yx64 hydra attenu	213	97.5	5.5	2894	2	Q7KRX2_DROME	Q7kxr2 drosophila
141	106.5	6.0	4138	2	Q811Y3_PLAAT	Q811y3 plasmodium	214	97.5	5.5	2898	2	Q688Z9_DROME	Q688z9 drosophila
142	106.5	6.0	897	2	Q9J1Y3_ARATH	Q9j1y2 arabidopsis	215	97.5	5.5	452	2	Q5N0Y6_SYNP6	Q5n0y6 synecococc
143	106	6.0	323	2	Q6FHB1_HUMAN	Q6fht1 homo sapien	216	97	5.5	484	2	Q26475_SCHAM	Q26475 schistocerc
144	105.5	6.0	329	1	CD86_HUMAN	P42081 homo sapien	217	97	5.5	773	1	Q60HT1_EPTBU	P01832 oryctolagus
145	105.5	6.0	329	2	Q6GTE4_HUMAN	Q6gte4 homo sapien	218	97	5.5	347	2	Q60HT1_EPTBU	Q6ht1 eptatretus
146	105.5	6.0	335	2	Q9PWR4_CHICK	Q9pwr4 gallus gall	219	96.5	5.4	368	2	Q6RWT3_BOVIN	Q6rwt3 bos taurus
147	105.5	6.0	398	2	Q9J1E1_MOUSE	Q9j1e1 mus musculu	220	96.5	5.4	375	2	Q6RWT4_BOVIN	Q6rwt4 bos taurus
148	105.5	6.0	245	2	Q566N1_BRARE	Q566n1 brachydano	221	96.5	5.4	402	2	Q4TZL0_ASF	Q4tzl0 african swi
149	105	5.9	397	1	CD244_MOUSE	Q07763 mus musculu	222	96.5	5.4	402	2	Q895L0_ASF	Q895l0 african swi
150	105	5.9	319	2	Q9UTU7_PIG	Q9utn0 canis famli	223	96.5	5.4	432	2	Q6RWT6_BOVIN	Q6rwt6 bos taurus
151	104.5	5.9	1271	2	Q8A321_BACTN	Q8a321 bacteroides	224	96.5	5.4	432	2	Q6RWT6_BOVIN	Q6rwt6 bos taurus
152	104.5	5.9	1656	2	Q50S97_ENTHI	Q50s97 entamoeba h	225	96.5	5.4	493	2	Q6P5Y4_HUMAN	Q6p5y4 homo sapien
153	104.5	5.9	555	2	Q92016_MOUSE	Q92018 mus musculu	226	96.5	5.4	533	2	Q8N818_HUMAN	Q8ncb8 homo sapien
154	104	5.9	435	2	Q9EQT7_MOUSE	Q9eqt7 mus musculu	227	96.5	5.4	534	2	Q5ZPR3_HUMAN	Q5zpr3 homo sapien
155	104	5.9	1220	2	Q94191_PABAR	Q94191 paracoccidi	228	96.5	5.4	534	2	Q5ZPR3_HUMAN	Q5zpr3 homo sapien
156	104	5.9	319	2	Q9UTU8_CANPA	Q9utn0 canis famli	229	96.5	5.4	1896	2	Q91AJ1_XENIA	Q91aj1 xenopus lae
157	103.5	5.8	323	2	Q9BDB8_CERTO	Q9bdb8 cercocebus	230	96.5	5.4	339	2	Q91AJ1_XENIA	Q91aj1 xenopus lae
158	103.5	5.8	323	2	Q8R373_MOUSE	Q8r373 mus musculu	231	96	5.4	341	2	Q61354_MOUSE	Q61354 mus musculu
159	103.5	5.8	406	2	Q8N778_HUMAN	Q8n778 homo sapien	232	96	5.4	359	1	LACH_DROME	Q24372 drosophila
160	103.5	5.8	1062	2	Q8AXC7_FUGRU	Q8axc7 fuigu rubrip	233	96	5.4	484	2	Q5QSL1_XENIR	Q5qsl1 xenopus tro
161	103	5.8	1078	2	Q8AXC8_FUGRU	Q8axc8 fuigu rubrip	234	96	5.4	494	2	Q6VAN1_HUMAN	Q6van1 homo sapien
162	103	5.8	1479	2	Q7KOPS_DROME	Q7kps5 drosophila	235	96	5.4	526	1	Q6VAN1_HUMAN	Q6van1 homo sapien
163	103	5.8	304	2	Q8ISPI_ASF	Q8isp1 african swi	236	96	5.4	526	1	Q6VAN1_HUMAN	Q6van1 homo sapien
164	102.5	5.8	323	2	Q9BDM4_MACMU	Q9bdm4 macaca mula	237	96	5.4	526	1	Q6VAN1_HUMAN	Q6van1 homo sapien
165	102.5	5.8	335	2	Q9YGH1_CHICK	Q9ygh1 gallus gall	238	96	5.4	526	2	Q6VAN3_HUMAN	Q6van3 homo sapien
166	102.5	5.8	335	2	Q4KLE4_XENIA	Q4kle4 xenopus lae	239	96	5.4	1087	2	Q6FRA_XENIA	Q6fra1 xenopus lae
167	102.5	5.8	359	2	Q92085_MOUSE	Q92085 mus musculu	240	96	5.4	1451	1	MYOM1_HUMAN	P52179 homo sapien
168	102.5	5.8	373	2	Q92085_MOUSE	P16573 rattus norv	241	96	5.4	1451	1	Q6ZUO_HUMAN	Q6zu0 homo sapien
169	102.5	5.8	519	1	Q94YV0_DROME	Q94yv0 drosophila	242	96	5.4	1685	2	Q6H969_HUMAN	Q6h969 homo sapien
170	102	5.8	1482	2	Q22271_ARATH	Q22271 arabidopsis	243	96	5.4	304	2	Q6UHT7_ASF	Q6ht7 african swi
171	101.5	5.7	324	2	Q4SPD7_TETNG	Q4spd7 tetradon n	244	95.5	5.4	340	2	Q61349_MOUSE	Q61349 mus musculu
172	101	5.7	324	2	Q4SPD7_TETNG	Q4spd7 tetradon n	245	95.5	5.4	365	1	Q6UHT7_ASF	Q6ht7 african swi
173	101	5.7	349	1	Q6VAN1_HUMAN	Q6van1 homo sapien	246	95.5	5.4	448	2	Q9JHL7_RAT	Q9jhl7 rattus norv
174	101	5.7	349	1	LACH_SCHAM	Q26197 schistocerc	247	95.5	5.4	458	2	Q63093_RAT	Q63093 rattus norv
175	101	5.7	365	2	Q6VAN6_BOVIN	Q6van6 bos taurus	248	95.5	5.4	459	2	Q9JHL6_RAT	Q9jhl6 rattus norv
176	101	5.7	372	2	Q6VAN6_BOVIN	Q6van6 bos taurus	249	95.5	5.4	463	2	Q6VAN7_MOUSE	Q6van7 mus musculu
177	101	5.7	429	2	Q6VAN7_MOUSE	Q6van7 bos taurus	250	95.5	5.4	463	2	Q6VAN7_MOUSE	Q6van7 mus musculu

251	95.5	5.4	463	2	Q66U72_XENIA	Q66J72_xenopus lae	324	92	5.2	2828	2	Q9NR99_HUMAN	Q9NR99_homo sapien
252	95.5	5.4	628	1	Q7S405_NEUCR	Q7S409 neurospora	325	91.5	5.2	160	2	Q8C254_MOUSE	Q8C254_mus musculus
253	95.5	5.4	700	1	PTPRE_HUMAN	P23469 homo sapien	326	91.5	5.2	226	2	Q8NH11_HUMAN	Q8NH11_homo sapien
254	95.5	5.4	700	2	Q5VMH4_HUMAN	Q5VMH4 homo sapien	327	91.5	5.2	230	2	Q8UV30_BRARE	Q8UV30_brachydantio
255	95.5	5.4	771	1	PIGR_MOUSE	Q70570 mus musculus	328	91.5	5.2	230	2	Q90286_BRARE	Q90286_brachydantio
256	95.5	5.4	822	1	CAN3_SHERP	Q9ctth8 ovis aries	329	91.5	5.2	306	1	BR1A_MOUSE	Q7ceaz3 mus musculus
257	95.5	5.4	1684	2	Q7RIAS_PLAYO	Q7RIAS plasmodium	330	91.5	5.2	527	2	Q4SZU1_TETNG	Q4SZU1_tetradodon n
258	95	5.4	316	2	Q6UX12_HUMAN	Q6UX12 homo sapien	331	91.5	5.2	725	2	Q4VWT3_9PIPI	Q4VWT3_xenopus sp.
259	95	5.4	577	2	Q5REH9_PONPY	Q5REH9 pongo pygma	332	91.5	5.2	943	2	Q7PRK4_ANOGA	Q7PRK4_anophelis g
260	95	5.4	589	2	Q5R770_PONPY	Q5R770 pongo pygma	333	91.5	5.2	1079	2	Q9YWS6_MESEPV	Q9YWS6_melanoplus
261	95	5.4	772	2	Q5U495_XENIA	Q5U495 xenopus lae	334	91.5	5.2	3005	2	Q5OLG3_ALTRA	Q5OLG3_alternaria
262	95	5.4	814	1	PUNC_HUMAN	Q81VU1 homo sapien	335	91	5.1	308	2	Q68EY1_XENIA	Q68EY1_xenopus lae
263	95	5.4	1237	2	Q610C8_CABER	Q610C8 caenothabdi	336	91	5.1	388	2	Q8NC34_HUMAN	Q8NC34_homo sapien
264	94.5	5.3	280	2	Q8UWK3_ICTPU	Q8UWK3 ictalurus p	337	91	5.1	467	2	Q91VT9_MOUSE	Q91VT9_mus musculus
265	94.5	5.3	379	2	Q8BLX5_MOUSE	Q8BLX5 mus musculus	338	91	5.1	467	2	Q8C6F2_MOUSE	Q8C6F2_mus musculus
266	94.5	5.3	397	2	Q8BFX8_MOUSE	Q8BFX8 m mus muscu	339	91	5.1	491	1	KCN33_RABIT	Q9CT17_oryctolagus
267	94.5	5.3	404	2	Q5R8X4_PONPY	Q5R8X4 pongo pygma	340	91	5.1	510	2	Q9BGV6_MACFA	Q9BGV6_macaca fasc
268	94.5	5.3	588	2	Q6MG92_RAT	Q6MG92 rattus norv	341	91	5.1	722	2	Q4KMG2_HUMAN	Q4KMG2_homo sapien
269	94	5.3	233	1	GP42_RAT	P23505 rattus norv	342	91	5.1	822	1	CAN3_BOVIN	Q6PCX3_mus musculus
270	94	5.3	269	2	Q5C8P0_9ADEN	Q5C8P0 simlan aden	343	91	5.1	1150	2	Q6PCX3_MOUSE	Q6PCX3_tetradodon n
271	94	5.3	336	2	Q8WNV8_FELICA	Q8WNV8 felis silve	344	91	5.1	1379	2	Q4SMF3_TETNG	Q4SMF3_homo sapien
272	94	5.3	419	2	Q96GOL5_HUMAN	Q96GOL5 homo sapien	345	91	5.1	1496	2	Q92626_HUMAN	Q92626_mus musculus
273	94	5.3	828	2	Q8C8T7_MOUSE	Q8C8T7 mus musculus	346	91	5.1	1848	1	JADID_MOUSE	Q62240_mus musculus
274	94	5.3	1088	1	NCA11_XENIA	P16170 xenopus lae	347	91	5.1	1840	2	Q9J103_RAT	Q9J103_rattus norv
275	93.5	5.3	365	1	CXAR_RAT	Q9CT066 rattus norv	348	91	5.1	2053	1	DSCL1_HUMAN	Q81D84_homo sapien
276	93.5	5.3	403	2	Q5W7A4_RAT	Q5W7A4 rattus norv	349	90.5	5.1	230	2	Q81A22_HUMAN	Q81A22_brachydantio
277	93.5	5.3	491	2	Q5BLW6_BOVIN	Q5BLW6 bos taurus	350	90.5	5.1	243	2	Q61A22_HUMAN	Q61A22_homo sapien
278	93.5	5.3	572	2	Q4R854_TETNG	Q4R854 tetradodon n	351	90.5	5.1	325	2	Q6PSW9_PIG	Q6PSW9_sus scrofa
279	93.5	5.3	840	2	Q4VYD6_SPICT	Q4VYD6 spiropasma	352	90.5	5.1	391	2	Q5U334_RAT	Q5U334_rattus norv
280	93.5	5.3	1039	2	Q5T377_HUMAN	Q5T377 homo sapien	353	90.5	5.1	412	2	Q5U334_RAT	Q5U334_rattus norv
281	93.5	5.3	1098	2	Q4RR1T_TETNG	Q4RR1T tetradodon n	354	90.5	5.1	412	2	Q63611_RAT	Q63611_rattus norv
282	93	5.2	316	2	Q9EXR1_HUMAN	Q9EXR1 homo sapien	355	90.5	5.1	412	2	Q9R1B1_RAT	Q9R1B1_rattus norv
283	93	5.2	339	2	Q7KR15_DROME	Q7KR15 drosophila	356	90.5	5.1	474	2	Q5FV48_FUGRU	Q5FV48_fugu rubrip
284	93	5.2	342	2	Q91B00_9PERC	Q91B00 epirochloides	357	90.5	5.1	483	2	Q7SX76_BRARE	Q7SX76_brachydantio
285	93	5.2	419	1	PSG4_HUMAN	Q00888 homo sapien	358	90.5	5.1	795	2	Q5ONM7_ENTHI	Q5ONM7_entameoba n
286	93	5.2	419	1	PSG7_HUMAN	Q13046 homo sapien	359	90.5	5.1	901	2	Q6IR38_MOUSE	Q6IR38_mus musculus
287	93	5.2	535	1	PSYR3_SPICT	P52200 spiropasma	361	90.5	5.1	922	2	Q9JTL7_ARATH	Q9JTL7_arabidopsis
288	93	5.2	661	2	Q9JW1_MOUSE	Q5J1W1 mus musculus	362	90.5	5.1	1012	1	ROBO4_MOUSE	Q8C310_mus musculus
289	93	5.2	752	2	Q9DGN6_CHICK	Q9DGN6 gallus gall	363	90.5	5.1	1596	2	Q5CPM9_CRYPV	Q5CPM9_cryptospori
290	93	5.2	813	2	PUNC_MOUSE	Q8BDC3 mus musculus	364	90.5	5.1	1905	1	Y659_PASMU	Q9CMZ1_pasteurella
291	93	5.2	949	2	Q6FKB0_CANGA	Q6FKB0 candida gla	365	90	5.1	240	2	Q5T325_HUMAN	Q5T325_homo sapien
292	93	5.2	1788	2	Q91AJ0_XENIA	Q91AJ0 xenopus lae	366	90	5.1	250	2	Q5U053_HUMAN	P19265_homo sapien
293	92.5	5.2	160	2	Q8C239_MOUSE	Q8C239 mus musculus	367	90	5.1	309	2	Q91YV7_MOUSE	Q91YV7_homo sapien
294	92.5	5.2	299	1	JWMT_HUMAN	Q9Y624 homo sapien	368	90	5.1	348	2	MEGR1_MOUSE	Q91YV7_mus musculus
295	92.5	5.2	299	2	Q6TIB4_HUMAN	Q6TIB4 homo sapien	369	90	5.1	419	1	PGS1_HUMAN	Q80C24_mus musculus
296	92.5	5.2	330	1	CD86_RABIT	P42071_oryctolagus	370	90	5.1	419	1	Q6ICR4_HUMAN	P11464_homo sapien
297	92.5	5.2	491	2	Q5E9J9_BOVIN	Q5E9J9 bos taurus	371	90	5.1	515	2	Q4RP84_TETNG	Q4RP84_homo sapien
298	92.5	5.2	733	2	Q5ONS6_BRARE	Q5ONS6 brachydantio	372	90	5.1	541	2	IL1BR_HUMAN	Q13478_homo sapien
299	92.5	5.2	931	2	BTNL9_HUMAN	Q7Z285 homo sapien	373	90	5.1	541	2	Q52LIC9_HUMAN	Q52LIC9_homo sapien
300	92.5	5.2	535	1	Q7Z285_BRARE	Q9D460 brachydantio	374	90	5.1	609	2	Q9WHY7_9PARA	Q9WHY7_rinderpest
301	92.5	5.2	544	2	CD166_BRARE	Q61QX4 brachydantio	375	90	5.1	771	2	Q4KMG7_HUMAN	Q4KMG7_homo sapien
302	92.5	5.2	564	1	Q610X4_BRARE	Q6EBB5 shewanella	376	90	5.1	1179	2	Q7QXR2_GIALA	Q7QXR2_giardia lam
303	92.5	5.2	760	2	Q8EBB5_SHEON	Q8EBB5 brachydantio	377	90	5.1	1297	2	Q6WLBS_9DIPT	Q6WLBS_chaetopsis
304	92.5	5.2	767	2	Q9C9S3_ARATH	Q9C9S3 arabidopsis	378	90	5.1	1297	2	Q4RVK8_TETNG	Q4RVK8_tetradodon n
305	92.5	5.2	777	2	Q7RAO7_PLAYO	Q7RAO7 plasmodium	379	90	5.1	1431	2	Q80U60_MOUSE	Q80U60_mus musculus
306	92.5	5.2	777	2	Q8B3U9_9GAMA	Q8B3U9 porcine lym	380	90	5.1	1495	2	Q4RB92_TETNG	Q4RB92_tetradodon n
307	92.5	5.2	782	2	Q8U1B8_9GAMA	Q8U1B8 porcine lym	381	90	5.1	243	1	CD48_HUMAN	Q4RB92_homo sapien
308	92.5	5.2	782	2	Q5R1P6_BRARE	Q5R1P6 brachydantio	382	89.5	5.1	339	2	Q5U055_HUMAN	Q5U055_homo sapien
309	92.5	5.2	5533	2	Q63476_RAT	Q63476 rattus norv	383	89.5	5.1	243	2	Q4T512_TETNG	Q4T512_tetradodon n
310	92	5.2	297	2	Q68CR6_HUMAN	Q68CR6 homo sapien	384	89.5	5.1	349	1	OMPA_BUCAI	P57414_buchnera ap
311	92	5.2	419	2	PSG8_HUMAN	Q4ZLY1 homo sapien	385	89.5	5.1	508	2	Q5KUB8_GROXA	Q5KUB8_grebacillus
312	92	5.2	426	1	Q4ZPT1_HUMAN	Q4ZPT1 homo sapien	386	89.5	5.1	570	2	Q5R640_PONPY	Q5R640_pongo pygma
313	92	5.2	491	2	Q9YKD7_9PARA	Q9YKD7 rinderpest	387	89.5	5.1	756	2	Q8CUN2_MOUSE	Q8CUN2_streptococce
314	92	5.2	609	2	KIRK2_MOUSE	Q6P1W7 homo sapien	388	89.5	5.1	770	2	Q81UN9_BRACO	Q81UN9_bredythrilo
315	92	5.2	700	1	Q6P1W7_HUMAN	Q6P1W7 homo sapien	389	89.5	5.1	821	2	CAN3_PIG	P43368_sus scrofa
316	92	5.2	743	2	Q71512_BACTO	Q71512 bacillus th	390	89.5	5.1	833	2	Q9BPQ7_HALRO	Q9BPQ7_halocynthia
317	92	5.2	829	2	Q9ZOX3_ARATH	Q9ZOX3 arabidopsis	391	89.5	5.1	845	2	SLIK2_HUMAN	Q9N156_homo sapien
318	92	5.2	882	1	FRM4A_MOUSE	Q8B1E6 mus musculus	392	89.5	5.1	845	2	Q6A113_HUMAN	Q6A113_homo sapien
319	92	5.2	1020	1	Q7XTP6_OYRSA	Q7XTP6 cryza acatv	393	89.5	5.1	1024	1	FRM4A_HUMAN	Q9P2Q2_homo sapien
320	92	5.2	1025	2	Q6PDY4_MOUSE	Q6PDY4 mus musculus	394	89.5	5.1	1170	2	Q4YR55_PLABE	Q4YR55_plasmodium
321	92	5.2	1031	2	Q7ZY71_XENIA	Q7ZY71 xenopus lae	395	89.5	5.1	1644	2	Q9W3D2_DROME	Q9W3D2_drosophila
322	92	5.2	1087	2	Q4SRX6_TETNG	Q4SRX6 tetradodon n	396	89.5	5.1				
323	92	5.2	2008	2	Q4SRX6_TETNG	Q4SRX6 tetradodon n							

397	89.5	5.1	1671	2	Q9W3D3_DROME	Q9x3d3 drosophila	470	87.5	4.9	302	2	Q4JX57_CORJX	Q4ix57 corynebacte
398	89.5	5.1	1716		Q61ZV2_CAEBR	Q61z2v2 caenorhabdi	471	87.5	4.9	325	2	Q02838_PIG	Q02838 sus scrofa
399	89.5	5.1	2214	1	SVTL_HUMAN	Q95425 homo sapien	472	87.5	4.9	332	2	Q640U3_XENTR	Q640u3 xenopus tro
400	89.5	5.1	3193	2	Q7RL38_PLAYO	Q7rl38 plasmidium	473	87.5	4.9	406	2	Q8VE47_MOUSE	Q8ve47 mus musculu
401	89	5.0	240	2	Q9BRW0_HUMAN	Q9brw0 homo sapien	474	87.5	4.9	413	2	Q65A45_BRARE	Q65a45 brachydanio
402	89	5.0	262	2	Q80T70_MOUSE	Q80t70 mus musculu	475	87.5	4.9	422	1	KI3L1_RAT	P83556 ratu
403	89	5.0	309	1	CD66_MOUSE	P40082 mus musculu	476	87.5	4.9	464	2	Q6GL25_XENTR	Q6gl25 xenopus tro
404	89	5.0	309	2	Q549Q9_MOUSE	Q549q9 mus musculu	477	87.5	4.9	487	1	PERL1_CHICK	Q722h2 gallu
405	89	5.0	314	2	Q61238_MOUSE	Q61238 mus musculu	478	87.5	4.9	547	2	Q6MG93_RAT	Q6mg93 ratu
406	89	5.0	322	2	Q9PTR8_SPERC	Q9ptr8 speroeloides	479	87.5	4.9	581	2	Q6BN45_DEBHA	Q6bn45 debaryomyc
407	89	5.0	323	2	Q8MKZ7_DROME	Q8mkz7 drosophila	480	87.5	4.9	583	1	CD166_MOUSE	Q61490 mus musculu
408	89	5.0	356	2	Q64381_MOUSE	Q64381 mus musculu	481	87.5	4.9	583	1	CD166_RAT	Q35112 ratu
409	89	5.0	368	2	Q5BI25_DROME	Q5bi25 drosophila	482	87.5	4.9	583	2	Q54AJ5_MOUSE	Q54aj5 mus musculu
410	89	5.0	434	2	Q6DN72_HUMAN	Q6dn72 homo sapien	483	87.5	4.9	652	2	Q89703_YITRU	Q89703 xenopus
411	89	5.0	438	2	Q5C724_SCHJA	Q5c724 schistosoma	484	87.5	4.9	699	2	Q6IV11_CAEBR	Q6iv11 caenorhabdi
412	89	5.0	466	2	Q551Y7_CRYNE	Q551y7 cryptococcu	485	87.5	4.9	723	2	Q5HZP8_XENTLA	Q5hzp8 xenopus lae
413	89	5.0	506	2	Q6MG91_RAT	Q6mg91 ratu	486	87.5	4.9	769	1	PIGR_RAT	P51083 ratu
414	89	5.0	821	1	CAN3_HUMAN	P20807 homo sapien	487	87.5	4.9	1087	2	Q9PUF6_CHICK	Q9puf6 gallu
415	89	5.0	1803	2	Q5CMK4_CRYHO	Q5cmk4 cryptocospori	488	87.5	4.9	2307	2	Q80IV2_PPTCO	Q80iv2 theiler's-1
416	89	5.0	5175	2	Q810U3_CAEBL	Q810u3 caenorhabdi	489	87.5	4.9	2340	2	Q78DX7_MOUSE	Q78dx7 mus musculu
417	89	5.0	5198	2	Q76518_CAEBL	Q76518 caenorhabdi	490	87.5	4.9	4162	2	Q89VU8_CHICK	Q89v8 gallu
418	89.5	5.0	271	1	OX2V_HHV8	P88963 human herpe	491	87.5	4.9	4283	2	Q9ERV0_RAT	Q9erv0 ratu
419	88.5	5.0	271	2	Q40948_HHV8	Q40948 human herpe	492	87.5	4.9	17903	2	Q7RTL4_DROME	Q7rtl4 drosophila
420	88.5	5.0	271	2	Q4S7L7_TETNG	Q4s7l7 tetradodon n	493	87.5	4.9	18074	2	Q917U4_DROME	Q917u4 drosophila
421	88.5	5.0	315	2	Q9DGT5_CHICK	Q9dgt5 gallu	494	87.5	4.9	156	2	Q5APG8_CANAL	Q5apf8 candida alb
422	88.5	5.0	316	2	Q5F3J1_CHICK	Q5f3j1 gallu	495	87.5	4.9	225	2	Q5NH27_PRAIT	Q5nh27 francisella
423	88.5	5.0	325	2	Q8UWL3_ICTPU	Q8uwl3 ictalurus p	496	87.5	4.9	229	2	Q9R121_RAT	Q9r121 ratu
424	88.5	5.0	327	1	MOX2R_RAT	Q9e858 ratu	497	87.5	4.9	291	2	KO152_MOUSE	Q6xq13 mus musculu
425	88.5	5.0	344	2	Q93242_CHICK	Q93242 gallu	498	87.5	4.9	337	2	Q5Z8W6_ORYSA	Q5z8w6 oryza sativ
426	88.5	5.0	532	2	Q8WVW6_HUMAN	Q8wvw6 homo sapien	499	87.5	4.9	341	2	Q61353_MOUSE	Q61353 mus musculu
427	88.5	5.0	534	2	Q96SAR_HUMAN	Q96sae2 homo sapien	500	87.5	4.9	344	2	Q568F7_BRARE	Q568f7 brachydanio
428	88.5	5.0	534	2	Q9W4R3_DROME	Q9w4r3 drosophila	501	87.5	4.9	403	2	Q9CYD6_MOUSE	Q9cyd6 mus musculu
429	88.5	5.0	782	2	Q61G13_DROME	Q61g13 drosophila	502	87.5	4.9	415	2	Q8C6X8_MOUSE	Q8c6x8 mus musculu
430	88.5	5.0	820	2	Q4S143_TETNG	Q4s143 tetradodon n	503	87.5	4.9	457	1	CD4_MOUSE	P06332 mus musculu
431	88.5	5.0	1081	2	Q8T4N8_PENRS	Q8t4n8 penaeus sem	504	87.5	4.9	491	1	KCN53_HUMAN	Q9bqz1 homo sapien
432	88.5	5.0	1283	2	Q7R0P8_PLAYO	Q7r0p8 plasmidium	505	87.5	4.9	491	2	Q8B0Z8_MOUSE	Q8b0z8 mus musculu
433	88.5	5.0	1390	1	MET_HUMAN	P05581 homo sapien	506	87.5	4.9	514	2	Q8BH18_MOUSE	Q8bh18 m mus muscu
434	88.5	5.0	1769	2	Q4YQ03_PLABE	Q4yq03 plasmidium	507	87.5	4.9	521	1	CD166_FABIT	Q46651 oycetolagus
435	88	5.0	320	2	Q737C6_BACCI	Q737c6 bacillus ce	508	87.5	4.9	522	1	Q8F7F1_LEPIN	Q8f7f1 leptospira
436	88	5.0	324	2	Q7TMA2_MOUSE	Q7tma2 mus musculu	509	87.5	4.9	543	2	Q4R603_MACPA	Q4r603 macaca fasc
437	88	5.0	329	2	Q9TTP2_CANPA	Q9tte2 canis famli	510	87.5	4.9	551	2	Q4Q0E7_SCNMA	Q4q0e7 schistosoma
438	88	5.0	337	2	Q91AZ4_SPERC	Q91az4 spheoeloides	511	87.5	4.9	583	1	CD166_HUMAN	Q51740 homo sapien
439	88	5.0	339	2	Q91B09_SPERC	Q91b09 spheoeloides	512	87.5	4.9	609	2	Q7EYK0_ORYSA	Q7eyk0 oryza sativ
440	88	5.0	343	2	Q8R4Y0_MOUSE	Q8r4y0 mus musculu	513	87.5	4.9	1272	2	Q4UDP5_BRARE	Q4ud5 brachydanio
441	88	5.0	363	1	MURG_BORBU	Q51708 borrelia bu	514	87.5	4.9	1272	2	Q5G1T3_BRARE	Q5g1t3 brachydanio
442	88	5.0	419	2	Q6P520_HUMAN	Q6p520 homo sapien	515	87.5	4.9	1284	2	Q5KLIV6_CRYNE	Q5kliv6 cryptococcu
443	88	5.0	422	2	Q58124_PYRHO	Q58124 pyrococcus	516	87.5	4.9	1403	3	Q6DCY7_XENTLA	Q6dcy7 xenopus lae
444	88	5.0	457	2	Q61396_MOUSE	Q61396 mus musculu	517	87.5	4.9	1451	2	Q55Y32_CRYNE	Q55y32 cryptococcu
445	88	5.0	508	1	CPED5_DROME	Q9yfp1 drosophila	518	87.5	4.9	1497	2	Q5XIV4_MOUSE	Q5xiv4 mus musculu
446	88	5.0	509	1	SHPS1_RAT	P97710 r tyrosine-	519	87.5	4.9	1501	2	Q7RTI7_MOUSE	Q7rti7 mus musculu
447	88	5.0	530	1	PVRS1_MOUSE	P32507 mus musculu	520	87.5	4.9	1569	2	Q6PAC0_MOUSE	Q6pac0 mus musculu
448	88	5.0	530	2	Q80XJ5_MOUSE	Q80xj5 mus musculu	521	87.5	4.9	1666	1	MYOM1_MOUSE	Q62234 mus musculu
449	88	5.0	607	2	Q4LPC1_9BURK	Q4lpc1 burkholderi	522	87.5	4.9	1666	2	Q546T8_MOUSE	Q546t8 mus musculu
450	88	5.0	623	2	Q7PUC7_ANGCA	Q7puc7 anopheles g	523	87.5	4.9	1904	2	Q64699_MOUSE	Q64699 mus musculu
451	88	5.0	639	2	Q6PA27_XENTLA	Q6pa27 xenopus lae	524	87.5	4.9	1907	2	Q4JBC7_MOUSE	Q4jfc7 mus musculu
452	88	5.0	699	1	P7PR8_MOUSE	P49446 mus musculu	525	87.5	4.9	2673	2	Q96SC3_HUMAN	Q96sc3 homo sapien
453	88	5.0	699	2	Q61042_MOUSE	Q61042 mus musculu	526	87.5	4.9	3160	1	FREM2_MOUSE	Q05793 mus musculu
454	88	5.0	821	1	CAN3_RAT	P16259 ratu	527	87.5	4.9	3707	1	PGBM_MOUSE	Q05793 mus musculu
455	88	5.0	837	2	Q8G518_BIFLO	Q8g518 bifidobacte	528	87.5	4.9	5635	2	Q5TRY7_HUMAN	Q5try7 homo sapien
456	88	5.0	986	2	Q8UTR9_PUGRU	Q8utr9 figu rubrip	529	86.5	4.9	210	2	Q4RTW7_MACPA	Q4rtw7 macaca fasc
457	88	5.0	1092	1	NCA12_XENTLA	P36335 xenopus lae	530	86.5	4.9	237	2	Q6IB65_HUMAN	Q6ib65 homo sapien
458	88	5.0	1112	2	Q60U10_CAEBR	Q60u10 caenorhabdi	531	86.5	4.9	240	2	Q6MG36_RAT	Q6mg36 ratu
459	88	5.0	1337	2	Q4RKW0_TETNG	Q4rkwo tetradodon n	532	86.5	4.9	293	2	Q8AXN8_CYPCA	Q8axn8 cyprinus car
460	88	5.0	1379	2	Q81387_PLAF7	Q81387 plasmidium	533	86.5	4.9	313	2	Q35531_RAT	Q35531 ratu
461	88	5.0	1925	1	PLXDI_HUMAN	Q9y4d7 homo sapien	534	86.5	4.9	324	2	Q91AY9_SPERC	Q91ay9 speroeloides
462	88	5.0	1946	2	Q4S290_TETNG	Q4s290 tetradodon n	535	86.5	4.9	354	2	Q5R412_PONPY	Q5r412 pongo pygma
463	88	5.0	2802	2	Q53T68_HUMAN	Q53t68 homo sapien	536	86.5	4.9	354	2	Q5R645_PONPY	Q5r645 pongo pygma
464	88	5.0	3007	2	Q14215_HUMAN	Q14215 homo sapien	537	86.5	4.9	384	2	Q4SY83_TETNG	Q4sy83 tetradodon n
465	88	5.0	6669	1	NEBU_HUMAN	P20929 homo sapien	538	86.5	4.9	443	1	EX7L_VIBVU	Q7fme3 vibrio vuln
466	88	5.0	11696	2	Q5CV09_CRYPV	Q5cv09 cryptocospori	539	86.5	4.9	443	1	EX7L_VIBVU	Q7fme3 vibrio vuln
467	87.5	4.9	265	1	CEAM7_HUMAN	Q14002 homo sapien	540	86.5	4.9	474	2	P79355_FELICA	P79355 felis silve
468	87.5	4.9	276	2	Q98822_ADB41	Q98822 human adeno	541	86.5	4.9	528	2	Q9RTP5_DEIRA	Q9rtp5 delinococcus
469	87.5	4.9	276	2	Q64861_YADEN	Q64861 human adeno	542	86.5	4.9	530	2	Q5FVCS_RAT	Q5fvc5 ratu

543	86.5	4.9	626	2	04SM56_TETNG	04sm56 tetradon n	616	85.5	4.8	1587	2	0705D1_ANOGA	0755d1 anopheles g
544	86.5	4.9	650	2	068BN9_PBSM	068bn9 pseudomonas	617	85.5	4.8	1947	2	07ROQ4_PLAYO	07rgq4 plasmidium
545	86.5	4.9	711	2	06LJAI_PHOPR	06ljai photobacter	618	85.5	4.8	2115	2	08IB55_PLAP7	08ib55 plasmidium
546	86.5	4.9	846	1	SLIKX2_MOUSE	0810c0 mus musculu	619	85.5	4.8	2129	2	06FUN0_CANGA	06fun0 candida gla
547	86.5	4.9	1028	2	06INB5_XENTIA	06inb5 xenopus lae	620	85.5	4.8	2225	2	05AC68_DICD1	05ac68 dictyosteli
548	86.5	4.9	1029	2	04Y4R9_PLACH	04y4r9 plasmidium	621	85.5	4.8	2414	2	059E23_HUMAN	059e23 homo sapien
549	86.5	4.9	2752	2	07OKD0_ANOGA	07okd0 anopheles g	622	85.5	4.8	2491	1	MPRI_HUMAN	MPRI17 homo sapien
550	86	4.9	235	2	04S001_TETNG	04s001 tetradon n	623	85.5	4.8	2491	1	06PFT5_HUMAN	06pft5 homo sapien
551	86	4.9	259	2	09Y5B2_HUMAN	09y5b2 homo sapien	624	85.5	4.8	2588	1	NSDI_MOUSE	NSDI491 mus musculu
552	86	4.9	265	2	0695R3_YADEN	0695r3 simian aden	625	85.5	4.8	2623	2	06WRIO_HUMAN	06wr10 homo sapien
553	86	4.9	280	2	08UMK1_ICTPU	08umk1 ictalurus p	626	85	4.8	280	2	0870G0_PODAN	0870g0 podospora a
554	86	4.9	330	2	06PEUT_MOUSE	06peut mus musculu	627	85	4.8	224	2	08UWL1_ICTPU	08wl1 ictalurus p
555	86	4.9	339	2	09IAZI_9PERC	09iazi spheroeoides	628	85	4.8	293	2	06MG56_RAT	06mg56 leptospira
556	86	4.9	348	1	NEGRI_RAT	0920j8 rattus norv	629	85	4.8	332	2	07F52_TEPIC	07f52 leptospira
557	86	4.9	354	1	VGLI_VZVD	P09258 varicella-z	630	85	4.8	332	2	08BX51_LEPIN	08bx51 leptospira
558	86	4.9	354	2	0775H3_HHV3	0775h3 human heppe	631	85	4.8	375	2	093GD6_DESAP	093gd6 desautl
559	86	4.9	354	2	077JF6_HHV3	077jf6 human heppe	632	85	4.8	379	1	JAML1_MOUSE	08u19 mus musculu
560	86	4.9	354	2	098VN1_HHV3	098vn1 human heppe	633	85	4.8	402	1	RAGR_RAT	063495 rattus norv
561	86	4.9	354	2	077NM4_HHV3	077nm4 human heppe	634	85	4.8	402	1	06MG66_RAT	06mg66 rattus norv
562	86	4.9	413	2	06ZNI1_HUMAN	06zni1 homo sapien	635	85	4.8	428	1	PEG3_HUMAN	06ng86 homo sapien
563	86	4.9	428	2	09BRW2_HUMAN	09brw2 homo sapien	636	85	4.8	475	2	06NZH8_XENTR	06nz8 xenopus tro
564	86	4.9	434	2	06IKI8_CABBR	06iki8 caenorhabdi	637	85	4.8	570	2	06GLY1_XENTIA	06gly1 xenopus lae
565	86	4.9	486	2	082N16_STPAM	082ni6 streptomyce	638	85	4.8	583	1	CD166_BOVIN	09ph13 bos taurus
566	86	4.9	487	2	082M13_STPAM	082ni3 streptomyce	639	85	4.8	684	2	0211J8_CAEEL	0211j8 caenorhabdi
567	86	4.9	545	2	09VCT4_DROME	09vct4 drosophila	640	85	4.8	709	2	09XSJ2_PIG	09xsj2 sus scrofa
568	86	4.9	556	2	058EQ1_BRARE	058eq1 brachydanio	641	85	4.8	712	2	09EB31_HUMAN	09eb31 homo sapien
569	86	4.9	648	2	06DJ24_XENTR	06dj24 xenopus tro	642	85	4.8	821	1	CAN3_MOUSE	064691 mus musculu
570	86	4.9	687	2	09MAJ5_ARATH	09maj5 arabidopsis	643	85	4.8	875	2	091ZV7_MOUSE	091zv7 mus musculu
571	86	4.9	728	2	0762C8_HUMAN	0762c8 homo sapien	644	85	4.8	880	2	06A7L8_PROAC	06a7l8 propionibac
572	86	4.9	731	2	08SP16_MACEU	08sp16 macropus eu	645	85	4.8	976	2	058N28_9CAUD	058n28 cynophaga
573	86	4.9	885	1	RFL1_ARATH	0813r3 arabidopsis	646	85	4.8	1168	2	04UBU6_THBAN	04ueu6 thelieria a
574	86	4.9	1070	2	04S2F2_TETNG	04s2f2 tetradon n	647	85	4.8	1376	2	08A223_9GAMA	08a223 porcine lym
575	86	4.9	1187	2	098TF0_CYPICA	098tf0 cyprinus ca	648	85	4.8	1384	2	076915_BOVIN	076915 bos taurus
576	86	4.9	1252	2	06CUN6_KULIA	06cun6 kluyveromyc	649	85	4.8	1389	2	04VA61_MOUSE	04va61 mus musculu
577	86	4.9	1337	2	01S070_HUMAN	01s070 homo sapien	650	85	4.8	1598	2	09P214_HUMAN	09p214 homo sapien
578	86	4.9	18412	2	07Z261_BRARE	07z261 brachydanio	651	85	4.8	1723	2	08CHB2_MOUSE	08chb2 mus musculu
579	85.5	4.8	230	2	05SNP6_BRARE	05snp6 brachydanio	652	85	4.8	1805	2	058EX2_HUMAN	05ex2 homo sapien
580	85.5	4.8	235	2	06GWM6_HUMAN	06gwm6 homo sapien	653	85	4.8	2487	2	09N1T0_ORNAN	09n1t0 ornithorhyn
581	85.5	4.8	249	2	06XJV6_MOUSE	06xjv6 mus musculu	654	85	4.8	210	2	07PVM1_ANOGA	07pvm1 anopheles g
582	85.5	4.8	266	2	04NV83_GDELT	04nv83 ananomyxob	655	84.5	4.8	238	2	04T426_TETNG	04t426 geobacter s
583	85.5	4.8	324	2	09UPK5_HUMAN	09upk5 homo sapien	656	84.5	4.8	241	2	04T426_TETNG	04t426 geobacter s
584	85.5	4.8	326	2	09UPK8_HUMAN	09upk8 homo sapien	657	84.5	4.8	263	2	04SQO2_TETNG	04sqo2 tetradon n
585	85.5	4.8	332	2	04RFH3_TETNG	04rfh3 tetradon n	658	84.5	4.8	280	2	0899D0_CLOTE	0899d0 clostridium
586	85.5	4.8	333	2	0752J3_HUMAN	0752j3 homo sapien	659	84.5	4.8	289	2	05HZV8_XENTR	05hzv8 xenopus tro
587	85.5	4.8	335	2	075237_HUMAN	075237 homo sapien	660	84.5	4.8	292	1	KO152_HUMAN	041165 homo sapien
588	85.5	4.8	347	2	04R908_MACEA	04r908 macaca fasc	661	84.5	4.8	303	2	09UKJ1_HUMAN	09ukj1 homo sapien
589	85.5	4.8	393	2	07TNZ6_RAT	07tnz6 rattus norv	662	84.5	4.8	308	2	04YCN2_PLARE	04ycn2 plasmidium
590	85.5	4.8	488	2	05FYV4_SPHBL	05fyv4 sphingomona	663	84.5	4.8	337	2	06SUQ7_MOUSE	06sqj7 mus musculu
591	85.5	4.8	510	2	05U557_XENTIA	05u557 xenopus lae	664	84.5	4.8	352	1	NEGRI1_HUMAN	0753j1 mus musculu
592	85.5	4.8	527	2	06YW20_ORYSA	06yw20 oryza sativ	665	84.5	4.8	354	2	05VT21_HUMAN	05vt21 homo sapien
593	85.5	4.8	620	2	0481C0_TETNG	0481c0 tetradon n	666	84.5	4.8	394	2	09D0G8_MOUSE	09d0g8 m mus muscu
594	85.5	4.8	622	2	05OXJ4_ENTHI	05oxj4 entamoeba h	667	84.5	4.8	397	2	06XRC3_HUMAN	06xrc3 homo sapien
595	85.5	4.8	650	2	08NA84_HUMAN	08na84 homo sapien	668	84.5	4.8	533	2	04IND9_GIBZE	04ind9 gibberella
596	85.5	4.8	657	2	093D79_BACTU	093d79 bacillus th	669	84.5	4.8	605	2	04UG78_THBAN	04ug78 thelieria a
597	85.5	4.8	767	2	05LKB5_BACER	05lkb5 bacillus th	670	84.5	4.8	756	2	004533_ARATH	004533 arabidopsis
598	85.5	4.8	767	2	064SY4_BACFN	064sy4 bacteroides	671	84.5	4.8	798	2	086K66_DICD1	086k66 dictyosteli
599	85.5	4.8	788	2	053Z20_BACTU	053z20 bacillus th	672	84.5	4.8	840	2	07VO12_CANBP	07vo12 candidatus
600	85.5	4.8	789	2	069270_BACTU	069270 bacillus th	673	84.5	4.8	1164	2	08PX58_METMA	08px58 methanosarc
601	85.5	4.8	789	2	045792_BACTU	045792 bacillus th	674	84.5	4.8	1211	1	M1OL1_HUMAN	09pxc6 homo sapien
602	85.5	4.8	789	2	045793_BACTU	045793 bacillus th	675	84.5	4.8	1485	2	04RH47_TETNG	04rh47 tetradon n
603	85.5	4.8	789	2	05XKQ5_BACTU	05xkq5 bacillus th	676	84.5	4.8	1608	2	08PVI0_METMA	08pvi0 methanosarc
604	85.5	4.8	789	2	079SG2_BACTU	079sg2 bacillus th	677	84.5	4.8	237	2	07YOK5_CANFA	07yok5 canis famli
605	85.5	4.8	789	2	058133_BACTU	058133 bacillus th	678	84	4.7	4311	2	05VSN2_BRARE	05vsn2 brachydanio
606	85.5	4.8	789	2	058X12_BACTU	058x12 bacillus th	679	84	4.7	262	2	09PTR7_9PERC	09ptr7 spheroeoides
607	85.5	4.8	789	2	093821_BACTU	093821 bacillus th	680	84	4.7	333	2	091B04_9PERC	091b04 spheroeoides
608	85.5	4.8	789	2	04VYTO_BACTU	04vyto bacillus th	681	84	4.7	343	2	08BY54_MOUSE	08by54 mus musculu
609	85.5	4.8	789	2	04U3F4_BACTU	04u3f4 bacillus th	682	84	4.7	363	2	066OAB_BORGA	066oab borrelia ga
610	85.5	4.8	789	1	KPM5_P5VMD	P00545 feline sarc	683	84	4.7	381	2	05VGF5_HALMA	05vgf5 haloarcula
611	85.5	4.8	1101	2	07XDJ5_ORYSA	07xdj5 oryza sativ	684	84	4.7	403	2	08EN15_OCCRH	08en15 oceanobacti
612	85.5	4.8	1101	2	09FML8_ORYSA	09fml8 oryza sativ	685	84	4.7	418	2	0501T5_BRARE	0501t5 brachydanio
613	85.5	4.8	1354	2	09VIC7_DROME	09vic7 drosophila	686	84	4.7	453	2	05ICKR5_CRINE	05ickr5 crytococcu
614	85.5	4.8	1363	2	053P57_ORYSA	053p57 oryza sativ	687	84	4.7	457	2	06FAG8_ACTIAD	06fag8 actinobact
615	85.5	4.8	1416	2	04P2B6_USITWA	04p2b6 usitlago ma	688	84	4.7	464	2	04KFA6_PSEF5	04kfa6 pseudomonas

689	84	4.7	466	2	Q5KCR4_CRYNE	Q5KCR4_CRYPTOCOCCU	762	83	4.7	281	2	Q6CJF8_MESAU	Q6CJF8_MESOCICCTU
690	84	4.7	509	2	Q6P6I8_MOUSE	Q6P6I8_mus musculus	763	83	4.7	305	2	Q6ZS95_HUMAN	Q6ZS95_homo sapien
691	84	4.7	556	2	Q7Z2U8_BRARE	Q7Z2U8 brachydanto	764	83	4.7	339	2	Q9IA22_SPERC	Q9IA22_spheroctides
692	84	4.7	593	2	Q5AYU9_EMENTI	Q5AYU9 aspergillus	765	83	4.7	369	2	Q9J3E5_DESDE	Q9J3E5_desulfovibr
693	84	4.7	593	2	Q8NKB1_EMENTI	Q8NKB1 emericiella	766	83	4.7	373	2	Q8TU74_METAC	Q8TU74_methanosarc
694	84	4.7	594	2	Q5L8S3_BACFN	Q5L8S3 bacteroides	767	83	4.7	401	2	Q08835_CERAE	Q08835_cercopithec
695	84	4.7	611	2	Q5EDK0_ORYSA	Q5EDK0 oryza sativ	768	83	4.7	420	2	Q68DM9_HUMAN	Q68DM9_homo sapien
696	84	4.7	611	2	Q7JTM6_MYCPA	Q7JTM6 mycobacteri	769	83	4.7	424	2	Q6CLX2_KUJLA	Q6CLX2_kluveromyc
697	84	4.7	668	1	P8B2_YEAST	P8B2 yeast	770	83	4.7	437	2	Q9OW14_CHICK	Q9OW14 gallus gall
698	84	4.7	685	1	Q54HG9_DICDI	Q54HG9 dictyostelm	771	83	4.7	438	2	Q4RKP5_TETNG	Q4RKP5 tetradon n
699	84	4.7	775	2	Q97754_RABIT	Q97754 coryctolagus	772	83	4.7	448	2	Q6LU33_PHOPR	Q6LU33 photobacter
700	84	4.7	800	2	Q8H329_ORYSA	Q8H329 oryza sativ	773	83	4.7	463	1	STHA_PSEB1	Q5U139 pseudomonas
701	84	4.7	810	2	Q8T3U2_DROME	Q8T3U2 dirosophila	774	83	4.7	514	2	Q9HOC3_HUMAN	Q9HOC3_homo sapien
702	84	4.7	811	2	Q9VKS4_DROME	Q9VKS4 dirosophila	775	83	4.7	538	2	Q9DFU0_SPAU	Q9DFU0 sparus atra
703	84	4.7	812	2	Q8W257_DROME	Q8W257 dirosophila	776	83	4.7	545	2	Q5OZ57_ENTHI	Q5OZ57 entameba h
704	84	4.7	851	2	Q9UX76_SUILO	Q9UX76 sulfolobus	777	83	4.7	555	2	Q59HD7_HUMAN	Q59HD7_homo sapien
705	84	4.7	880	2	P91643_DROME	P91643 dirosophila	778	83	4.7	577	2	Q9D2Z1_MOUSE	Q9D2Z1_mus muscu
706	84	4.7	984	2	Q4TMP4_GIBZE	Q4TMP4 gibbeterella	779	83	4.7	594	2	Q64NY2_MOUSE	Q64NY2 bacteroides
707	84	4.7	1028	2	Q4TMP4_GIBZE	Q4TMP4 gibbeterella	780	83	4.7	702	2	Q4S767_TETNG	Q4S767 tetradon n
708	84	4.7	1028	2	Q4TMP4_GIBZE	Q4TMP4 gibbeterella	781	83	4.7	757	1	P1GR_BOVIN	P1GR_bos taurus
709	84	4.7	1062	2	Q997A4_PBRON	Q997A4 american pi	782	83	4.7	845	1	Q5VVP5_HUMAN	Q5VVP5_homo sapien
710	84	4.7	1115	2	Q5UM15_BRARE	Q5UM15 brachydanto	783	83	4.7	873	1	VIDLR_HUMAN	Q9B155_homo sapien
711	84	4.7	1193	2	Q5GPR6_MOUSE	Q5GPR6 mus musculu	784	83	4.7	873	2	Q5VVP6_HUMAN	Q5VVP6_homo sapien
712	84	4.7	1206	2	Q4IHZ8_DROME	Q4IHZ8 dirosophila	785	83	4.7	873	2	Q5S4M1_MACMU	Q5S4M1 macaca mula
713	84	4.7	1300	1	INSRR_MOUSE	INSRR mouse	786	83	4.7	925	2	Q9U4B4_CABEL	Q9U4B4 caenorhabdi
714	84	4.7	1379	1	MER_MOUSE	MER mouse	787	83	4.7	925	2	Q9UB94_CABEL	Q9UB94 caenorhabdi
715	84	4.7	1499	2	Q90815_CHICK	Q90815 gallus gall	788	83	4.7	925	2	Q9UB95_CABEL	Q9UB95 caenorhabdi
716	84	4.7	1671	2	Q57119_MOUSE	Q57119 mus musculu	789	83	4.7	925	2	Q44191_CABEL	Q44191 caenorhabdi
717	84	4.7	1903	2	Q5GPR6_MOUSE	Q5GPR6 mus musculu	790	83	4.7	1099	2	Q61KCI_CABEL	Q61KCI caenorhabdi
718	84	4.7	3034	1	CERRL_MOUSE	C35161 mus musculu	791	83	4.7	1106	1	ACTLY_CABEL	P53585 caenorhabdi
719	83.5	4.7	284	2	Q4SM17_TETNG	Q4SM17 tetradon n	792	83	4.7	1106	2	Q1BIB5_PLA7	Q1BIB5 plasmodium
720	83.5	4.7	284	2	Q9GLJ3_BOVIN	Q9GLJ3 bos taurus	793	83	4.7	1254	2	Q674V1_PODCA	Q674V1 podocoryne
721	83.5	4.7	289	2	Q8KJ3_MERUN	Q8KJ3 meriones un	794	83	4.7	1382	2	Q64RK4_BRARE	Q64RK4 brachydanto
722	83.5	4.7	298	1	JAM2_HUMAN	P57087 homo sapien	795	83	4.7	1419	2	Q4RMP2_TETNG	Q4RMP2 tetradon n
723	83.5	4.7	306	2	Q6PYW4_PYRHO	Q6PYW4 schistosoma	796	83	4.7	2421	2	Q95MJ1_LEMCA	Q95MJ1 lemur cacta
724	83.5	4.7	315	2	Q6F5F0_MOUSE	Q6F5F0 mus musculu	797	83	4.7	2489	2	Q06116_YEAST	Q06116 saccharomyc
725	83.5	4.7	391	2	Q6F5F0_MOUSE	Q6F5F0 mus musculu	798	83	4.7	140	2	Q5VWH6_HUMAN	Q5VWH6_homo sapien
726	83.5	4.7	392	2	Q76708_CABEL	Q76708 caenorhabdi	799	83	4.7	154	2	Q5VWH5_HUMAN	Q5VWH5_homo sapien
727	83.5	4.7	408	2	Q8BVFF_MOUSE	Q8BVFF mus musculu	800	83	4.7	155	2	Q96P81_HUMAN	Q96P81_homo sapien
728	83.5	4.7	408	2	Q8KQ94_MOUSE	Q8KQ94 mus musculu	801	83	4.7	218	2	Q4U114_IACRE	Q4U114 lactobacilli
729	83.5	4.7	408	2	Q91WPI_MOUSE	Q91WPI mus musculu	802	83.5	4.7	230	2	Q8UV76_BRARE	Q8UV76 brachydanto
730	83.5	4.7	429	2	Q5Z4H1_MAGCR	Q5Z4H1 magnaporthe	803	83.5	4.7	239	2	Q618J5_CABER	Q618J5 caenorhabdi
731	83.5	4.7	450	2	Q6UX10_HUMAN	Q6UX10 homo sapien	804	83.5	4.7	319	1	Q7YS40_PIG	Q7YS40_porc
732	83.5	4.7	450	2	Q96R60_HUMAN	Q96R60 homo sapien	805	83.5	4.7	319	1	GPAJ3_MOUSE	Q9JKA5 mus musculu
733	83.5	4.7	515	2	Q96PJ5_HUMAN	Q96PJ5 homo sapien	806	83.5	4.7	330	2	P97269_CAVPO	P97269 cavia porce
734	83.5	4.7	528	2	P91670_DROME	P91670 dirosophila	807	83.5	4.7	332	2	Q565E6_RAT	Q565E6 rattus norv
735	83.5	4.7	577	2	Q8IH34_BACCR	Q8IH34 bacillus ce	808	83.5	4.7	341	1	BTNL1_MOUSE	Q79E50 mus musculu
736	83.5	4.7	580	2	Q6CTP7_YARLI	Q6CTP7 yarrowia li	809	83.5	4.7	347	1	Q529W7_MAGCR	Q529W7 magnaporthe
737	83.5	4.7	646	2	Q899Y4_CLOTE	Q899Y4 clostridium	810	83.5	4.7	364	2	Q4KK51_PSEFS	Q4KK51 pseudomonas
738	83.5	4.7	725	2	Q512D5_CANFA	Q512D5 canis famli	811	83.5	4.7	377	2	Q4R920_MACFA	Q4R920 macaca fasc
739	83.5	4.7	738	2	Q4YB64_PLABE	Q4YB64 plasmodium	812	83.5	4.7	378	1	LEPAT4_ARATH	Q81472 arabidopsis
740	83.5	4.7	847	2	Q512D7_CANFA	Q512D7 canis famli	813	83.5	4.7	382	2	Q6VEU7_MOUSE	Q6VEU7 mus musculu
741	83.5	4.7	862	2	Q4SAP3_TETNG	Q4SAP3 tetradon n	814	83.5	4.7	437	2	Q51ZV9_STRT1	Q51ZV9 streptococc
742	83.5	4.7	1028	2	Q5R6D4_PONPY	Q5R6D4 pongo pygma	815	83.5	4.7	437	2	Q5M4H0_STRT2	Q5M4H0 streptococc
743	83.5	4.7	1059	2	Q9DE49_BRARE	Q9DE49 brachydanto	816	83.5	4.7	446	2	Q5B2Q4_EMENTI	Q5B2Q4 aspergillus
744	83.5	4.7	1101	2	Q5YTB6_BRARE	Q5YTB6 brachydanto	817	83.5	4.7	446	2	Q8NKO3_EMENTI	Q8NKO3 emericiella
745	83.5	4.7	1160	2	Q6G587_BABRE	Q6G587 bartonella	818	83.5	4.7	468	2	Q6PJ50_MOUSE	Q6PJ50 mus musculu
746	83.5	4.7	1273	2	Q4T5J1_TETNG	Q4T5J1 tetradon n	819	83.5	4.7	540	2	Q582E7_TRYRP	Q582E7 trypanosoma
747	83.5	4.7	1332	2	Q6PRX7_CANCA	Q6PRX7 candida gla	820	83.5	4.7	576	2	Q8TOKO_METAC	Q8TOKO methanosarc
748	83.5	4.7	1463	2	Q5S124_MOUSE	Q5S124 mus musculu	821	83.5	4.7	676	2	Q4S1P9_TETNG	Q4S1P9 tetradon n
749	83.5	4.7	1483	2	Q5CYR5_CRYPV	Q5CYR5 cryptospori	822	83.5	4.7	773	1	MS22_CABEL	Q17514 caenorhabdi
750	83.5	4.7	1501	2	Q9QW00_PMTRI	Q9QW00 rattus sp.	823	83.5	4.7	789	2	Q4U3F5_BACTU	Q4U3F5 bacillus th
751	83.5	4.7	1501	2	Q4UJF8_RAT	Q4JF18 rattus norv	824	83.5	4.7	833	2	Q9VHG1_DROME	Q9VHG1 dirosophila
752	83.5	4.7	1556	2	Q83NPF_TROW8	Q83NPF tropheryma	825	83.5	4.7	840	2	Q84BZ6_SPIKU	Q84BZ6 spiroplasma
753	83.5	4.7	1802	2	Q9J5C2_FOPPV	Q9J5C2 fowlpox vir	826	83.5	4.7	840	2	Q84BZ7_SPIKU	Q84BZ7 spiroplasma
754	83.5	4.7	1863	2	Q64605_RAT	Q64605 rattus norv	827	83.5	4.7	986	2	Q6DG17_BRARE	Q6DG17 brachydanto
755	83.5	4.7	3354	2	Q7PL03_ANOGA	Q7PL03 anopheles g	828	83.5	4.7	994	2	Q6167_PLA7	Q6167 plasmodium
756	83.5	4.7	4651	2	Q7PL01_ANOGA	Q7PL01 anopheles g	829	83.5	4.7	994	2	Q610Q4_CABER	Q610Q4 caenorhabdi
757	83	4.7	151	2	Q7YS89_PIG	Q7YS89 porc scrofa	830	83.5	4.7	1028	1	CNTN6_HUMAN	Q9JUS2_homo sapien
758	83	4.7	231	2	Q8WY66_HUMAN	Q8WY66 homo sapien	831	83.5	4.7	1209	2	Q7PG72_ANOGA	Q7PG72 anopheles g
759	83	4.7	234	2	Q7RT27_MOUSE	Q7RT27 mus musculu	832	83.5	4.7	1215	2	Q7OEC1_ANOGA	Q7OEC1 anopheles g
760	83	4.7	237	2	Q6DQX5_RABIT	Q6DQX5 oryctolagus	833	83.5	4.7	1241	2	Q83GG1_TROWT	Q83GG1 tropheryma
761	83	4.7	273	2	Q5VY16_HUMAN	Q5VY16 homo sapien	834	83.5	4.7	1345	2	Q9BUP3_OXYTR	Q9BUP3 oxytricha c

981	81	4.6	423	2	Q9UAG6_DICDI	Q9uag6 dictyosteli	1054	80.5	4.5	823	2	Q39594_CHIRE	Q39594 chlamydomon
982	81	4.6	423	2	Q54D73_DICDI	Q54d73 dictyosteli	1055	80.5	4.5	932	2	Q7TQ14_PAT	Q7tq14 rattus norv
983	81	4.6	425	2	Q61FM2_CABBR	Q61fm2 caenorhabdi	1056	80.5	4.5	976	2	Q8TRD5_BRARE	Q8trd5 brachydanio
984	81	4.6	451	2	Q8DDA0_VIBVU	Q8dda0 vibrio vuln	1057	80.5	4.5	976	2	Q8JFR5_BRARE	Q8jfr5 brachydanio
985	81	4.6	481	2	Q5K374_BRARE	Q5k374 brachydanio	1058	80.5	4.5	976	2	Q9W755_BRARE	Q9w755 brachydanio
986	81	4.6	489	1	CP3102_DROME	Q9ngx9 drosophilla	1059	80.5	4.5	1079	2	Q5QGS4_MOUSE	Q5qgs4 mus musculu
987	81	4.6	507	2	Q9U315_CABERL	Q9u315 caenorhabdi	1060	80.5	4.5	1114	2	Q5QGS4_MOUSE	Q5qgs4 mus musculu
988	81	4.6	517	2	Q4RFQ2_TETNG	Q4rfq2 caenorhabdi	1061	80.5	4.5	1293	2	Q6WLN9_9DIP1	Q6wln9 heterostemu
989	81	4.6	521	1	CD166_CANFA	Q46634 canis famli	1062	80.5	4.5	1304	2	Q5A2D6_CANAL	Q5a2d6 candida alb
990	81	4.6	580	2	Q54D58_DICDI	Q54d58 dictyosteli	1063	80.5	4.5	1364	1	Q5F475_CHICK	Q5f475 xenopus lae
991	81	4.6	617	2	Q5MW54_BRARE	Q5mw54 brachydanio	1064	80.5	4.5	1389	2	Q7Z3Y2_HUMAN	Q7z3y2 homo sapien
992	81	4.6	624	2	Q94AX9_ARATH	Q94ax9 arabidopsis	1065	80.5	4.5	1465	2	Q6UA06_CYEID	Q6ua06 cretopharyn
993	81	4.6	643	2	Q7T231_ARATH	Q7t231 arabidopsis	1066	80.5	4.5	1677	2	Q4R321_TETNG	Q4r321 tetradon n
994	81	4.6	648	2	Q6WTL5_XENLA	Q6wtl5 xenopus lae	1067	80.5	4.5	1702	2	PPERS_HUMAN	PPERS homo sapien
995	81	4.6	700	2	Q4Q3A0_LEIMA	Q4q3a0 leihsmania	1068	80.5	4.5	1948	1	Q5CGS0_CRYPO	Q5cgs0 cryptocospori
996	81	4.6	745	2	Q6NNX7_DROME	Q6nnx7 drosophilla	1069	80.5	4.5	2170	2	Q5CQ17_CRYPA	Q5cq17 cryptocospori
997	81	4.6	760	1	YC85_YEAST	P25574 saccharomyc	1070	80.5	4.5	2253	2	Q8JY20_PPCIC	Q8jy20 ljunigan vir
998	81	4.6	769	2	Q971S9_CIOAB	Q971s9 clostridium	1071	80.5	4.5	2253	2	Q8JY20_PPCIC	Q8jy20 ljunigan vir
999	81	4.6	829	1	CADH3_HUMAN	P22223 homo sapien	1072	80.5	4.5	2358	2	Q95MJ2_MACRG	Q95mj2 macropus ru
1000	81	4.6	837	2	Q8G4P3_BIFLO	Q8g4p3 bifidobacte	1073	80.5	4.5	2398	2	Q872P1_NEUCR	Q872p1 neurospora
1001	81	4.6	937	2	Q5RDT6_PONPY	Q5rdt6 pongo pygma	1074	80.5	4.5	3267	2	Q5DUA4_MOUSE	Q5dua4 mus musculu
1002	81	4.6	1079	2	Q6E7G6_CANFA	Q6e7g6 canis famli	1075	80.5	4.5	3267	2	Q5DUA5_MOUSE	Q5dua5 mus musculu
1003	81	4.6	1150	2	Q4SL82_TETNG	Q4sl82 tetradon n	1076	80.5	4.5	3337	2	Q9TWY4_CABERL	Q9twy4 caenorhabdi
1004	81	4.6	1180	2	Q5IS40_PANTR	Q5is40 pan troglod	1077	80.5	4.5	3343	1	CAD3_CABERL	CAD3 caenorhabdi
1005	81	4.6	1196	2	Q9BTF1_CYPCA	Q9btf1 cypinus ca	1078	80.5	4.5	3352	2	Q5DUJ3_MOUSE	Q5duj3 mus musculu
1006	81	4.6	1200	2	Q9P3A8_SCHPO	Q9p3a8 schizosacch	1079	80.5	4.5	3354	1	CAD23_MOUSE	CAD23 mouse
1007	81	4.6	1324	1	NRCAM_HUMAN	Q92823 homo sapien	1080	80.5	4.5	3358	1	CSRG2_MOUSE	CSRG2 mouse
1008	81	4.6	1335	2	Q6ZPE0_MOUSE	Q6zpe0 mus musculu	1081	80.5	4.5	5992	2	Q5W615_CABERL	Q5w615 caenorhabdi
1009	81	4.6	1355	2	Q51EY2_ENTHI	Q51ey2 entamoeba h	1082	80.5	4.5	6632	1	UNC89_CABERL	UNC89 caenorhabdi
1010	81	4.6	1478	2	Q59H90_HUMAN	Q59h90 homo sapien	1083	80.5	4.5	7122	2	Q5W616_CABERL	Q5w616 caenorhabdi
1011	81	4.6	1498	2	Q64604_RAT	Q64604 rattus norv	1084	80.5	4.5	7441	2	Q7Z120_CABERL	Q7z120 caenorhabdi
1012	81	4.6	1891	2	Q7UI70_RHOBA	Q7ui70 rhodospirell	1085	80.5	4.5	8081	2	Q8WV18_HUMAN	Q8wv18 homo sapien
1013	81	4.6	2219	2	Q88M19_LACPL	Q88m19 lactobacill	1086	80.5	4.5	184	2	Q9UKJ0_HUMAN	Q9ukj0 homo sapien
1014	81	4.6	2283	2	Q4N957_THERPA	Q4n957 theileria p	1087	80.5	4.5	227	2	Q9UKJ0_HUMAN	Q9ukj0 homo sapien
1015	81	4.6	2391	2	Q5HNO0_STABEQ	Q5hno0 staphylococ	1088	80.5	4.5	235	2	Q9M11_MOUSE	Q9m11 mus musculu
1016	81	4.6	2402	2	Q5HNR4_STABEQ	Q5hnr4 staphylococ	1089	80.5	4.5	240	2	Q5VSN6_BRARE	Q5vsn6 brachydanio
1017	81	4.6	2747	2	Q5GQM9_9CAUD	Q5gqm9 bacteriophia	1090	80.5	4.5	276	2	Q640S5_XENTR	Q640s5 xenopus tro
1018	80.5	4.5	261	2	Q9W6V1_CHICK	Q9w6v1 gallus gall	1091	80.5	4.5	327	2	Q4RTW7_TETNG	Q4rtw7 tetradon n
1019	80.5	4.5	290	2	Q8CRR9_STABEQ	Q8crr9 staphylococ	1092	80.5	4.5	337	2	Q8UV29_BRARE	Q8uv29 brachydanio
1020	80.5	4.5	291	2	Q5HNO0_STABEQ	Q5hno0 staphylococ	1093	80.5	4.5	338	1	LSAMP_RAT	LSAMP rattus norv
1021	80.5	4.5	346	1	EPNBI1_HUMAN	P98172 homo sapien	1094	80.5	4.5	341	1	K12L3_HUMAN	K12l3 rattus norv
1022	80.5	4.5	371	2	Q4WVPI_BACCE	Q4wvpi bacillus ce	1095	80.5	4.5	343	2	Q8X5J1_ECO57	Q8x5j1 escherichia
1023	80.5	4.5	371	2	Q633A8_BACCK	Q633a8 bacillus ce	1096	80.5	4.5	361	2	Q5M960_RAT	Q5m960 rattus norv
1024	80.5	4.5	371	2	Q6HCJ8_BACCK	Q6hcj8 bacillus th	1097	80.5	4.5	362	2	Q6XN16_ONCMY	Q6xn16 oncorhynzon
1025	80.5	4.5	371	2	Q72249_BACCI	Q72249 bacillus ce	1098	80.5	4.5	378	2	Q6XN16_ONCMY	Q6xn16 oncorhynzon
1026	80.5	4.5	371	2	Q816V2_BACCR	Q816v2 bacillus ce	1099	80.5	4.5	436	2	Q9N563_HUMAN	Q9n563 homo sapien
1027	80.5	4.5	376	1	GCPI1_ABATH	Q94d08 arabidopsis	1100	80.5	4.5	436	2	Q4NAS0_9MICC	Q4nas0 arthroabcte
1028	80.5	4.5	382	2	Q5X143_RAT	Q5x143 rattus norv	1101	80.5	4.5	440	2	Q8MK36_NACMU	Q8mk36 macaca mla
1029	80.5	4.5	385	2	Q4SOV8_TETNG	Q4sov8 tetradon n	1102	80.5	4.5	465	1	Q67TB8_STYTH	Q67tb8 symbiodace
1030	80.5	4.5	388	2	Q8R464_MOUSE	Q8r464 mus musculu	1103	80.5	4.5	482	1	ABCD_PSEAE	P16275 pseudomonas
1031	80.5	4.5	462	1	MURD_CIOAB	Q97db9 clostridium	1104	80.5	4.5	509	2	Q6UEG2_ASPPA	Q6ueg2 aspergillus
1032	80.5	4.5	472	2	Q811T8_MOUSE	Q811t8 mus musculu	1105	80.5	4.5	509	2	Q5CUC7_CRYPA	Q5cuc7 cryptocospori
1033	80.5	4.5	473	2	Q5RGHS_SALPA	Q5rghs salmonella	1106	80.5	4.5	529	2	Q81WX2_HUMAN	Q81wx2 homo sapien
1034	80.5	4.5	473	2	Q82809_SALTI	Q82809 salmonella	1107	80.5	4.5	516	2	FERLI1_MOUSE	Q91v87 mus musculu
1035	80.5	4.5	475	2	Q62056_MOUSE	Q62056 mus musculu	1108	80.5	4.5	535	1	Q6SJI2_BACLD	Q6sji2 bacillus li
1036	80.5	4.5	476	1	YCAM_ECOLI	P75835 escherichia	1109	80.5	4.5	535	2	Q58EG3_BRARS	Q58eg3 brachydanio
1037	80.5	4.5	498	2	Q886D9_PSEBM	Q886d9 pseudomonas	1110	80.5	4.5	574	2	Q62911_RINDK	Q62911 rinderpest
1038	80.5	4.5	507	2	Q5K4Q3_PIG	Q5k4q3 sus scrofa	1111	80.5	4.5	624	2	Q8LQ08_ARATH	Q8lq08 arabidopsis
1039	80.5	4.5	514	2	Q5SQUB_MOUSE	Q5squb mus musculu	1112	80.5	4.5	624	2	Q9VUD0_DROME	Q9vud0 drosophilla
1040	80.5	4.5	540	2	Q8XEB5_ECO57	Q8xeb5 escherichia	1113	80.5	4.5	633	2	Q7SXCI_BRARE	Q7sxc1 brachydanio
1041	80.5	4.5	546	2	Q80X70_MOUSE	Q80x70 mus musculu	1114	80.5	4.5	637	1	PBL1_CRYNV	Q98p2 cryptocococ
1042	80.5	4.5	548	2	Q99NB3_MOUSE	Q99nb3 mus musculu	1115	80.5	4.5	681	2	Q75JX7_DICDI	Q75jx7 dictyosteli
1043	80.5	4.5	556	2	Q9BDM4_VIBVU	Q9bdm4 vibrio vuln	1116	80.5	4.5	753	2	Q54KQ7_DICDI	Q54kq7 dictyosteli
1044	80.5	4.5	564	2	Q7ZU00_BRARE	Q7zu00 brachydanio	1117	80.5	4.5	865	2	Q68DA2_HUMAN	Q68da2 homo sapien
1045	80.5	4.5	602	2	Q6CYJ9_HUMAN	Q6cyj9 homo sapien	1118	80.5	4.5	902	1	BRCC4_CRIGR	Q9aym7 cricetus lae
1046	80.5	4.5	636	2	Q4FWB0_LEIMA	Q4fwb0 leihsmania	1119	80.5	4.5	957	2	Q641F3_XENLA	Q641f3 xenopus lae
1047	80.5	4.5	662	2	Q60926_HUMAN	Q60926 homo sapien	1120	80.5	4.5	960	2	Q6BXD5_DEBHA	Q6bxds deaeromyce
1048	80.5	4.5	683	2	Q5CRD8_CRYPA	Q5cprd8 cryptocospori	1121	80.5	4.5	1000	2	Q4TBK4_TETNG	Q4tbk4 tetradon n
1049	80.5	4.5	707	1	Q7XNT7_ORYSA	Q7xnt7 oryza sativ	1122	80.5	4.5	1005	2	P79921_XENLA	P79921 xenopus lae
1050	80.5	4.5	721	1	DP55_ASPPU	Q13479 aspergillus	1123	80.5	4.5	1040	2	CNTN2_HUMAN	Q02246 homo sapien
1051	80.5	4.5	739	2	Q53FL7_HUMAN	Q53fl7 homo sapien	1124	80.5	4.5	1040	2	Q5T054_HUMAN	Q5t054 homo sapien
1052	80.5	4.5	739	2	Q865F2_RABIT	Q865f2 oryctolagus	1125	80.5	4.5	1170	1	TSPI1_MOUSE	P35441 mus musculu
1053	80.5	4.5	789	2	Q8RSZ5_BACTU	Q8rsz5 bacillus th	1126	80.5	4.5				

1127	80	4.5	1192	2	081Y28_BACAN	081Y28 bacillus an	1200	79	4.5	323	2	08ND29_HUMAN	08nd29 mus saplien
1128	80	4.5	1310	2	081714_CABEL	081714 caenorhabdi	1201	79	4.5	340	2	06PK29_MOUSE	06pk29 mus musculu
1129	80	4.5	1431	2	08EW23_MYCPE	08ew23 mycoplasma	1202	79	4.5	342	2	08MK29_MACMU	08mk29 macaca mula
1130	80	4.5	1925	2	09YR83_YVIRP	09yr83 nudaurelia	1203	79	4.5	389	2	05U3R8_BRARR	05u3r8 brachydanio
1131	80	4.5	2195	2	0723M7_LISMF	0723m7 listeria mo	1204	79	4.5	406	2	08BP77_MOUSE	08bp77 mus musculu
1132	80	4.5	2456	2	081715_CABEL	081715 caenorhabdi	1205	79	4.5	410	2	081JPS_BACAN	081jps bacillus an
1133	80	4.5	3064	2	06UDW7_PLAFA	06udw7 plasmodium	1206	79	4.5	412	2	06MZS4_HUMAN	06mzs4 homo saplien
1134	80	4.5	5229	2	07RTF4_PLAYO	07rtf4 plasmodium	1207	79	4.5	429	2	08BE81_MOUSE	08bf81 m mus mucu
1135	79.5	4.5	151	2	08C2T1_MOUSE	08c2t1 mus musculu	1208	79	4.5	438	1	Y3532_METUA	08c289 methanococ
1136	79.5	4.5	236	2	06FIQ7_HUMAN	06fiq7 homo saplien	1209	79	4.5	440	2	08MK37_MACMU	08mk37 macaca mula
1137	79.5	4.5	237	2	06DHW4_HUMAN	06dhw4 homo saplien	1210	79	4.5	446	2	P79762_CHICK	P79762 gallus galli
1138	79.5	4.5	244	2	08SOB6_PIG	08sob6 sus scrofa	1211	79	4.5	446	2	09PWF8_CHICK	09pwf8 gallus galli
1139	79.5	4.5	249	1	MYP0_CHICK	P73301 gallus galli	1212	79	4.5	446	2	Q4VU46_CHICK	Q4vu46 gallus galli
1140	79.5	4.5	257	1	Q5WPT1_SHEEP	Q5wpt1 ovis aries	1213	79	4.5	446	2	Q4VU49_CHICK	Q4vu49 gallus galli
1141	79.5	4.5	289	2	Q97XZ7_SULSO	Q97xz7 sulfolobus	1214	79	4.5	446	2	Q4VU50_CHICK	Q4vu50 gallus galli
1142	79.5	4.5	321	2	Q5WRG0_SHEEP	Q5wrg0 ovis aries	1215	79	4.5	446	2	Q4VU57_CHICK	Q4vu57 gallus galli
1143	79.5	4.5	328	1	CYSP4_BRANA	P25251 brassica na	1216	79	4.5	446	2	Q4VU66_CHICK	Q4vu66 gallus galli
1144	79.5	4.5	345	2	Q6GM08_XENIA	Q6gm08 xenopus lae	1217	79	4.5	446	2	Q4VU63_CHICK	Q4vu63 gallus galli
1145	79.5	4.5	368	2	Q4VA91_MOUSE	Q4va91 mus musculu	1218	79	4.5	451	2	Q7MOR3_VIBRY	Q7mqe3 vibrio vuln
1146	79.5	4.5	399	2	Q8EMV2_OCBIR	Q8emv2 oceanobacti	1219	79	4.5	461	2	Q4RL18_CABEL	Q4rl18 caenorhabdi
1147	79.5	4.5	400	2	Q8ZHN7_YERPE	Q8zhn7 yerstinia pe	1220	79	4.5	463	1	STHA_PSEBK	Q8hkx8 pseudomonas
1148	79.5	4.5	400	2	Q666Z6_YERPS	Q666z6 yerstinia pe	1221	79	4.5	474	2	Q4V883_RAT	Q4v883 rattus norv
1149	79.5	4.5	401	2	Q93534_XENIA	Q93534 xenopus lae	1222	79	4.5	479	2	Q9K6X5_BACHD	Q9k6x5 bacillus ha
1150	79.5	4.5	418	2	Q7RL88_PLAYO	Q7rl88 plasmodium	1223	79	4.5	490	1	RLUD1_HUMAN	RLUD1_PONPY
1151	79.5	4.5	430	1	TPSN_CHICK	Q73895 gallus galli	1224	79	4.5	491	2	Q8GZP5_LYCES	Q8gzp5 lycopersico
1152	79.5	4.5	430	2	Q761J8_COTJA	Q761j8 coturnix co	1225	79	4.5	511	2	Q4IG29_GIBBEZ	Q4ig29 gibberella
1153	79.5	4.5	446	2	Q69885_STRCC	Q69885 streptomyce	1226	79	4.5	524	2	Q8LTK1_9CAUD	Q8ltk1 lactococcus
1154	79.5	4.5	453	2	Q4S5U7_TETNG	Q4s5u7 tetradodon n	1227	79	4.5	526	2	Q51SR0_MAGGR	Q51se0 magnaporthe
1155	79.5	4.5	474	2	Q7ZU93_BRARB	Q7zu93 brachydanio	1228	79	4.5	526	2	Q80WA6_MOUSE	Q80wa6 mus musculu
1156	79.5	4.5	490	1	TIME_ECOLI	Q47282 escherichia	1229	79	4.5	526	2	Q80Y89_MOUSE	Q80y89 mus musculu
1157	79.5	4.5	510	2	Q5E9Z9_BOVIN	Q5e9z9 bos taurus	1230	79	4.5	571	2	Q5B307_ICTPU	Q5b307 ictalurus p
1158	79.5	4.5	516	2	Q418S1_STAHU	Q418s1 staphylococ	1231	79	4.5	584	2	Q9Y3Y8_HUMAN	Q9y3y8 homo saplien
1159	79.5	4.5	520	2	Q8GDL8_PHOLU	Q8gdl8 haloarchabu	1232	79	4.5	586	2	Q5CFV6_CRYHO	Q5cfv6 cryptospori
1160	79.5	4.5	524	2	Q5V7K4_XENIA	Q5v7k4 halococcus	1233	79	4.5	590	2	Q9P4U4_CANTR	Q9p4u4 candida tro
1161	79.5	4.5	524	2	Q7PSU8_ANOGA	Q7psu8 anopheles g	1234	79	4.5	611	2	Q91BR6_XENIA	Q91bf6 xenopus lae
1162	79.5	4.5	641	2	Q8ESD2_CIOIN	Q8esd2 clona intes	1235	79	4.5	611	2	Q9PT10_XENIA	Q9pt10 xenopus lae
1163	79.5	4.5	686	2	Q75WK5_ORYLA	Q75wk5 oryzias lat	1236	79	4.5	617	2	Q51F12_BRARB	Q51f12 brachydanio
1164	79.5	4.5	729	2	Q4RFH6_TETNG	Q4rfh6 tetradodon n	1237	79	4.5	630	2	Q4WG72_ASPTU	Q4wg72 aspergillus
1165	79.5	4.5	740	1	PECAL_PIG	Q95242 sus scrofa	1238	79	4.5	644	2	Q6GINS_XENIA	Q6gins xenopus lae
1166	79.5	4.5	743	2	Q6P4H5_HUMAN	Q6p4h5 homo saplien	1239	79	4.5	653	2	Q4R819_USITMA	Q4r819 usellago ma
1167	79.5	4.5	821	2	Q8C7S6_MOUSE	Q8c7s6 mus musculu	1240	79	4.5	657	2	P73359_SYNY3	P73359 synecocyst
1168	79.5	4.5	845	2	Q91YY0_MOUSE	Q91yy0 mus musculu	1241	79	4.5	711	2	Q80Y89_MOUSE	Q80y89 mus musculu
1169	79.5	4.5	859	1	PM52_MOUSE	P54279 mus musculu	1242	79	4.5	778	2	Q9N4B1_CABEL	Q9n4b1 caenorhabdi
1170	79.5	4.5	873	1	VLDLR_MOUSE	P98156 mus musculu	1243	79	4.5	785	2	Q7N4B1_MOUSE	Q7n4p4 mus musculu
1171	79.5	4.5	875	2	Q4RKX6_TETNG	Q4rkx6 tetradodon n	1244	79	4.5	795	2	Q6O0V2_MYCHY	Q6o0v2 mycoplasma
1172	79.5	4.5	924	2	Q73LB0_TREDE	Q73l80 treponema d	1245	79	4.5	807	2	Q8PTR2_METMA	Q8ptr2 methanosarc
1173	79.5	4.5	961	1	ROBO4_RAT	Q80w87 rattus norv	1246	79	4.5	853	2	Q19372_CABEL	Q19372 caenorhabdi
1174	79.5	4.5	980	1	CSFIR_FELICA	P13369 felis silve	1247	79	4.5	917	2	Q767W4_PIG	Q767w4 sus scrofa
1175	79.5	4.5	1043	1	Q6PA07_XENIA	Q6pa07 xenopus lae	1248	79	4.5	928	2	Q61XY3_CABBR	Q61xy3 caenorhabdi
1176	79.5	4.5	1162	1	TFP2_HUMAN	Q9unv4 homo saplien	1249	79	4.5	977	2	Q8GZ40_ARATH	Q8gz40 arabidopsis
1177	79.5	4.5	1171	2	Q80YQ1_MOUSE	Q80yq1 mus musculu	1250	79	4.5	996	2	Q8BM64_DEBHA	Q8bme4 debaryomyce
1178	79.5	4.5	1171	2	Q8CGR2_MOUSE	Q8cgr2 mus musculu	1251	79	4.5	1017	2	Q4SK37_TETNG	Q4sk37 tetradodon n
1179	79.5	4.5	1197	2	Q4LWJ3_9BURK	Q4ljw3 burkholderi	1252	79	4.5	1030	2	Q7XTP4_ORYSA	Q7xtp4 oryza sativ
1180	79.5	4.5	1262	2	Q5AOK4_EMBNI	Q5aqk4 aspergillus	1253	79	4.5	1104	2	Q9FKR7_ARATH	Q9fkr7 arabidopsis
1181	79.5	4.5	1342	2	Q9GPP6_DROME	Q9gpp6 drosophila	1254	79	4.5	1177	2	Q6GGB1_XENIA	Q6ggb1 xenopus lae
1182	79.5	4.5	1342	2	Q9VPZ7_DROME	Q9vpz7 drosophila	1255	79	4.5	1218	2	Q4N9H0_THIEPA	Q4n9h0 theileria p
1183	79.5	4.5	1355	2	Q5TUE1_ANOGA	Q5tue1 anopheles g	1256	79	4.5	1228	1	ALAS_ARATH	Q9agq3 arabidopsis
1184	79.5	4.5	1465	1	MYOM2_HUMAN	P54296 homo saplien	1257	79	4.5	1264	2	P91767_MANSE	P91767 menduca sex
1185	79.5	4.5	1614	1	Q7RMN9_PLAYO	Q7rmn9 plasmodium	1258	79	4.5	1361	1	GLI4_XENIA	Q91661 xenopus lae
1186	79.5	4.5	1670	2	Q7QZP4_GIALA	Q7qzp4 giardia lam	1259	79	4.5	1382	1	MET_CANFA	Q75zy9 canis famli
1187	79.5	4.5	1838	2	Q88Z07_MOUSE	Q88z07 mus musculu	1260	79	4.5	1390	2	Q7RRL3_PLAYO	Q7rrl3 plasmodium
1188	79.5	4.5	2253	2	Q8ATV19_PPICO	Q8atv19 ljunjan vir	1261	79	4.5	1416	2	Q5AS50_EMBNI	Q5as50 aspergillus
1189	79.5	4.5	2256	2	Q8ATV19_PPICO	Q8atv19 ljunjan vir	1262	79	4.5	1465	2	Q6ZOR3_MOUSE	Q6z0r3 mus musculu
1190	79.5	4.5	2658	2	Q4G573_LEITMA	Q4g573 leishmania	1263	79	4.5	1887	2	Q9QW67_9MURI	Q9qw67 rattus sp.
1191	79.5	4.5	2706	2	Q97292_PLAF7	Q97292 plasmodium	1264	79	4.5	1905	2	Q5VVI9_HUMAN	Q5vvi9 homo saplien
1192	79	4.5	158	2	Q15225_HUMAN	Q15225 homo saplien	1265	79	4.5	1925	2	Q6BHV1_MOUSE	Q6bhv1 mus musculu
1193	79	4.5	210	2	Q9AC09_CAUCR	Q9ac09 caulobacter	1266	79	4.5	4010	1	FRAS1_MOUSE	Q5vfe8 homo saplien
1194	79	4.5	222	2	Q8WK98_MACPR	Q8wk98 macroscelid	1267	79	4.5	173	2	Q5VVF8_HUMAN	Q5vfe8 pongo pygma
1195	79	4.5	226	2	Q86P32_DROME	Q86p32 drosophila	1268	78.5	4.4	261	2	Q5R602_PONPY	Q5r602 pongo pygma
1196	79	4.5	244	2	Q927X2_LISIN	Q927x2 listeria in	1269	78.5	4.4	292	2	Q5HZR6_XENIA	Q5hzr6 xenopus lae
1197	79	4.5	260	2	Q53H40_HUMAN	Q53h40 homo saplien	1270	78.5	4.4	300	1	CEAL19_HUMAN	Q7z692 homo saplien
1198	79	4.5	271	2	Q95161_GADMO	Q95161 gadus moriu	1271	78.5	4.4	303	2	Q4X5M9_PLACH	Q4x5m9 placach
1199	79	4.5	274	2	Q5MD24_PIG	Q5md24 sus scrofa	1272	78.5	4.4	305	1	PEX26_MACFA	Q9pbe5 macaca fasc

1273	78.5	4.4	305	2	Q4HXQ1_GIBBE	Q4hxq1 gibberella	1346	78	4.4	353	1	CEPU1_CHICK	Q99773 gallus galli
1274	78.5	4.4	308	2	Q5MRG1_SHEEP	Q5wrg1 ovis aries	1347	78	4.4	375	2	Q65280_ASF	Q65280 african swi
1275	78.5	4.4	318	2	Q91664_XENLA	Q91664 xenopus lae	1348	78	4.4	399	1	V5IG4_HUMAN	Q9y279 homo sapien
1276	78.5	4.4	325	2	Q501V7_BRAR	Q501v7 brachydano	1349	78	4.4	402	2	Q35444_MOUSE	Q35444 mus musculus
1277	78.5	4.4	333	2	Q7MR78_MOLST	Q7mr78 molinia s	1350	78	4.4	412	2	Q8G6P7_BIFLO	Q8G6P7 bifidobacte
1278	78.5	4.4	341	2	Q59EM4_HUMAN	Q59em4 homo sapien	1351	78	4.4	423	2	Q9RB12_ACIAD	Q9rb12 acinetobact
1279	78.5	4.4	381	2	Q753P2_ASHGO	Q753p2 ashbya goes	1352	78	4.4	435	2	Q4TBP7_TETNG	Q4tbp7 tetradodon n
1280	78.5	4.4	388	2	Q8NFZ8_HUMAN	Q8nftz8 homo sapien	1353	78	4.4	446	2	Q4VU54_CHICK	Q4vnu54 gallus galli
1281	78.5	4.4	429	1	IGHF_RAT	P01855 rattus norv	1354	78	4.4	446	2	Q4VU62_CHICK	Q4vnu62 gallus galli
1282	78.5	4.4	431	2	Q8X022_NEUCR	Q8x022 neuropept	1355	78	4.4	452	2	Q4VOM5_CANBF	Q4vnu5 canidiatus
1283	78.5	4.4	434	2	Q4RFG0_TETNG	Q4rtfg0 tetradodon n	1356	78	4.4	452	2	Q4TOT8_TETNG	Q4tot8 tetradodon n
1284	78.5	4.4	439	2	Q5R6T5_PONPY	Q5r6t5 pongo pygma	1357	78	4.4	473	2	Q9VOS_DROME	Q9vvs drosophila
1285	78.5	4.4	432	2	Q76773_LUCPU	Q76773 lucilia cup	1358	78	4.4	473	2	Q4MOJ9_BACCE	Q4mqj9 bacillus ce
1286	78.5	4.4	459	2	Q9S839_ARATH	Q9s839 arabidopsis	1359	78	4.4	490	2	Q74491_SCHPO	Q74491 schizosacch
1287	78.5	4.4	463	2	Q4ML18_BACCE	Q4ml18 bacillus ce	1360	78	4.4	491	2	Q9VKX6_DROME	Q9vxx6 drosophila
1288	78.5	4.4	467	1	SIGL1_MOUSE	Q91y57 mus musculi	1361	78	4.4	515	2	Q4V518_DROME	Q4v518 drosophila
1289	78.5	4.4	471	2	Q9DAV5_MOUSE	Q9dav5 mus musculi	1362	78	4.4	550	2	Q61CK3_CAEBR	Q61ck3 caenorhabdi
1290	78.5	4.4	497	1	UBRD_ECO57	P58194 escherichia	1363	78	4.4	587	2	Q5A325_CANAL	Q5a325 candida alb
1291	78.5	4.4	537	2	Q93EIT_RHILT	Q93eit rhizobium l	1364	78	4.4	590	2	Q5TTP5_ANOCA	Q5ttp5 anopheles g
1292	78.5	4.4	539	2	Q04252_ARATH	Q04252 arabidopsis	1365	78	4.4	604	2	Q76PD3_SCHPO	Q76pd3 schizosacch
1293	78.5	4.4	542	2	Q6PAB8_XENLA	Q6pab8 xenopus lae	1366	78	4.4	606	2	Q6IRH8_RAT	Q6irh8 rattus norv
1294	78.5	4.4	556	2	Q8L6Z9_ARATH	Q8l6z9 arabidopsis	1367	78	4.4	606	2	Q9S837_MOUSE	Q9s887 mus musculi
1295	78.5	4.4	591	2	Q6NSU9_MOUSE	Q6nau9 mus musculi	1368	78	4.4	608	2	Q57826_BRUAB	Q57826 bruceella ab
1296	78.5	4.4	603	2	Q7S314_NEUCR	Q7s314 neuropept	1369	78	4.4	608	2	Q8YCV9_BRUME	Q8ycv9 bruceella me
1297	78.5	4.4	618	2	Q54BQ5_DICDI	Q54bq5 dicyostei	1370	78	4.4	608	2	Q8FVG6_BRUST	Q8fvg6 bruceella su
1298	78.5	4.4	628	1	LU_HUMAN	P50895 homo sapien	1371	78	4.4	609	1	H5MA_RINDK	P13567 rinderpest
1299	78.5	4.4	629	2	Q8L444_ARATH	Q8l444 arabidopsis	1372	78	4.4	612	2	Q7RE74_PLAYO	Q7re74 plasmodium
1300	78.5	4.4	638	2	Q9LFS4_ARATH	Q9lfs4 arabidopsis	1373	78	4.4	634	2	Q8X024_SHETE	Q8x024 cryptococcu
1301	78.5	4.4	651	2	Q8BBU0_PSRSM	Q8bbu0 pseudomonas	1374	78	4.4	634	2	Q6MXO_SHETE	Q6mxo cryptococcu
1302	78.5	4.4	708	1	KIRP2_HUMAN	Q6uwl6 homo sapien	1375	78	4.4	648	2	Q8R2Y2_MOUSE	Q8r2y2 mus musculi
1303	78.5	4.4	717	2	Q6C1H6_YARLI	Q6c1h6 yarrowia li	1376	78	4.4	653	2	Q762C5_MOUSE	Q762c5 mus musculi
1304	78.5	4.4	721	2	Q4XIR6_ASPFU	Q4xir6 aspergillus	1377	78	4.4	690	2	Q5ISU0_MACFA	Q5isl0 metacac fasc
1305	78.5	4.4	751	2	Q6FKY3_CANGA	Q6fk37 candida gla	1378	78	4.4	706	2	Q6YC14_MOUSE	Q6yc14 mus musculi
1306	78.5	4.4	831	1	SAS3_YEAST	P34218 saccharomyc	1379	78	4.4	802	2	Q8BM11_MOUSE	Q8bm11 mus musculi
1307	78.5	4.4	844	2	Q59YK6_CANAL	Q59y24 candida alb	1380	78	4.4	807	2	NCA12_HUMAN	P13592 homo sapien
1308	78.5	4.4	844	2	Q59YK6_CANAL	Q59y24 candida alb	1381	78	4.4	807	2	Q59FL7_HUMAN	Q59fl7 homo sapien
1309	78.5	4.4	844	2	Q75H9_CANAL	Q75h9 candida alb	1382	78	4.4	836	2	Q48483_BPSPP	Q48483 bacterioph
1310	78.5	4.4	847	1	CD22_HUMAN	P20273 homo sapien	1383	78	4.4	848	1	NCA11_HUMAN	P13591 homo sapien
1311	78.5	4.4	888	2	Q7ZMM9_XENLA	Q7zmm9 xenopus lae	1384	78	4.4	850	1	SEMLA_DROME	Q24322 drosophila
1312	78.5	4.4	901	2	Q57V64_9TRYP	Q57v64 trypanosoma	1385	78	4.4	850	2	Q4S3Y6_TETNG	Q4s3y6 tetradodon n
1313	78.5	4.4	927	1	PCDDG_HUMAN	Q9y5g3 homo sapien	1386	78	4.4	865	2	Q8Q7H7_9H1V1	Q8q7h7 human immun
1314	78.5	4.4	938	2	Q64BU3_9ARCH	Q64bu3 uncultured	1387	78	4.4	884	1	CADH8_XENLA	P31352 xenopus lae
1315	78.5	4.4	1018	2	Q65L89_BURPS	Q65l89 burkholderi	1388	78	4.4	884	2	Q6NTM0_XENLA	Q6ntm0 xenopus lae
1316	78.5	4.4	1029	2	Q596X0_CARAU	Q596x0 carassius a	1389	78	4.4	904	2	Q7QCM9_ANOGA	Q7qcm9 anopheles g
1317	78.5	4.4	1033	2	Q62C67_BURMA	Q62c67 burkholderi	1390	78	4.4	905	2	Q13955_SCHPO	Q13955 schizosacch
1318	78.5	4.4	1036	1	CNTN2_CHICK	P26885 gallus galli	1391	78	4.4	966	2	Q4RKM2_TETNG	Q4rk2 tetradodon n
1319	78.5	4.4	1038	2	Q8YSN0_ANASP	Q8ysn0 anabaena sp	1392	78	4.4	976	2	Q6LYF8_METMP	Q6lyf8 methanococc
1320	78.5	4.4	1143	2	Q69Z28_MOUSE	Q69z28 mus musculi	1393	78	4.4	993	1	DSG3_MOUSE	Q31902 mus musculi
1321	78.5	4.4	1198	2	Q60T65_CAEBR	Q60t65 caenorhabdi	1394	78	4.4	1002	2	Q4SP56_TETNG	Q4sp56 tetradodon n
1322	78.5	4.4	1225	2	Q4WK02_ASPFU	Q4wk02 aspergillus	1395	78	4.4	1009	2	Q33250_XENLA	Q33250 xenopus lae
1323	78.5	4.4	1341	2	Q4YB10_PLABE	Q4yb10 plasmodium	1396	78	4.4	1016	2	Q8A4W1_BACYN	Q8a4w1 bacteroides
1324	78.5	4.4	1465	2	Q8GVU3_ARATH	Q8gvu3 arabidopsis	1397	78	4.4	1040	1	CNTN2_MOUSE	Q61330 mus musculi
1325	78.5	4.4	1468	2	Q8SVE1_ARATH	Q8sve1 arabidopsis	1398	78	4.4	1071	2	Q75CA6_ASHGO	Q75ca6 ashbya goes
1326	78.5	4.4	1615	2	Q7ROM4_PLAYO	Q7rtm4 plasmodium	1399	78	4.4	1076	2	Q4RNS5_TETNG	Q4rns5 tetradodon n
1327	78.5	4.4	1638	2	Q61WTS_CAEBR	Q61wts caenorhabdi	1400	78	4.4	1147	2	Q9DDX1_MELGA	Q9ddx1 metacaris g
1328	78.5	4.4	1897	2	Q50TWS_ENTHI	Q50tws entamoeba h	1401	78	4.4	1209	2	Q54SA2_DICDI	Q54sa2 dictyosteli
1329	78.5	4.4	1915	2	Q9RPL0_9CIOT	Q9rpl0 acetiabrio	1402	78	4.4	1229	2	Q6CKW4_KIULA	Q6ckw4 kuuyeromyc
1330	78.5	4.4	1954	2	Q6ZP2_MOUSE	Q6zpp2 mus musculi	1403	78	4.4	1288	2	Q62AK5_CAEBR	Q62ak5 caenorhabdi
1331	78.5	4.4	2053	2	Q4WZ40_THERP	Q4wz40 theileria p	1404	78	4.4	1341	2	Q4RWS0_TETNG	Q4rws0 tetradodon n
1332	78.5	4.4	2176	2	Q6W4S5_MOUSE	Q6w4s5 mus musculi	1405	78	4.4	1458	2	Q5B164_DROME	Q5b164 drosophila
1333	78.5	4.4	2179	1	K0310_HUMAN	Q15027 homo sapien	1406	78	4.4	1503	2	Q7KIT4_DROME	Q7kit4 drosophila
1334	78.5	4.4	2829	2	Q61VD6_STRPU	Q61vd6 strongyloce	1407	78	4.4	1510	2	Q4IMKO_GIBZE	Q4imko gibberella
1335	78.5	4.4	194	2	Q6UXN2_HUMAN	Q6uxn2 homo sapien	1408	78	4.4	1677	2	Q54WH5_DICDI	Q54wh5 dictyosteli
1336	78.5	4.4	200	2	Q8NEU1_HUMAN	Q8neu1 homo sapien	1409	78	4.4	1924	2	Q7Z8U6_ASPOR	Q7z8u6 aspergillus
1337	78.5	4.4	236	2	Q8NEU1_HUMAN	Q8neu1 homo sapien	1410	78	4.4	1943	2	Q4RPP4_TETNG	Q4rpp4 tetradodon n
1338	78.5	4.4	257	1	UPPS_CLOAB	Q97162 clostridium	1411	78	4.4	3722	2	P94873_LYSIA	P94873 lysobacter
1339	78.5	4.4	272	2	Q8RINS_MOUSE	Q8rins mus musculi	1412	78	4.4	117	2	Q7Z267_BRAR	Q7z267 brachydano
1340	78.5	4.4	287	2	Q13984_HUMAN	Q13984 homo sapien	1413	78	4.4	128	2	Q8BUW2_HUMAN	Q8buw2 homo sapien
1341	78.5	4.4	292	2	Q6UY47_HUMAN	Q6uy47 homo sapien	1414	78	4.4	154	2	Q4QLO9_HAE18	Q4ql09 haemophilus
1342	78.5	4.4	299	2	Q5XJ15_HUMAN	Q5xj15 homo sapien	1415	78	4.4	172	2	Q619B9_CAEBR	Q619b9 caenorhabdi
1343	78.5	4.4	304	2	Q4J754_HUMAN	Q4j754 homo sapien	1416	78	4.4	172	2	Q19627_CABEL	Q19627 ixodes scap
1344	78.5	4.4	313	2	Q57596_CHICK	Q57596 gallus galli	1417	78	4.4	186	2	Q8MV99_TYOSC	Q8mv99 ixodes scap
1345	78.5	4.4	335	1	PSG5_HUMAN	Q15238 homo sapien	1418	78	4.4	202	2	Q7N6H1_PHOIL	Q7n6h1 photorhabdu

1419	77.5	4.4	214	2	Q99VY1_STRAU	Q99VY1	staphylococ
1420	77.5	4.4	214	2	Q7A716_STAN	Q7A716	staphylococ
1421	77.5	4.4	214	2	Q7A2T3_STAN	Q7A2T3	staphylococ
1422	77.5	4.4	214	2	Q7A1M5_STRAW	Q7A1M5	staphylococ
1423	77.5	4.4	214	2	Q6G136_STRAW	Q6G136	staphylococ
1424	77.5	4.4	214	2	Q6GBU6_STRAS	Q6GBU6	staphylococ
1425	77.5	4.4	214	2	Q5H134_STAAC	Q5H134	staphylococ
1426	77.5	4.4	216	1	YJL1_SCHPO	YJL1	schizosacch
1427	77.5	4.4	239	1	CD8A_FELCA	CD8A	felis silve
1428	77.5	4.4	246	1	Q58CX4_BOVIN	Q58CX4	bos taurus
1429	77.5	4.4	276	2	Q6P0R7_BRARE	Q6P0R7	brachydanio
1430	77.5	4.4	290	2	Q5TNT8_ANGA	Q5TNT8	anopheles g
1431	77.5	4.4	294	2	Q8K1Z5_MOUSE	Q8K1Z5	mus musculus
1432	77.5	4.4	295	2	Q61B19_CAEBR	Q61B19	caenorhabdit
1433	77.5	4.4	300	1	JAM1_RAT	Q9JHY1	rattus norv
1434	77.5	4.4	308	2	Q5O3N7_BRARE	Q5O3N7	brachydanio
1435	77.5	4.4	310	2	Q4V8T3_BRARE	Q4V8T3	brachydanio
1436	77.5	4.4	314	2	Q58YD8_BRARE	Q58YD8	brachydanio
1437	77.5	4.4	324	2	Q940M5_ARATH	Q940M5	arabidopsis
1438	77.5	4.4	326	2	Q91A23_PERIC	Q91A23	spheroeides
1439	77.5	4.4	331	2	Q675Z1_9URUC	Q675Z1	oikopleura
1440	77.5	4.4	333	1	CD1B1_CAVRO	Q9QZ22	cavia porce
1441	77.5	4.4	338	2	Q6RHD4_BRARE	Q6RHD4	brachydanio
1442	77.5	4.4	345	2	Q9G9W4_9ORTH	Q9G9W4	teleostylinu
1443	77.5	4.4	345	2	Q9G9W3_9ORTH	Q9G9W3	teleostylinu
1444	77.5	4.4	351	2	Q9ADX7_9RIZ	Q9ADX7	agrobacteri
1445	77.5	4.4	356	2	Q8AXL7_ONCMU	Q8AXL7	oncomyrmec
1446	77.5	4.4	360	2	Q7VAZ7_PROMA	Q7VAZ7	prochloroco
1447	77.5	4.4	368	2	Q6F5F1_MOUSE	Q6F5F1	mus musculus
1448	77.5	4.4	371	2	Q81KQ7_BACAN	Q81KQ7	bacillus an
1449	77.5	4.4	376	2	Q510N4_ENTHI	Q510N4	entamoeba h
1450	77.5	4.4	410	2	Q54V70_DICDI	Q54V70	dictyosteli
1451	77.5	4.4	410	2	Q4J0H4_AZOVU	Q4J0H4	azotobacter
1452	77.5	4.4	425	2	Q9CVU0_AZOVU	Q9CVU0	azotobacter
1453	77.5	4.4	428	2	Q72NX8_LEPTC	Q72NX8	leptospira
1454	77.5	4.4	428	2	Q8F7J7_LEPIN	Q8F7J7	leptospira
1455	77.5	4.4	433	2	Q5S054_MOUSE	Q5S054	mus musculus
1456	77.5	4.4	446	2	Q4V7T4_9GALL	Q4V7T4	streptococ
1457	77.5	4.4	448	1	EX7L_STR6	Q8D8m	strepococ
1458	77.5	4.4	460	2	Q7YTA8_BOMO	Q7YTA8	bombyx moti
1459	77.5	4.4	476	2	Q9CU34_MOUSE	Q9CU34	mus musculus
1460	77.5	4.4	481	2	Q5K373_BRARE	Q5K373	brachydanio
1461	77.5	4.4	490	1	CN108_MOUSE	Q8B163	mus musculus
1462	77.5	4.4	491	1	SYR8_HUMAN	Q86686	homo sapien
1463	77.5	4.4	495	2	Q4TBU0_TERING	Q4TBU0	terranodon n
1464	77.5	4.4	510	1	MOQ_WIGBR	Q8dlv2	wiggleswort
1465	77.5	4.4	513	1	SHPS1_MOUSE	P9J797	m tyrosine-
1466	77.5	4.4	516	2	Q6O5M2_METCA	Q6O5m2	methylococ
1467	77.5	4.4	536	2	Q7UZH7_PROMP	Q7UZH7	prochloroco
1468	77.5	4.4	539	2	Q9FX24_ARATH	Q9FX24	arabidopsis
1469	77.5	4.4	591	2	Q911K8_PSBAR	Q911K8	pseudomonas
1470	77.5	4.4	593	2	Q61NMS_XENLA	Q61NMS	xenopus lae
1471	77.5	4.4	602	2	Q5VPD3_ORYSA	Q5VPD3	oryza sativ
1472	77.5	4.4	603	1	MUTL_LISMP	Q71zr6	listeria mo
1473	77.5	4.4	611	1	Q70W32_ONCMY	Q70W32	oncomyrmec
1474	77.5	4.4	650	1	LIRB1_HUMAN	Q8n16	h leukocyte
1475	77.5	4.4	672	2	Q4Z489_PLABA	Q4Z489	plasmodium
1476	77.5	4.4	687	2	Q6CUX2_KLULA	Q6CUX2	kluyveromyc
1477	77.5	4.4	693	2	Q4FY44_LELMA	Q4FY44	leishmania
1478	77.5	4.4	717	2	Q8U7P9_AGRIS	Q8U7P9	agrobacteri
1479	77.5	4.4	725	2	Q6MQO9_BDBBA	Q6MQO9	belliobviri
1480	77.5	4.4	735	2	Q9FG24_ARATH	Q9FG24	arabidopsis
1481	77.5	4.4	735	2	Q8S606_9PLIV	Q8S606	human t-cel
1482	77.5	4.4	739	1	VCAM1_HUMAN	P19920	homo sapien
1483	77.5	4.4	757	1	DNM1_YEAST	P54661	saacharomyc
1484	77.5	4.4	785	2	Q6CTN0_KLULA	Q6CTN0	kluyveromyc
1485	77.5	4.4	823	2	Q517A3_ENTHI	Q517A3	entamoeba h
1486	77.5	4.4	829	2	Q64XJ3_BACFR	Q64XJ3	bacteroides
1487	77.5	4.4	873	2	Q4T602_TERING	Q4T602	terranodon n
1488	77.5	4.4	898	2	Q5R6T8_PONPY	Q5R6T8	pongo pygma
1489	77.5	4.4	912	2	Q6S1Q0_ORYSA	Q6S1Q0	oryza sativ
1490	77.5	4.4	925	2	Q5RBM3_PONPY	Q5RBM3	pongo pygma
1491	77.5	4.4	951	2	P91193_CAEBL	P91193	caenorhabdit

1492	77.5	4.4	959	2	Q5FH10_EHRGC	Q5FH10	ehrllichia r
1493	77.5	4.4	959	2	Q5BMO_EHRGW	Q5BMO	ehrllichia r
1494	77.5	4.4	991	2	Q9S7G6_ARATH	Q9S7G6	arabidopsis
1495	77.5	4.4	997	2	Q44087_CAEBL	Q44087	caenorhabdit
1496	77.5	4.4	1014	2	Q77813_RABIT	Q77813	oryctolagus
1497	77.5	4.4	1040	2	Q9W675_BRARE	Q9W675	brachydanio
1498	77.5	4.4	1082	2	Q8W0U0_SOREI	Q8W0U0	scorophyru bic
1499	77.5	4.4	1093	2	Q6GNA9_XENLA	Q6GNA9	xenopus lae
1500	77.5	4.4	1099	2	P90731_CAEBL	P90731	caenorhabdit

ALIGNMENTS

RESULT 1

SLAF7_HUMAN STANDARD: PRT: 335 AA.

ID SLAF7_HUMAN Q9N025; Q8N6Y8; Q8ND32; Q9NY08; Q9NY23; Q9N025; Q8N6Y8; Q8ND32; Q9NY08; Q9NY23; DT 13-SEP-2005 (Rel. 48, Created) DT 13-SEP-2005 (Rel. 48, Last sequence update) DT 13-SEP-2005 (Rel. 48, Last annotation update) DE SLAM family member 7 precursor (CD2-like receptor activating cytotoxic cells) (C8AC) (Protein 19A) (Membrane protein FOAP-12) (CD2 subset 1) (Novel Ly9). GN Name=SLAF7; Synonyms=CS1; ORFNames=UNQ576/PRO1138; OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; CC Homo. OK NCBI_Taxid=9606; [1] NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND TISSUE SPECIFICITY. RM MEDLINE=21115149; PubMed=11220635; DOI=10.1007/s002510000274; RA Bales K.S., Mathew P.A.; RT "Molecular cloning of CS1, a novel human natural killer cell receptor belonging to the CD2 subset of the immunoglobulin superfamily."; RN Immunogenetics 52:302-307(2001). [2] NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY. RP PubMed=11698418; RA Bouchon A., Cella M., Grieser H.L., Cohen J.I., Colonna M.; RT "Activation of NK cell-mediated cytotoxicity by a SAP-independent receptor of the CD2 family."; RN J. Immunol. 167:5517-5521(2001). [3] NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 3), FUNCTION, AND TISSUE SPECIFICITY. RP MEDLINE=21661458; PubMed=11802771; DOI=10.1042/0264-6021.3610431; RA Murphy J.J., Hobby P., Vilartino-Varela J., Bishop B., Iordanidou P., Sutton B.J., Norton J.D.; RT "A novel immunoglobulin superfamily receptor (19A) related to CD2 is expressed on activated lymphocytes and promotes homotypic B-cell adhesion."; RN Biochem. J. 361:431-436(2002). [4] NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1). RP TISSUE=Macrophage; RA Fujii Y., Takayama K., Teurittani K., Yajima Y., Anemiyu T., Uka Y., Naito K., Kawaguchi A.; RT "Homo sapiens mRNA for FOAP-12 protein, complete cds."; RN Submitted (May-1999) to the EMBL/Genbank/DBJ databases. [5] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]. RP MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; RA Clark H.P., Gurney A.L., Adaya E., Baker K., Baldwin D.T., Brush J., Chen J., Chow B., Chui C., Crowley C., Currie B., Devel B., Dowd P., Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M.R., Robbie B., Sanchez C., Schenfeld J., Sehnagiri S., Simmons L., Singh V., Smith V., Stinson J., Vagts A., Vanden R.L., Watanabe C., Wiand D., Woods K., Xie M.-H., Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RT Genome Res. 13:2265-2270(2003).
RN [6]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RC TISSUE=Lymph node;
RG Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
RN [7]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG Human chromosome 1 international sequencing consortium;
RG Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
RN [8]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC TISSUE=Fetal lung, and Fetal spleen;
RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mollany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schin J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RN PROTEIN SEQUENCE OF 23-37.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [10]
RN ALTERNATIVE SPLICING.
RX PubMed=15368295; DOI=10.1002/eji.200424917;
RA Lee J.K., Boles K.S., Mathew P.A.;
RT "Molecular and functional characterization of a CSI (CRACC) splice
RT variant expressed in human NK cells that does not contain
RT immunoreceptor tyrosine-based switch motifs.";
RL Eur. J. Immunol. 34:2791-2799(2004).
RN [11]
RN TISSUE SPECIFICITY, AND SAP-BINDING.
RX MEDLINE=2222696; PubMed=12242590; DOI=10.1007/s00251-002-0463-3;
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Plazuela P.,
RA Bosch J., Terhorst C., Engel P.;
RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT leukocyte cell-surface receptors.";
RL Immunogenetics 54:394-402(2002).
RN [12]
RN FUNCTION: Isoform 1 mediates NK cell activation through a SAP-
RN independent extracellular signal-regulated ERK-mediated pathway.
RN May play a role in lymphocyte adhesion. Isoform 3 does not mediate
RN any activation. SAP can bind the cytoplasmic tail of isoform 1
RN when phosphorylated in the presence of Fyn (in vitro).
RN -1- SUBCELLULAR LOCATION: Type I membrane protein.
RN -1- ALTERNATIVE PRODUCTS:
RN Event=Alternative splicing; Named isoforms=3;
RN Name=1; Synonyms=19A, CSI-L;
RN IsoId=G9NQ25-1; Sequence=Displayed;
RN Name=2;
RN IsoId=G9NQ25-2; Sequence=VSP_013781;

CC Note=No experimental confirmation available;
CC Name=3; Synonyms=19A24, CSI-S;
CC IsoId=G9NQ25-3; Sequence=VSP_013782;
CC TISSUE SPECIFICITY: Expressed in spleen, lymph node, peripheral
CC blood leukocytes, bone marrow, small intestine, stomach, appendix,
CC lung and trachea. Expression was detected in NK cells, activated
CC B-cells, NK-cell line but not in promyelocytic, B-, or T-cell
CC lines. The isoform 3 is expressed at much lower level than isoform
CC 1.
CC -1- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.
CC -1- CAUTION: Ref.3 (CAB76561) sequence differs from that shown due to
CC framehifts.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF291815; AAK11549.1; -; mRNA.
CC EMBL; AF390894; AAL26989.1; -; mRNA.
CC EMBL; AJ271869; CAB76561.1; ALT FRAME; mRNA.
CC EMBL; AJ276429; CAB81950.2; -; mRNA.
CC EMBL; AB027233; BAB61022.1; -; mRNA.
CC EMBL; AY358512; AAO88876.1; -; mRNA.
CC EMBL; AL834424; CAD39085.1; -; mRNA.
CC EMBL; AL121985; CAC00579.1; -; Genomic DNA.
CC EMBL; AL121985; CAH73507.1; -; Genomic DNA.
CC EMBL; AL121985; CAH73508.1; -; Genomic DNA.
CC EMBL; BC027867; AAH27867.1; -; mRNA.
CC EMBL; ENSG0000026751; Homo sapiens.
CC HGNC; HGNC:21394; SLAMF7.
CC MIM; 606625; -.
CC DR GO; GO:0016020; C:membrane; NAS.
CC DR GO; GO:0007155; P:cell adhesion; NAS.
CC DR GO; GO:0030101; P:natural killer cell activation; NAS.
CC DR GO; GO:0042267; P:natural killer cell mediated cytotoxicity; NAS.
CC DR InterPro; IPR007110; Ig-Like.
CC DR PROSITE; PS50835; IG_LIKE; 1.
CC KW Alternative splicing; Direct protein sequencing; Glycoprotein;
CC Immunoglobulin domain; Receptor; Signal; Transmembrane.
CC -----
CC SIGNAL 1 22
CC CHAIN 23 335 SLAM family member 7
CC TOPO_DOM 23 226 Extracellular (Potential).
CC TRANSMEM 227 247 Potential.
CC TOPO_DOM 248 335 Cytoplasmic (Potential).
CC DOMAIN 131 206 Ig-like C2-type.
CC CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 176 176 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 204 204 N-linked (GlcNAc...) (Potential).
CC DISULFID 145 215 Potential.
CC DISULFID 151 195 By similarity.
CC DISULFID 151 195 Missing (in isoform 2).
CC VARSPLIC 19 125 /FTid=VSP_013781.
CC VARSPLIC 258 296 -> NNPGRSRKYGLHCGNTEKDGKSLVTHADARHTAIC
CC L (in isoform 3).
CC /FTid=VSP_013782.
CC M -> L (in Ref. 3).
CC SQ SEQUENCE 335 AA; 37421 MW; D09ABBCF74B8D4 CRC64;
CC -----
CC Query Match 100.0%; Score 1772; DB 1; Length 335;
CC Best Local Similarity 100.0%; Pred. No. 2.2e-139; Indels 0; Gaps 0;
CC Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC 1 MAGSPCTCTLTLYIIMQLTGSAAAGPVKELVSGGAVTFPLSKSKVQYDSIVTFTNTPL 60
CC 1 MAGSPCTCTLTLYIIMQLTGSAAAGPVKELVSGGAVTFPLSKSKVQYDSIVTFTNTPL 60

Qy 61 VTIOPEGGTTIYTONRNRERVDPPGGYSLKSLKLNKNDSGIYYGYISSSLQOPSTOEY 120
 Db 61 VTIOPEGGTTIYTONRNRERVDPPGGYSLKSLKLNKNDSGIYYGYISSSLQOPSTOEY 120
 Qy 121 VLHYEHHSKPKRMGMGLOSNNGTCVTNLTCOMHEGSEDDVYTWKALGOANESHSIL 180
 Db 121 VLHYEHHSKPKRMGMGLOSNNGTCVTNLTCOMHEGSEDDVYTWKALGOANESHSIL 180
 Qy 181 PISMRGSDMTFTICVARNPVSRNESPILARKLCEGAADPDSSMVLCLLVLPLLSL 240
 Db 181 PISMRGSDMTFTICVARNPVSRNESPILARKLCEGAADPDSSMVLCLLVLPLLSL 240
 Qy 241 FVLGLFLMFLKREGEYIEKKRVDICRETPNICPHSGENTYDTIPIHRTIKEDPA 300
 Db 241 FVLGLFLMFLKREGEYIEKKRVDICRETPNICPHSGENTYDTIPIHRTIKEDPA 300
 Qy 301 NTVYSTVAFPKKMPHSLTMTPTPRLPAYENV 335
 Db 301 NTVYSTVAFPKKMPHSLTMTPTPRLPAYENV 335
 Db 301 NTVYSTVAFPKKMPHSLTMTPTPRLPAYENV 335

RESULT 2
 SLAF_MOUSE STANDARD; PR7; 333 AA.
 ID SLAF7_MOUSE Q8BHT2; Q8CJ63; Q8CJ64; Q8CJ65; Q91XA0;
 AC Q8BHK6; Q8BHT2; Q8CJ63; Q8CJ64; Q8CJ65; Q91XA0;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE SLAM family member 7 precursor (leukocyte cell-surface antigen) (Novel
 Ly9).
 GN Name=Slamf7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muridea; Muridae; Murinae; Mus.
 NC NCB1 TaxID=10090;
 RX NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 2 AND 3).
 RP STRAIN=BA1B/C; and C57BL/6; TISSUE=Thymus;
 RC MEDLINE=2222696; PubMed=12242590; DOI=10.1007/s00251-002-0483-3;
 RX MEDLINE=2222696; PubMed=12242590; DOI=10.1007/s00251-002-0483-3;
 RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Flizcucta P.,
 Bosch V., Terhorst C., Engel P.;
 RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
 leukocyte cell-surface receptors.";
 RT Immunogenetics 54:394-402(2002).
 RL [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).
 RP STRAIN=C57BL/6J; TISSUE=Aorta, Testis, and Vein;
 RC MEDLINE=2234683; PubMed=1246851; DOI=10.1038/nature01266;
 RX MEDLINE=2234683; PubMed=1246851; DOI=10.1038/nature01266;
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 Schmitt L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 Blake J.A., Bradt D., Brusci V., Chochia S., Corbani L.B., Cousins S.,
 Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 Gassmann S., Guelinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 Kani A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 Konoigawa A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,
 Maglott D.R., Maltais L., Marchionni L., McKensie L., Miki H.,
 Nagaishi T., Numa K., Okido T., Pavan W.J., Petrea G., Peocle G.,
 Petrovsky N., Pillai R., Pontius U.V., Qi D., Ramachandran S.,
 Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 Sandelin A., Schneider C., Sempile C.A., Setou M., Shinada K.,
 Sultana R., Takekura Y., Taylor M.S., Teasdale R.D., Tomita K.,
 Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
 Yuan Z., Zavanian M., Zhu Y., Zimmer A., Carrinci P., Hayatsu N.,
 Hitozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 Shitaka T., Waki K., Kawai J., Aizawa K., Aikawa T., Fukuda S.,
 Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 4).
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Uddin T.B., Toshitsuki S., Carrinci P., Prange C.,
 Raha S.S., Loguélano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McGowan P.U., McKernan K.J., Malek J.A., Gamaralle P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,
 Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Mediates NK cell activation through a SAP-independent
 extracellular signal-regulated BRK-mediated pathway. May play a
 role in lymphocyte adhesion (By similarity). Isoform 1 does not
 bind SAP (in vitro).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: Type I membrane protein.
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=Q8BHK6-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8BHK6-2; Sequence=VSP_013784;
 CC Name=3;
 CC IsoId=Q8BHK6-3; Sequence=VSP_013783, VSP_013784;
 CC Name=4;
 CC IsoId=Q8BHK6-4; Sequence=VSP_013783;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Expressed in spleen, lymph node, bone marrow
 and testis. Lower levels detected in thymus. Expressed in NK cells
 and B-cells.
 CC -1- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
 domain.
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to a
 frameshift in position 255.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 CC EMBL, AF467909; AAN63158.1; -; mRNA.
 CC EMBL, AF467910; AAN63159.1; -; mRNA.
 CC EMBL, AF467911; AAN63160.1; -; mRNA.
 CC EMBL, AK030135; AAC6801.1; -; mRNA.
 CC EMBL, AK030148; BAC26810.1; -; mRNA.
 CC EMBL, AK040678; BAC30665.1; -; mRNA.
 CC EMBL, AK089525; BAC40914.1; -; mRNA.
 CC EMBL, BC011154; AAH11154.1; ALT FRAMES; mRNA.
 CC EMBL, ENSMUSG0000038179; Mus musculus.
 CC MGI, MGI:1922595; Slmf7.
 CC GO, GO:0016021; C:integral to membrane, TAS.
 CC InterPro, IPR007110; Ig-like.
 CC PROSITE, PS50835; Ig-like; 1.
 CC Alternative splicing; Glycoprotein; Immunoglobulin domain; Receptor;
 KW

```

KW Signal; Transmembrane.
FT SIGNAL 1 22 By similarity.
FT CHAIN 23 333 SLAM family member 7.
FT TOPO DOM 23 224 Extracellular (Potential).
FT TRANSMEM 225 245 Potential.
FT TOPO DOM 246 333 Cytoplasmic (Potential).
FT DOMAIN 128 203 Ig-like C2-type.
FT CARBOHYD 42 42 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 95 95 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 139 139 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 145 145 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 156 156 N-linked (GlcNAc . . .) (Potential).
FT DISULFID 142 212 Potential.
FT DISULFID 148 192 By similarity.
FT VARSPLIC 255 289 Missing (in isoform 3 and isoform 4).
FT VARSPLIC 312 333 /FTID=VSP_013783.
/FTID=VSP_013784.
/FTID=VSP_013784.
CONFLICT 118 118 V -> A (in Ref. 1; AAN63158).
CONFLICT 248 248 T -> M (in Ref. 1; AAN63158 and 2).
CONFLICT 253 253 G -> R (in Ref. 1; AAN63159 and 3).
SQ SEQUENCE 333 AA; 37187 MW; 8D40B823FEBB7129 CRC64;

Query Match 46.0%; Score 815; DB 1; Length 333;
Best Local Similarity 49.3%; Pred. No. 1.7e-59;
Matches 167; Conservative 58; Mismatches 104; Indels 10; Gaps 3;

QY 1 MAGSTCTLTLYITLQNGSANGSPVKELVSGVGVFPLSKYKQVDYVTFNTPL 60
DB 1 MARSTYITFTSVLCQLYTATASGTUKVAGLDDSVFTTLITETIKDYVMTNTPL 60
QY 61 VTIOEGGTLITVTONRNRERVDPDGYSLSKLKSKLKDSDGIVYVSSSLQDPSTOEY 120
DB 61 AMVKDQ---VTSQSNKRIYFPGLYSMKLSQKNDSDGAYRAEIVTSSQASLIDEX 117
QY 121 VLAHYEHLSKPYNTMGLDSNKKGTCTVNTITCMEHGEEDVYTTKQLGQAANESHGSL 180
DB 118 VLAHYKHLSRPKYITIDROSNNKGTCTVNTITCSTDDEGVYVSMKAVGCGDNQFHDGATL 177
QY 181 PISWWSGSDMTFICVARNPVRNFSPIARLCEGAADDDSSMWLLCLLVPLSL 240
DB 178 SIAMSGEKDQALTCARNPVNSSTFVPQKLCEDATDITLSLGLIYLCFSAVLIL 237
QY 241 FVLGLFL----WFLKREROEYIEBKRVYDICTEPNLCPSHGENTYDTPHTNRTILK 296
DB 238 FAVLLTHTHTTWIKKGKGE---EDKRVDRHQEMDCLPHLENAVDTYITTEKRRPE 294
QY 297 EDPANTVSTVEIPIKGMENPHSLTMPDTPRLFAVENVI 335
DB 295 EDPANTFYSTVQIPKVVKSPSSLPAKFLVPRSLSPENVI 333

RESULT 3
ID 015430 HUMAN PRELIMINARY; PRT; 328 AA.
AC 015430; O8WLP1;
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Leukocyte antigen CD84 (leukocyte differentiation antigen CD84 isoform CD84c) (MAX.3 cell surface antigen precursor) (CD84 antigen).
GN Name=CD84; ORFNames=RP11-528G1.3-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=97454416; PubMed=9310491;
RA de la Fuente M.A., Pizcueta P., Nadal M., Bosch J., Engel P.,
"CD84 leukocyte antigen is a new member of the Ig superfamily.";

```

```

RL Blood 90:2398-2405(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Palou E., Sole J., Piroto F., Gaya A.
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86188202; PubMed=3008886;
RA Andreesen R., Bros K.J., Osterholz J., Emmrich F.,
"Human macrophage maturation and heterogeneity: analysis with a newly
generated set of monoclonal antibodies to differentiation antigens.";
RL Blood 67:1257-1264(1986).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20164057; PubMed=10698700; DOI=10.1042/0264-6021.3460729;
RA Krause S.W., Rehl M., Heinz S., Ebner R., Andreesen R.,
"Characterization of MX3 antigen, a glycoprotein expressed on mature
macrophages, dendritic cells and blood platelets: identity with
CD84.";
RL Biochem. J. 346:729-736(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Boesak S.A., McGraw P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.J., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,
Schurch A., Schein J.R., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=lymph;
RA Director MGC Project;
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RA Lad H.,
Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.
DR EMBL, U82988; AAB84364.1; -, mRNA.
DR EMBL, AF054815; AAF21721.1; -, mRNA.
DR EMBL, AJ223324; CAA11264.1; -, mRNA.
DR EMBL, BC020063; AAH20063.1; -, mRNA.
DR EMBL, AL138930; CAI15158.1; -, Genomic DNA.
DR Ensemble; ENSG0000065294; Homo sapiens.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0006952; P:defense response; TAS.
DR GO; GO:0007156; P:homophilic cell adhesion; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG_1; IG-like.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 328 MAX.3 cell surface antigen.
SQ SEQUENCE 328 AA; 36871 MW; 6C9A99206A6D0344 CRC64;

Query Match 20.5%; Score 362.5; DB 2; Length 328;

```

Best Local Similarity 31.5%; Pred. No. 1e-21;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

QY 14 LMOL-----TGSAAAGPYKELV---GSVGAATPPLK-SKYKQVDSIWTNTPTPLVITQ 64
DB 6 LMIILLCLQTPPEAKGKSEIFTYNGILGESVTPEPNIQEPKQVITAMTSKTSVAAYTP 65
QY 65 PEGGT---IITYONRRERVDPPDGYSLKLSKLKKNDSGIYVGIYSSSLQQPSTQERY 121
DB 66 GDSERAPVYVTHRYRHYRIHALGPNVNLVSLDMEDAGDKADINQADPYTTTKRYN 125
QY 122 LHYEHLKPYVTMGLQSNKNGTCVTNLTCCMEHGEEDVITYWKALGOANESHGSLTP 181
DB 126 LQIYRLCKPKITQSLMASVNSTCMTLTCSVEKEKVTYWSPLGE-----EGNVLIQ 179
QY 182 ISMRGSDMTFICVARNPVSRNPSPIIARLCEGADDDPS-----SMVLCLLILVP 235
DB 180 IFQPEDELTYTCTAONPVSN-SDSISARQLCADIMGFTHTTGLSLVAMPFLVLT 238
QY 236 LLSLFLVGLFLMFLKRRQERYIEKKRVDCRETPNICPHSGENTEXDTPHTNRITL 295
DB 239 ILSVFLRLP-----KRRQDAASKITITYIMASRTQF--ASRIYDELIGSKVLPS 290
QY 296 KEDPANTYVSTVEIPKXENPHSLTMDPTPLPAYENVI 335
DB 291 KEBPVNTYSEVQFADKKMGKASTQDSKP--PQTSSEYELV 328

RESULT 4

Q9Z178 MOUSE
ID Q9Z178 MOUSE PRELIMINARY; PRT; 329 AA.

AC 09Z178;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD84 leukocyte antigen.
GN Name=CD84; Synonyms=CD84;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peritoneum;
RX MEDLINE=99180614; PubMed=10079287; DOI=10.1007/s002510050490;
RA de la Fuente M.A., Tovar V., Pizcueta P., Nadal M., Bosch J.,
RA Engel P.;
RT "Molecular cloning, characterization, and chromosomal localization of
RT the mouse homologue of CD84, a member of the CD2 family of cell
RT surface molecules.";
RL Immunogenetics 49:249-255(1999).
DR EMBL; AF043445; AAD02273.1; -; mRNA.
DR Ensembl; ENSMUSG0000038147; Mus musculus.
DR MGI; MGI:1336885; CD84.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 329 AA; 37345 MW; 43BBIAM5AF1989E0 CRC64;

Query Match 20.5%; Score 362.5; DB 2; Length 329;
Best Local Similarity 30.5%; Pred. No. 1e-21;
Matches 105; Conservative 62; Mismatches 136; Indels 41; Gaps 14;

QY 11 IYILQULGSAAGPYKELV---GSVGAATPPLK-SKYKQVDSIWTNTPTPLVITQ 65
DB 8 IWLFLCLQWTSAAAGCADAPVWNGILGESVTPLMIQEKIKDINAMT-SQSSVAFIRCG 66
QY 66 -EGGTIIVTONRRERVDPPDGYSLKLSKLKKNDSGIYVGIYSSSLQQPSTQERYLHV 124
DB 67 VKAKAVTITQGYKRIEIIIDQKYLVIKIDLMEDAGTYKADINEN-EEITTKIYIYLI 125

QY 125 YEHLKPYVTMGLQSNKNGTCVTNLTCCMEHGEEDVITYWKALGOANESHGSLTPISW 184
DB 126 YRLKTPKITQSLISLINTCNITLTCSVEKEKQVTSWSPFGSKSN-----VLQIVH 179
QY 185 RWGSDMTFICVARNPVSRNPSPIIARLCEGA-----ADDPSSMVLCLLILVPL 237
DB 180 SPMQCKLTYTCTAONPVSN-SSDSVTVQPCPTDPSFPHRAVLPGGLAVFLILIPML 238
QY 238 LSLFLVGLFLMFLKRRQERYIEKKRVDCRETPNICPHSGENTE---YDTIPTHNRT 293
DB 239 AFLPRL-----YKRRDRITLQD--DVSKITVAVSKNAQPTESRITDEIPOSGL 289
QY 294 ILKEDPANTYVSTVEIPKXENPHSLTMDP--TPRLPAYENVI 335
DB 290 SKCKDPVTITVSSVQLSEKMKETN---MKDRSLPKALGNELIV 329

RESULT 5

Q8WW18 HUMAN
ID Q8WW18 HUMAN PRELIMINARY; PRT; 339 AA.

AC 08WW18;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Leukocyte differentiation antigen CD84 precursor (CD84 antigen)
DE (Leukocyte antigen).
GN Name=CD84; ORFNames=RP11-528G1.3-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaye A.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lad H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y12632; CAA73181.1; -; mRNA.
DR EMBL; AL138930; CAI15159.1; -; Genomic_DNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 21
FT CHAIN 22 339
SQ SEQUENCE 339 AA; 38082 MW; E78D6D5CAC893604 CRC64;

Query Match 20.3%; Score 359; DB 2; Length 339;
Best Local Similarity 31.6%; Pred. No. 2.1e-21;
Matches 111; Conservative 51; Mismatches 143; Indels 46; Gaps 12;

QY 14 LMOL-----TGSAAAGPYKELV---GSVGAATPPLK-SKYKQVDSIWTNTPTPLVITQ 64
DB 6 LMIILLCLQTPPEAKGKSEIFTYNGILGESVTPEPNIQEPKQVITAMTSKTSVAAYTP 65
QY 65 PEGGT---IITYONRRERVDPPDGYSLKLSKLKKNDSGIYVGIYSSSLQQPSTQERY 121
DB 66 GDSERAPVYVTHRYRHYRIHALGPNVNLVSLDMEDAGYKADINQADPYTTTKRYN 125
QY 122 LHYEHLKPYVTMGLQSNKNGTCVTNLTCCMEHGEEDVITYWKALGOANESHGSLTP 181
DB 126 LQIYRLCKPKITQSLMASVNSTCMTLTCSVEKEKVTYWSPLGE-----EGNVLIQ 179
QY 182 ISMRGSDMTFICVARNPVSRNPSPIIARLCEGADDDPSM-----VLLCLLIV 234
DB 180 IFQPEDELTYTCTAONPVSN-SDSISARQLC-----ADIMGFTHTTGLSLVLA 232
QY 235 PLLSLFLVGLFLMFLKRRQ-----EYIEKKRV-DICRETPNICPHSGENTEX 284

DB 223 PFLVLIISVYLFPLFKRQSCINTPTKMPYAAASKTITYYIMASRTOP--AESRY 290
QY 285 DTIPHTNRLKEDPANTVYSTVEIPKKNENPHSLTMPDRLPAYENVI 335
DB 291 DELLQSKVLPSEBEPVNTVYSEVQPADKKKASTQDSKP--FGTSYEYVI 339

RESULT 6
GENZB6 MOUSE
ID Q6NZB6 MOUSE PRELIMINARY; PRT; 645 AA.
AC Q6NZB6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Ly9 protein (fragment).
GN Name=Ly9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dietzenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosack S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Gough J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalek U., Smalls D.E.,
RA Scheraga A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.L.
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC066212; AAH66212.1; -; mRNA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
PT NON TER
SQ SEQUENCE 645 AA; 71884 MW; 316EFL83DFD510B CRC64;

Query Match 20.2%; Score 358.5; DB 2; Length 645;
Best Local Similarity 27.9%; Pred. No. 5,1e-21;
Matches 119; Conservative 51; Mismatches 138; Indels 119; Gaps 16;

QY 14 LMQL-TGSA-----AGPVEKLVGSGAVTPPLK-SKYQVDSIYWTFTPLVITIQ 67
DB 229 IWQCTGASRRKTAAG--KTVVGIIGEPYTLPLEFATRTATKVVWVFNTS--VISQERR 284
QY 68 GIIITVQNR-----NRRVDPDGGSLSKLKNKDSGIYVGVYSSLSQPSQEVYL 122
DB 285 GAATADSRKPKPGSEERRVITSDQDSLKISQLKEDAGPHAYVCSASRDPSTVNHFTL 344

QY 123 HYVEHLSPKTYTMGLQSRNGCTVTNLTCCMEHEGEDIYTWKALGQANSHNGSIPI 182
DB 345 LVYKRLKRPSTYKSPVHMANNNGICEVVLTCVDGGNNVTYTMPLQNKRAVMSQGRSHLV 404
QY 183 SWRMGESDMTFLCVARNPVSRNPFSPILARKLCEGAADDPSSMWLCLLVPLLSLFV 242
DB 405 SWESEHLPNTCTAHNPVS--NSSQPSGGITCSG---PRNRKFMILLLVLLMLLI 459
QY 243 LGLFLMFLKRE-----ROEYIEE-----KKRVDCRETPNCP- 276
DB 460 GGCFILRKQKQCSLATRYQAEVPAIIPETPTGHGQFVLSQRYKIDMSAKTRHQPT 519
QY 277 -----HSGENTR---YDIPHTN----- 291
DB 520 PISDTSASSATTEBDEKTRMHSYANRNQVYTLVTHQDIAHALAYGQVEYEAITEPD 579
QY 292 -----RTLL--KEDPANTVYSTVEIPKK-MENPHSLTMPPTP 326
DB 580 KYDGSMEEDPRAIYQVSLNAGETPLPKKEDSNITVCSQKPKTAQTPQDASPEPTP 639
QY 327 RLFAVEN 333
DB 640 ---TYEN 643

RESULT 7
Q9UIB8 HUMAN
ID Q9UIB8 HUMAN PRELIMINARY; PRT; 345 AA.
AC Q9UIB8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Leukocyte differentiation antigen CD84 isoform CD84a (CD84 antigen)
DE (Leukocyte antigen).
GN Name=CD84; ORFNames=RP11-528G1.3-003;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Palou E., Sole J., Pirotto F., Gaya A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lad H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF054816; AAF21722.1; -; mRNA.
DR EMBL; AL138930; CAI5160.1; -; Genomic DNA.
DR Ensembl; ENSG0000066294; Homo sapiens.
DR HGNC; HGNC:1704; CD84.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KV Immunoglobulin domain.
SQ SEQUENCE 345 AA; 38782 MW; DA06BC5A682E62D CRC64;

Query Match 20.2%; Score 358; DB 2; Length 345;
Best Local Similarity 30.8%; Pred. No. 2.6e-21;
Matches 110; Conservative 52; Mismatches 143; Indels 52; Gaps 11;

QY 14 LMQL-----TGSAGSPVKELY---GSGVAVTPPLK-SKYQVDSIYWTFTPLVITIQ 64
DB 6 LMILLICITQTPKPAKGSIFITVNGILIGESVTFPVNIQERQVKIIMTSTISVAIYTP 65
QY 65 PEGGT---IIVTQNRNRVDPDGGSLSKLKNKDSGIYVGVYSSLSQPSQEVYL 121
DB 66 GDSFAIPAVVTYTHRYRIRHALGPNVNLVSLDLMEDAGDYKADINQADPYTTTKRYN 125
QY 122 LHVYHLSPKTYTMGLQSRNGCTVTNLTCCMEHEGEDIYTWKALGQANSHNGSIPI 181


```

Db      126 LQIYRLKPKITQSLMASVNSTCVTLTCSYEKEKNTYVMSPLGE-----EGNVLQ 179
Qy      182 ISWRMGSDMTFICVARNPVSNFSSPIIARLCEGADDDPPSSM-----VLLCLLLV 234
Db      180 IFQTEDEDELITTCYANPNVSN--SDSISARQLC-----ADIMGFRTHTGLISVLAM 232
Qy      235 PLLLSLFLVGLFLMFLKERQREYIEKKRVDCRETP-----NICPMS 278
Db      233 FFLVLLISSVFLPLFKRQRIPEBSCCLNTPFKNFPAASKTITYYIMASRTQTP-- 290
Qy      279 GENTYEDTTPHTNRITLKEDPANTYTYSTVEIPKKNENPHSLTMDTRELPAIYENVI 335
Db      291 AESRIYDEILQSKVLPSEKPEPVTVSYEVOFADKKMGKASTODSKP--PQTSSYEIYI 345

```

```

RESULT 8
Q6FHA8_HUMAN
Q6FHA8_HUMAN PRELIMINARY; PRT; 328 AA.
AC Q6FHA8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CD84 protein (Fragment).
GN Name=CD84;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Mkomdinye M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zhuo D., Hu Y., Labber J.,
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR541847; CAG46645.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 328
SQ SEQUENCE 328 AA; 36861 MW; 6C9A8BDD45BD0344 CRC64;

```

```

Query Match      20.0%; Score 354.5; DB 2; Length 328;
Best Local Similarity 31.2%; Pred. No. 4.8e-21;
Matches 106; Conservative 55; Mismatches 144; Indels 35; Gaps 10;

Qy      14 LMQL-----TGSAAAGPVKELY---GSVCGAVTTPPLK-SKVQVDSIVTFTPTPLVTLQ 64
Db      6 LWILLICLTQMPBAAGKQSEITTVNGILGESVTFPNIOEPKQKIANTSKTISVAAYTP 65
Qy      65 PEGGT---IIVTONNRERVDPPDGYSIKLSKLKKNDGIIYVVGISSSLOQPSIOEYV 121
Db      66 GDSERAPAVTVTHRYNRYRIHALGPVYNLVISDLKREDAGDKADINTQADPYTTTKRYN 125
Qy      122 LHVYHLSPKRYTMGIQSNKNGTCTVNTLTCCMEHGEEDVITYWKALQGANSHNGSILPI 181
Db      126 LQIYRLKPKITQSLMASVNSTCVTLTCSYEKEKNTYVMSPLGE-----EGNVLQ 179
Qy      182 ISWRMGSDMTFICVARNPVSNFSSPIIARLCEGADDDPS-----SWLLCLLLV 235
Db      180 IFQTEDEDELITTCYANPNVSN--SDSISARQLCADIANGFRTHTGLISVLAMFFLLV 238
Qy      236 LLLSLFVLGLFLMFLKERQREYIEKKRVDCRETPNICPSGENTYEDTTPHTNRITL 295
Db      239 ILSVFLPLF-----KRDQAASKTITYYIMASRTQTP--AESRIYDEILQSKVLP 290
Qy      296 KEDPANTYTYSTVEIPKKNENPHSLTMDTRELPAIYENVI 335
Db      291 KESVNTVYSEVOFADKKMGKASTODSKP--PQTSSYEIYI 328

```

```

RESULT 9
Q7TMP7_MOUSE
Q7TMP7_MOUSE PRELIMINARY; PRT; 649 AA.
AC Q7TMP7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lys protein (Fragment).
GN Name=Lys9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Carrinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullaby S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalske U., Smallus D.E.,
RA Scherch A., Schin J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055380; AAH5380.1; -; mRNA.
DR HSSP; P08921; IHNG.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 1
SQ SEQUENCE 649 AA; 72414 MW; AD6A09381C063B34 CRC64;

```

```

Query Match      20.0%; Score 354.5; DB 2; Length 649;
Best Local Similarity 27.6%; Pred. No. 1.1e-20;
Matches 118; Conservative 52; Mismatches 139; Indels 119; Gaps 16;

Qy      14 LMQL-----ASGPVKELYSGVAVTPEPLSK-VKQVDSIVTFTPTPLVTLQ 67
Db      233 IWFQCTGASRRKTAAG--KTVVGLIGEPVTLPLEFRATRTATNVAVVENTS--VISQERR 288
Qy      68 GTTIYTQNR-----NRKAVDPPDGYSIKLSKLKKNDGIIYVVGISSSLOQPSIOEYV 122
Db      289 GAATDSSRRKPKGSEERRVRTSDQSLKISQIKREDAGPFAHYVCSASRDPVRAHTL 348
Qy      123 HVYHLSPKRYTMGIQSNKNGTCTVNTLTCCMEHGEEDVITYWKALQGANSHNGSILPI 182
Db      349 LVYKLEPSTYKSVYHAMNGICEVVLTCVSDGGNNVTYTMPLQNKAAVMSQGSHLNV 408
Qy      183 ISWRMGSDMTFICVARNPVSNFSSPIIARLCEGADDDPSNWLLCLLLVPLLSLFLV 242

```

Db 409 SWESGEHLPNFTCTAHNPVS-NSSQSFSSGTCG---PERNKRFMLLLVLLMLI 463
Qy 243 LGLPLMLKRB-----ROEYIEE-----KKRVDICRETPNICP- 276
Db 464 GGYFLRRKKQCSLATRYQAEVPAHLEPPTPGHGQSVLSQRREKIDMSAKTTRHQPT 523
Qy 277 -----HSGENTB---YDTIPPTN----- 291
Db 524 PTDSTSSSSATTEDEDEKTRAHSTANSGRMQYDLVTHQDIAMALAYGQVEYEAITPYD 583
Qy 292 -----RTL--KEDPANTVYSGVLEPRK-MENPHSLTMPTP 326
Db 584 KVDGSMDEEGMAIYOVSLNAGETPLPKCKEDSNITVCSVQKPKXTAOTPODAESPETP 643
Qy 327 RLPAVEN 333
Db 644 ---TYEN 647

RESULT 10
LY9_MOUSE STANDARD; PRT; 654 AA.
ID LY9_MOUSE
AC 001365; O9ES29; O9ES35; O9ES36;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE T-Lymphocyte surface antigen Ly-9 precursor (Lymphocyte antigen 9)
DE (Cell-surface molecule Ly-9).
GN Name=Ly9; Synonyms=Ly-9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
NP NUCLEOTIDE SEQUENCE, AND POLYMORPHISM.
RC STRAIN=129/Sv, BALB/c, and C57BL/6; TISSUE=Spleen;
RA MEDLINE=92373005; PubMed=1506686;
RX Tovar V., de la Fuente M.A., Pizcueta P., Bosch J., Engel P.;
RT "Gene structure of the mouse leukocyte cell surface molecule Ly9";
RL Immunogenetics 51:788-793(2000).
[2]
RP NUCLEOTIDE SEQUENCE OF 22-654, AND PROTEIN SEQUENCE OF 48-59.
RX MEDLINE=92373005; PubMed=1506686;
RA Sandrin M.S., Gumley T.P., Henning M.M., Vaughan H.A., Genez L.J.,
RA Trippari J.A., McKenzie I.F.C.;
RT "Isolation and characterization of cDNA clones for mouse Ly-9";
RL J. Immunol. 149:1636-1641(1992).
CC -1- FUNCTION: May participate in adhesion reactions between T
CC lymphocytes and accessory cells by homophilic interaction.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Lymphocytes.
CC -1- SIMILARITY: Contains 2 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC -1- SIMILARITY: Contains 2 Ig-like V-type (immunoglobulin-like)
CC domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF244131; AAG14997.1; -; mRNA.
DR EMBL; AF244131; AAG14996.1; -; genomic_DNA.
DR EMBL; AF246701; AAG13268.2; -; genomic_DNA.
DR EMBL; AF245117; AAG13268.2; JOINED; Genomic_DNA.
DR EMBL; AF245506; AAG13268.2; JOINED; Genomic_DNA.
DR EMBL; AF245118; AAG13268.2; JOINED; Genomic_DNA.
DR EMBL; AF245507; AAG13268.2; JOINED; Genomic_DNA.
DR EMBL; AF245508; AAG13268.2; JOINED; Genomic_DNA.
DR EMBL; AF245509; AAG13268.2; JOINED; Genomic_DNA.
DR EMBL; AF245510; AAG13268.2; JOINED; Genomic_DNA.

DR EMBL; AF246699; AAG13268.2; JOINED; Genomic_DNA.
DR EMBL; AF246700; AAG13268.2; JOINED; Genomic_DNA.
DR HSSP; P08921; IHNG.
DR Ensemble; ENSMUSG0000004707; Mus musculus.
DR MGI; MGI:96885; Ly9.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane, TAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 2.
DR PROSITE; PS50835; Ig-LIKE; 2.
KW Antigen; Cell adhesion; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin domain; Polymorphism; Repeat; Signal; Transmembrane.
FT SIGNAL 1 47
FT CHAIN 1
FT TOPO_DOM 48 654
FT TRANSMEM 48 453
FT TOPO_DOM 454 474
FT DOMAIN 475 654
FT DOMAIN 48 158
FT DOMAIN 159 243
FT DOMAIN 250 362
FT DOMAIN 353 453
FT CARBOHYD 68 68
FT CARBOHYD 120 120
FT CARBOHYD 121 231
FT CARBOHYD 231 231
FT CARBOHYD 284 284
FT CARBOHYD 390 390
FT CARBOHYD 412 412
FT CARBOHYD 423 423
FT CARBOHYD 434 434
FT DISULFID 172 242
FT DISULFID 178 222
FT DISULFID 376 445
FT DISULFID 382 426
FT VARIANT 10 10
FT VARIANT 14 14
FT VARIANT 79 79
FT VARIANT 91 91
FT VARIANT 130 130
FT VARIANT 139 139
FT VARIANT 362 362
FT VARIANT 366 366
FT VARIANT 377 377
FT VARIANT 550 550
FT VARIANT 592 592
FT VARIANT 283 283
FT CONFLICT 499 499
FT CONFLICT 560 560
FT CONFLICT 647 654
SQ SEQUENCE 654 AA; 73143 MW; 1CB8B9708A88EE7 CRC64;
Query Match 20.0%; Score 354.5; DB 1; Length 654;
Beet Local Similarity 27.6%; Pred. No. 11e-20;
Matches 118; Conservative 52; Mismatches 138; Indels 119; Gaps 16;
Qy 14 LMOL-TGSA-----ASGPVKEIVSGVAVTPPLKSK-VKQVDSIVWTNTPLVTIQPEG 67
Db 238 IWQFTGSRKRTKTAG--KTVVGILGEPTVPLEPRARAKRVNVWVNTS--VISQRR 293
Qy 68 GTIIVTONR-----NREKVPDPDGYSLKSLKKNDSGIYVGVSSLSQOPSTQEVYL 122
Db 294 GAATADSRKPKKSGSERVRVTSDDQSLKISQLKMEADGPHAVYCSASRDPVRFPTL 353
Qy 123 HYVEHLSPKXTYMGISKNKGTCTYNTLTCEMEHEGEDIYTWKALGQAANSHSGSLPI 182
Db 354 LVYKLEKPSYTKSPVHMNNGICEVVLICVSDGNGNNTYTWMPLOKNAVWSQGSRLNV 413
Qy 183 SMRWGESMTFLCYAARNPVSRNFSPLIARLCEGAADDPSSWVLLCLLVPLLSLFLV 242
Db 414 SWESGEHLPNFTCTAHNPVS-NSSQSFSSGTCG---PERNKRFMLLLVLLMLI 468


```
QY 243 LGLFLWFLKRE-----ROEYIEB-----KKRYDICREFPNICP- 276
DB 469 GGYFLLRKKKCCSSLATRYROAEVPAIPEPTPTGHGQPSVLSQRYEKUDMSAKTTRHOPT 528
QY 277 -----HSGENTE---YDTPPTN----- 291
DB 529 PFTSSTSSSSATBERDEKTRMHSNANRNOYDLYTHQDIAHALAYGQVEYEAITPYD 588
QY 292 -----RTLL--KEDPANTVSTVEIIPKK-MENPHSLATMPDTP 326
DB 589 KVDSDMEEDMAYIQVSLNVOGEFPLPKCKEDSNITYSVQKPKKTAQTPOODASPEPTP 648
QY 327 RLFAVEN 333
DB 649 ---TYEN 652

RESULT 11
Q8C2D4 MOUSE PRELIMINARY; PRT; 544 AA.
ID Q8C2D4
AC Q8C2D4
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
DE length enriched library, clone: B430026K15 product: lymphocyte antigen
DE 9, full insert sequence.
GN Name: Ly9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kaenkawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glass C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirni L.M., Stuhli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Kono H., Balarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guenichon S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombereite P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohntunki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RA The FANTOM Consortium;
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RL "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RN [4]
```

```
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagata S., Sasaki N., Carninci P.,
RA Kono H., Akiyama U., Nishi K., Kitesuna T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaihiagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiroka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai C., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK088815; BAC04591.1; -; mRNA.
DR Ensembl; ENSMUSG0000004707; Mus musculus.
DR MGI; MGI:96885; Ly9.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR Pfam; PF00047; IG_1.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG LIKE; 2.
KW Immunoglobulin domain.
SQ
SEQUENCE 544 AA; 6161 MW; AAED977F3B25914 CRC64;

Query Match 19.9%; Score 353.5; DB 2; Length 544;
Best Local Similarity 27.6%; Pred. No. 1.1e-20;
Matches 118; Conservative 52; Mismatches 138; Indels 119; Gaps 16;

QY 14 LWOL-TGSA---ASGPKELVSGVAGATPPLKSK-VKQVDSIVYTRNTPTLYTIGR 67
DB 128 IWQCTGASRRKTAAG--KTVAGILGEPVTLPLEFRARFARAKNVVWVNTS--VYSQRR 183
QY 68 GTIIVTQNR-----NREVDPPDGYSLKSKLKKNSGIYVGVYSSLSQSPQOEYVL 122
DB 184 GAATPADSRKPKGSEERVTRTSDQDSIKTSQLKMEADGPHAYAVCSASDPSVRAFTL 243
QY 123 HVEYHLSPKRYTMGLQSNKNGCTVTNLTCMEHEGEDVITYTKALGQANSHNGSLPI 182
DB 244 LVYKRLKRPSTVNSPVYHMMGICVAVLTCSVDGGNNVTYTMPLQNKAVWSQGSHTLV 303
QY 183 SWRWGESDWTFCVARNPVSNNFSSPIIARLCEGADDPSSNWLCLLVLPLLSIFV 242
DB 304 SWESGEHLNPTCTAHPVVS--NSSSOFSSGTCISG---PRNNRRFWILLVLVLVLLMI 358
QY 243 LGLFLWFLKRE-----ROEYIEB-----KKRYDICREFPNICP- 276
DB 359 GGYFLLRKKKCCSSLATRYROAEVPAIPEPTPTGHGQPSVLSQRYEKUDMSAKTTRHOPT 418
```

QY	277	-----HSGENTE-----YDTRIPHN-----	291
Db	419	PTSDTSSSSATTEEDEXTRIJHSTANSNOYVDLHTHODIALAHALAYEQVEAYEALTIPYD	478
QY	292	-----RTIL--SEBANTVYSVTEIIPK--MENPHSLTWTPTP	326
Db	479	KYDSEMDSEDMAYIYQVSLNVOGETPLPKCKEBSNITLYCSVQKPKTKTAQTPQDASPERP	538
QY	327	RLFAVEN 333	
Db	539	---TYEN 542	
	RESULT 12		
	Q4VBG4_MOUSE		
ID	Q4VBG4_MOUSE PRELIMINARY;	PRT;	654 AA.
AC	Q4VBG4;		
DT	13-SEP-2005 (TREMBLrel. 31, Created)		
DT	13-SEP-2005 (TREMBLrel. 31, Last sequence update)		
DT	13-SEP-2005 (TREMBLrel. 31, Last annotation update)		
DE	ly9 protein.		
GN	Name=ly9;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muroidea; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=NM1; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Straube R.L., Fellngold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemen G.D.,		
RA	Altschul S.F., Zeeberg B., Bueto K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Boek S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,		
RA	Fabry J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,		
RA	Scherer A., Schein J.E., Jones S.J.M., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=NM1; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;		
RG	NIH MGC Project;		
RL	Submitted (May-2005) to the EMBL/Genbank/DBS databases.		
DR	EMBL; BC095921; AA95921.1; -- mRNA.		
DR	MGJ; M68865; Ly9.		
DR	InterPro; IPR003599; I9.		
DR	InterPro; IPR007110; I9-like.		
DR	PFam; PF00047; I9; 1.		
DR	SMART; SM00409; I9; 2.		
DR	PROSITE; PS00835; I9-LIKE; 2.		
KM	Immunoglobulin domain.		
SO	SEQUENCE 654 AA; 73154 MW; 8C3ABPB571482B2C CRC64;		
	Query Match	19.9%; Score 353.5; DB 2; Length 654;	
	Best Local Similarity	27.6%; Pred. No. 1.4e-20;	
	Matches 118; Conservative 52; Mismatches 138; Indels 119; Gaps 16		
QY	14	LMQ--TSGA---ASGPVKEIVSGVAGATVPLK--VKQVDSIVTNTTTLVLTIOEG 67	

Db	228	1WQFCTGASRRTKTAAG--KTWVGILGEPTVLEBFRATPATKQNVVFNPTS--VISQERR	293
Qy	68	GTITVTONR-----NRERVPDPGGYSILKSLTKKNDSGIYYVGIYSSSLQPSITQEVYL	122
Db	294	GAATADSRKPKGSEBERVRTSDQOQSILKISQLKQEDADAPYAAVVCSEASRDPVHFLL	353
Qy	123	HYVHEHLSKPYTMGIQSKNGKVCYNLTCCMEHGEEDVLYTWKALQQAANESNGSILPI	182
Db	354	LVYKRLKEPVSYNSEFVHMNGIKCVLLTCSYDGGGNNVYTWMPILQNKVMGQSKHLNV	413
Qy	183	SWRMGESMTFICVARNPNSRPFSSPILARLKCEGAADPDSSMVLICLLVPLLSLFV	242
Db	414	SWSESEHLPNPLCTAHNPVS--NSSQFSSGTTCSG-----PERKKRPMILLVLVLLMLI	468
Qy	243	LGLFLPMFLKRE-----ROEYLTIE-----KKRVDCIETPNICP-	276
Db	469	GGYFLIRKKQOSSLATRYRQAEVPAEIPETPYTHGQGFVLSQRVEKILMMSATTTHQPT	528
Qy	277	-----HSEANTE--YDITTPHN-----	291
Db	529	PTSDTSSESSATTEDEDEKTRIHSTANSNQYDVLVTHODIALALAYEQVEYEAITPYD	588
Qy	292	-----RTLL--KEDAPTYSVVEIPIPK-MENPHSLTWPDPIT	326
Db	569	KYDESMEDEDAIYQVLSLVNGGETFLPKCKEDSNITTCYSVQKPKTTAQTLPDQABSPFIT	648
Qy	327	RLFAVEN 333	
Db	649	---TYEN 652	
RESULT 13			
Q96A28 HUMAN			
AC	Q96A28	HUMAN PRELIMINARY;	PRT; 289 AA.
DT	01-DEC-2001	(TREMBLrel. 19, Created)	
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)	
DT	10-MAY-2005	(TREMBLrel. 30, Last annotation update)	
DE	CD84-H1	(CD2 family 10) (SLAM family member 9).	
GN	Name=SLAMF9;		
OS	Homo sapiens	(Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Butleria; Buarchontoglires; Primates; Catarrhini; Homiidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
OX	NCBI_TaxID=9606;		
NP	NUCLEOTIDE SEQUENCE.		
RL	Zhang W., Wan T., Li N., He L., Yuan Z., Yu M., Cao X.;		
RL	Submitted (JUN-2000) to the EMBL/Genbank/DBCP databases.		
NP	NUCLEOTIDE SEQUENCE.		
RP	MEDLINE=2154111; PubMed=11685473; DOI=10.1007/s002510100364;		
RA	Fennelly J.A., Tiwari B., Davis S.J., Evans E.J.;		
RT	"CD2F-10: a new member of the CD2 subset of the immunoglobulin		
RT	superfamily.";		
RT	Immunogenetics 53:599-602(2001).		
RL	[3]		
NP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Pooled tissue;		
RC	MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Scheen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schenfer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Caetano T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bohak S.A., McWen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulky S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,
 RA Butterfield J.S.N., Krzywinski M.I., Skalski U., Smailus D.B.,
 RA Schnerch A., Schin J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pooled tissue;
 RA Director MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF25725; AAK69052.1; -; mRNA.
 DR EMBL; AY034613; AAK61389.1; -; mRNA.
 DR EMBL; BC074754; AAH74754.1; -; mRNA.
 DR Ensembl; ENSG0000162723; Homo sapiens.
 DR InterPro; IPR003599; IG-like.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 269 AA; 32436 MW; 2FB67EB8B4D18205 CRC64;
 Query Match 18.7%; Score 330.5; DB 2; Length 289;
 Best Local Similarity 30.6%; Pred. No. 4.1e-19;
 Matches 87; Conservative 60; Mismatches 102; Indels 35; Gaps 10;
 QY 1 MAGSTCTCTLYI-----LMQLTGSAAGPVKEINSGVGAATVPFK-SKVKQVDSIV 52
 DB 1 MCAFWMLLLLLLOSGQRRLRMWGS-----EEVAVLQESISLPLEIPPEEVENII 54
 QY 53 WFTNTPLVTIOP--EG--GTTIVQNNRBERVDPDGGYSKLKSKLKKNDGSIYYVGIY 108
 DB 55 WSSHSK-LATVPGKEGHPATIMVTPHYQGVSLDYSLSHINLMEBSGLYQAOY 113
 QY 109 SSSLOQPSIOEVYLVHYEHLSEKPYTMGLQSNKNGCTVNTLCCMEHGEEDVIYTKALG 168
 DB 114 LRTSGISIMQGVNLCVYRMLSPQITVNPESGEGACMSLVCSEKAGMDWTYFWLSRG 173
 QY 169 QAANSHNGSIIPISWRGSESDMTPTICVARNPVSNRFPSSPIARLKLCEG-----AAD 220
 DB 174 DSTYTFHGSPVLTSTWRPDSLTSTCRANPDISVSSCP-----PDGPFYADPNVASE 228
 QY 221 DPDSMVLCL-LVYPLLISLPLVLGLPLMFLKREGEYIEKK 263
 DB 229 KPSTAFCLAKGLIFLLVLVLMG--LWVIRVQKHKKPRKK 270
 RESULT 14
 ID Q8C9E4_MOUSE PRELIMINARY; PRT; 538 AA.
 AC Q8C9E4;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
 DE library, clone:A630078M16 product:lymphocyte antigen 9, full insert
 DE sequence. (Fragment).
 GN Name:Ly9;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_taxid=10090;
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi T., Fukuda S.,
 RA Atkawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kaenaka T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stebbins F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gattungich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
 RA Noadone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Welt C., Whitaker C., Wilming L.,
 RA Hayashizaki Y.;
 RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Konteski S.,
 RL "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RA The FANTOM Consortium,
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwa K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki K.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashiura W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nihi K., Nomura X., Numazaki R., Ohno M., Ohashi N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK042288; BAC1215.1; -; mRNA.
 DR HSSP; P08921; IHNG.
 DR MGI; MGI:96885; Ly9.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.

DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00409; IG; 2.
DR PROSITE: PS50835; IG LIKE; 2.
FT NON TER 538 538
SQ SEQUENCE 538 AA; 60040 MW; 7DC7FB9C64BFE9A6 CRC64;

Query Match 18.6%; Score 329; DB 2; Length 538;
Best Local Similarity 31.5%; Pred. No. 1.2e-18;

Matches 96; Conservative 51; Mismatches 130; Indels 28; Gaps 12;

QY 14 LMOL-TGSA-----ASGPYKELVSGAVTFPLKSK-VKQVDSIYWTPTPLVTIQTGEBG 67
DB 238 IWOFCETGASRRRTAG--KTIVGILGEPYTLPEFRATRTATNVAWVFNITS--VISOERR 293
QY 68 GTIIVTQNR-----NREKVDPPDGGYSLKSLKKNDSGIYVYGSISSLOOPTQOEYVL 122
DB 294 GAATPDSRRKRGSRERVRYSDDQSLKISQLKHEADGPHYAVYCSERAPSVRHFTL 353
QY 123 HVEYHLSKPYTMGLQSNKNGTCVTNLTCCMEHGEEDVITYWKALGOANESHNGSILPI 182
DB 354 LVYKRLKRPSTYKSPVHMANGICEVVLTCSDVGGANNVYTWMPLONKAVNSQKSHLV 413
QY 183 SWRGESEMTPLCVARNPVSRNFSPIILARKLCEGADDPDSMTVLCLLVPLILSLFV 242
DB 414 SWEGSEHLPNFTCTAHNPVS-NSSSQFSSGTICSG---PERNKRFWLLILLVLLMLI 468
QY 243 LGLFWFLKRREROEYIEEK-KRVDICRETPNICPHSGE---NTEYDTIPIHNTIILKE 297
DB 469 GGYFL--LRKKQCSILATRRQAEVPAIEPTFGHGQFSVLSQRYEKIDMSAKT-TRH 525
QY 298 DPANT 302
DB 526 QPTPT 530

RESULT 15
Q5JRR0 HUMAN
ID Q5JRR0 HUMAN PRELIMINARY; PRT; 289 AA.
AC Q5JRR0;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DB SLAM family member 9.
GN Name=SLAMF9; ORFNames=RP11-48020.3-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL; AL513485; CA114607.1; -; Genomic DNA.
DR Ensembl; ENSG00000162723; Homo sapiens.
DR HGNC; HGNC:18430; SLAMF9.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain; Transmembrane.
SQ SEQUENCE 289 AA; 32436 MW; 2BA22CBAC2E7F275 CRC64;

Query Match 18.5%; Score 328.5; DB 2; Length 289;
Best Local Similarity 30.3%; Pred. No. 6e-19;
Matches 86; Conservative 61; Mismatches 102; Indels 35; Gaps 10;

QY 1 MAGSPYCTLLIYI-----LMQLTGSASAGPVKEIVSGAVTFPLK-SKYKQVDSIV 52
DB 1 MCAFPWLLILLILLOGSGQRRLRMKGS-----EEVAVLVQESISISPLEIPDPDEVENTI 54
QY 53 WFTNTPLVTIQTG--EG--GTIIVTQNRNRRERVDPPDGGYSLKSLKKNDSGIYVYGIV 108

DB 55 WSHKRS-LATVVPQKRGHPATIMWTNPNYQGVSTLDPSTSLHISNLSWEDSGLYQAVN 113
QY 109 SSSIQQPSTQEYVLHVEYHLSKPYTMGLQSNKNGTCVTNLTCCMEHGEEDVITYWKALG 168
DB 114 LRTSQISTMQQYNICVTRKMLSEPIITVNFESSGGAGCSMSLVCSEYKAGMDMTYSWLSRG 173
QY 169 QANESHNGSILPISRWGESDMTFICVARNPVSRNFSPIILARKLCEG-----AAD 220
DB 174 DSTYTFHGGPVLSTSWRPGDSALSYTCRANPNISVSSCP1-----PDGPFYADPNVASE 228
QY 221 DPDSMTVLCL-LVPLILSLFVGLFLWFLKRREROEYIEKK 263
DB 229 KPSTAFCLIAQLIFLLVILAMG--LWVIRVQRRHMPRMCK 270

Search completed: December 16, 2005, 10:45:18
Job time : 272 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 10:40:47 (Search time 49 Seconds

(without alignments)
565.232 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 1772

Sequence: 1 MAGSPTCLTYILMQTGS.....PHSLTMDPTPLFAVENVI 335

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: /cgn2_6/prodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/7_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/8_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/9_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/BACKFILES1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1772	100.0	335	2	US-09-991-181-253
2	1772	100.0	335	2	US-09-990-444-253
3	1772	100.0	335	2	US-09-997-333-253
4	1772	100.0	335	2	US-09-992-598-253
5	498	28.1	97	2	US-09-513-999C-4472
6	362.5	20.5	328	2	US-09-949-016-6428
7	362.5	20.5	329	2	US-09-149-476-483
8	362.5	20.5	332	2	US-09-949-016-7327
9	186	10.5	343	1	US-08-348-792-10
10	186	10.5	343	1	US-08-462-738-10
11	186	10.5	343	2	US-09-199-955-10
12	186	10.5	343	2	US-08-880-875-10
13	182.5	10.3	335	1	US-08-348-792-2
14	182.5	10.3	335	1	US-08-462-738-2
15	182.5	10.3	335	2	US-09-199-955-2
16	182.5	10.3	335	2	US-08-880-875-2
17	182.5	10.3	335	2	US-09-369-248A-3
18	182.5	10.3	335	2	US-09-949-002-349
19	182.5	10.3	351	2	US-09-949-002-418
20	180	10.2	307	1	US-08-348-792-8
21	180	10.2	307	1	US-08-462-738-8
22	180	10.2	307	2	US-09-199-955-8
23	180	10.2	307	2	US-08-880-875-8
24	170	9.6	365	2	US-09-949-016-6907
25	164.5	9.3	305	1	US-08-348-792-6
27	164.5	9.3	305	1	US-08-462-738-6

28	164.5	9.3	305	2	US-09-199-955-6	Sequence 6, Appl1
29	164.5	9.3	305	2	US-08-880-875-6	Sequence 6, Appl1
30	158.5	8.9	329	1	US-08-348-792-12	Sequence 12, Appl1
31	158.5	8.9	329	1	US-08-462-738-12	Sequence 12, Appl1
32	158.5	8.9	329	2	US-09-199-955-12	Sequence 12, Appl1
33	158.5	8.9	329	2	US-08-880-875-12	Sequence 12, Appl1
34	152	8.6	298	1	US-08-348-792-4	Sequence 4, Appl1
35	152	8.6	298	1	US-08-462-738-4	Sequence 4, Appl1
36	152	8.6	298	2	US-09-199-955-4	Sequence 4, Appl1
37	152	8.6	298	2	US-08-880-875-4	Sequence 4, Appl1
38	150.5	8.5	285	2	US-09-369-248A-2	Sequence 2, Appl1
39	141	8.0	149	2	US-09-227-357-443	Sequence 443, App
40	141	8.0	149	2	US-09-973-278-571	Sequence 571, App
41	140.5	7.9	142	2	US-09-973-278-252	Sequence 252, App
42	140.5	7.9	143	2	US-09-227-357-192	Sequence 192, App
43	136.5	7.7	351	2	US-08-466-465-6	Sequence 6, Appl1
44	136.5	7.7	351	2	US-09-730-465-6	Sequence 6, Appl1
45	128	7.2	225	1	US-08-328-152A-31	Sequence 31, Appl1
46	128	7.2	321	6	5169835-17	Patent No. 5169835
47	125.5	7.1	464	1	US-08-602-725-32	Sequence 32, Appl1
48	125.5	7.1	464	2	US-09-949-016-6116	Sequence 6116, Ap
49	125.5	7.1	464	2	US-09-949-016-7525	Sequence 7525, Ap
50	124.5	7.0	365	2	US-09-949-016-7591	Sequence 7591, Ap
51	123	6.9	199	1	US-08-328-152A-36	Sequence 36, Appl
52	122	6.9	316	2	US-09-397-243D-13	Sequence 13, Appl
53	120	6.8	352	2	US-09-991-181-505	Sequence 505, App
54	120	6.8	352	2	US-09-990-444-505	Sequence 505, App
55	120	6.8	352	2	US-09-997-333-505	Sequence 505, App
56	120	6.8	352	2	US-09-992-598-505	Sequence 505, App
57	119.5	6.7	365	1	US-08-979-424-3	Sequence 3, Appl1
58	119.5	6.7	365	2	US-09-272-496-2	Sequence 2, Appl1
59	119.5	6.7	365	2	US-09-949-016-6064	Sequence 6064, Ap
60	119.5	6.7	383	2	US-09-949-016-11050	Sequence 11050, A
61	119.5	6.7	418	2	US-08-630-172-18	Sequence 18, Appl
62	119.5	6.7	448	2	US-09-375-419-18	Sequence 18, Appl
63	117.5	6.6	344	1	US-08-602-725-34	Sequence 34, Appl
64	117.5	6.6	365	2	US-08-928-383B-2	Sequence 2, Appl1
65	116.5	6.6	319	1	US-08-597-495B-22	Sequence 22, Appl
66	116.5	6.6	319	2	US-09-068-051A-82	Sequence 82, Appl
67	116.5	6.6	319	2	US-09-336-536-67	Sequence 67, Appl
68	116.5	6.6	319	2	US-09-254-465A-6	Sequence 6, Appl1
69	116.5	6.6	319	2	US-09-953-499-6	Sequence 6, Appl1
70	115.5	6.5	184	2	US-08-630-172-2	Sequence 2, Appl1
71	115.5	6.5	184	2	US-09-375-419-2	Sequence 2, Appl1
72	114.5	6.5	642	1	US-08-217-299-1	Sequence 1, Appl1
73	114.5	6.5	698	1	US-08-602-725-36	Sequence 36, Appl
74	114.5	6.5	702	2	US-09-949-016-6484	Sequence 6484, Ap
75	114.5	6.5	734	1	US-08-389-455A-17	Sequence 17, Appl
76	114.5	6.5	734	2	US-08-987-867A-17	Sequence 17, Appl
77	114.5	6.5	740	2	US-09-949-016-8168	Sequence 8168, Ap
78	113	6.4	373	2	US-09-991-181-503	Sequence 503, App
79	113	6.4	373	2	US-09-999-833A-59	Sequence 59, Appl
80	113	6.4	373	2	US-09-990-444-503	Sequence 503, App
81	113	6.4	373	2	US-09-997-333-503	Sequence 503, App
82	113	6.4	373	2	US-09-992-598-503	Sequence 59, Appl
83	113	6.4	373	2	US-10-020-445A-59	Sequence 59, Appl
84	111.5	6.3	174	1	US-08-765-536-2	Sequence 2, Appl1
85	111.5	6.3	174	4	PCT-US95-08401-2	Sequence 2, Appl1
86	110.5	6.2	365	2	US-09-899-634C-4	Sequence 4, Appl1
87	109.5	6.2	315	2	US-09-910-174B-28	Sequence 28, Appl
88	109.5	6.2	315	2	US-09-620-461-28	Sequence 28, Appl
89	109	6.2	324	2	US-09-910-174B-6	Sequence 6, Appl1
90	109	6.2	324	2	US-09-620-461-6	Sequence 6, Appl1
91	105.5	6.0	323	2	US-09-651-200-21	Sequence 21, Appl
92	105.5	6.0	323	2	US-09-441-411-22	Sequence 22, Appl
93	105.5	6.0	323	2	US-09-915-789A-16	Sequence 16, Appl
94	105.5	6.0	323	4	PCT-US94-09642-2	Sequence 2, Appl1
95	105.5	6.0	329	1	US-08-456-104-2	Sequence 2, Appl1
96	105.5	6.0	329	1	US-08-101-624-2	Sequence 2, Appl1
97	105.5	6.0	329	2	US-08-479-744A-2	Sequence 2, Appl1
98	105.5	6.0	329	2	US-08-280-757B-2	Sequence 2, Appl1
99	105.5	6.0	329	2	US-08-205-697A-23	Sequence 23, Appl
100	105.5	6.0	329	2	US-08-702-525-23	Sequence 23, Appl

101	105.5	6.0	329	2	US-08-403-253A-4	Sequence 4, Appli	174	91.5	5.2	230	2	US-09-869-388-4	Sequence 4, Appli
102	105.5	6.0	329	2	US-08-435-816A-4	Sequence 4, Appli	175	91.5	5.2	341	2	US-09-401-636-9	Sequence 9, Appli
103	105.5	6.0	329	2	US-09-425-762-2	Sequence 2, Appli	176	91.5	5.1	251	6	5185441-38	Patent No. 5185441
104	105.5	6.0	329	2	US-09-837-867A-23	Sequence 23, Appli	177	91	5.1	316	2	US-09-915-789A-3	Sequence 3, Appli
105	105.5	6.0	329	2	US-09-206-132-2	Sequence 2, Appli	178	90.5	5.1	521	2	US-08-996-338-20	Sequence 20, Appli
106	105.5	6.0	329	2	US-09-441-411-26	Sequence 26, Appli	179	90.5	5.1	521	2	US-09-556-972-20	Sequence 20, Appli
107	105.5	6.0	329	2	US-09-425-516-2	Sequence 2, Appli	180	90	5.1	156	2	US-09-370-838-210	Sequence 210, App
108	105.5	6.0	329	2	US-09-350-202-4	Sequence 4, Appli	181	90	5.1	156	2	US-09-854-133-210	Sequence 210, App
109	105.5	6.0	329	2	US-08-592-711-4	Sequence 4, Appli	182	90	5.1	222	1	US-08-328-152A-8	Sequence 8, Appli
110	105.5	6.0	329	2	US-09-349-915B-4	Sequence 4, Appli	183	90	5.1	240	1	US-07-940-861-12	Sequence 12, Appli
111	105.5	6.0	329	4	PCT-US95-02576-23	Sequence 23, Appli	184	90	5.1	240	1	US-08-459-512-12	Sequence 12, Appli
112	105.5	6.0	372	2	US-09-949-016-1132	Sequence 11132, A	185	90	5.1	240	1	US-08-460-132-12	Sequence 12, Appli
113	104.5	5.9	329	2	US-09-667-135-32	Sequence 32, Appli	186	90	5.1	240	1	US-08-466-465-4	Sequence 4, Appli
114	104	5.9	349	2	US-09-924-103-4	Sequence 4, Appli	187	90	5.1	240	2	US-09-730-465-4	Sequence 4, Appli
115	102	5.8	144	2	US-09-513-999C-4353	Sequence 4353, Ap	188	90	5.1	240	4	PCT-US92-02050-12	Patent No. 5185441-36
116	101.5	5.7	270	2	US-09-254-465A-24	Sequence 24, Appli	189	90	5.1	240	6	5185441-36	Patent No. 5185441
117	101.5	5.7	270	2	US-09-953-499-24	Sequence 24, Appli	190	90	5.1	240	6	5223394-4	Patent No. 5223394
118	101.5	5.7	273	2	US-09-254-465A-26	Sequence 26, Appli	191	90	5.1	240	6	5223394-6	Patent No. 5223394
119	101.5	5.7	273	2	US-09-953-499-26	Sequence 26, Appli	192	90	5.1	250	1	US-07-940-861-10	Sequence 10, Appli
120	100.5	5.7	638	2	US-09-228-986-74	Sequence 74, Appli	193	90	5.1	250	1	US-08-459-512-10	Sequence 10, Appli
121	100.5	5.7	638	2	US-10-101-464A-74	Sequence 74, Appli	194	90	5.1	250	1	US-08-459-657-10	Sequence 10, Appli
122	100	5.6	365	2	US-08-928-383B-23	Sequence 23, Appli	195	90	5.1	250	1	US-08-460-132-10	Sequence 10, Appli
123	98.5	5.6	365	2	US-08-928-383B-23	Sequence 23, Appli	196	90	5.1	250	2	US-08-466-465-2	Sequence 2, Appli
124	98.5	5.6	732	2	US-09-818-247-5	Sequence 5, Appli	197	90	5.1	250	2	US-09-730-465-2	Sequence 2, Appli
125	98	5.5	503	2	US-08-999-689A-6	Sequence 6, Appli	198	90	5.1	250	4	PCT-US92-02050-10	Patent No. 5185441-36
126	98	5.5	503	2	US-09-944-807-4	Sequence 4, Appli	199	90	5.1	250	4	PCT-US92-02050-10	Patent No. 5185441-36
127	97	5.5	773	2	US-08-434-000A-2	Sequence 2, Appli	200	90	5.1	250	6	5223394-1	Patent No. 5223394
128	97	5.5	773	2	US-09-312-157-2	Sequence 2, Appli	201	90	5.1	253	2	US-09-949-016-10124	Sequence 10124, A
129	97	5.5	773	2	US-09-717-888-2	Sequence 2, Appli	202	90	5.1	419	6	5169835-2	Patent No. 5169835
130	97	5.5	773	2	US-09-818-247-6	Sequence 6, Appli	203	90	5.1	541	1	US-08-604-333-2	Sequence 2, Appli
131	96.5	5.4	534	2	US-09-651-200-6	Sequence 6, Appli	204	90	5.1	541	2	US-09-110-618-2	Sequence 2, Appli
132	96.5	5.4	534	2	US-09-651-200-24	Sequence 24, Appli	205	90	5.1	541	2	US-09-173-151A-28	Sequence 28, Appli
133	96	5.4	440	2	US-09-651-200-2	Sequence 2, Appli	206	90	5.1	541	2	US-09-578-178-2	Sequence 2, Appli
134	96	5.4	440	2	US-09-651-200-4	Sequence 4, Appli	207	90	5.1	541	2	US-09-577-806-2	Sequence 2, Appli
135	96	5.4	526	2	US-09-910-174B-9	Sequence 9, Appli	208	90	5.1	541	2	US-09-621-502-4	Sequence 4, Appli
136	96	5.4	526	2	US-09-620-461-9	Sequence 9, Appli	209	90	5.1	541	2	US-09-949-002-360	Sequence 360, App
137	96	5.4	526	2	US-09-949-016-6122	Sequence 6122, Ap	210	90	5.1	546	2	US-09-949-002-489	Sequence 489, App
138	96	5.4	540	2	US-09-949-016-11644	Sequence 11644, A	211	90	5.1	821	2	US-08-836-734E-8	Sequence 8, Appli
139	95.5	5.4	365	2	US-08-928-383B-26	Sequence 26, Appli	212	90	5.1	821	2	US-08-836-734E-9	Sequence 9, Appli
140	95.5	5.4	417	2	US-09-949-016-6729	Sequence 6729, Ap	213	89.5	5.1	215	2	US-09-915-789A-20	Sequence 20, Appli
141	95.5	5.4	771	2	US-08-434-000A-8	Sequence 8, Appli	214	89.5	5.1	215	2	US-09-479-744A-23	Sequence 23, Appli
142	95.5	5.4	771	2	US-09-312-157-8	Sequence 8, Appli	215	89.5	5.1	423	2	US-09-181-339-9	Sequence 9, Appli
143	95.5	5.4	771	2	US-09-717-888-8	Sequence 8, Appli	216	89	5.0	303	2	US-09-651-200-23	Sequence 23, Appli
144	95.5	5.4	771	2	US-09-818-247-4	Sequence 4, Appli	217	89	5.0	303	2	US-09-441-411-15	Sequence 15, Appli
145	95	5.4	316	2	US-09-999-833A-137	Sequence 137, App	218	89	5.0	303	2	US-09-441-411-20	Sequence 20, Appli
146	95	5.4	316	2	US-10-020-445A-137	Sequence 137, App	219	89	5.0	309	1	US-08-456-104-4	Sequence 4, Appli
147	93.5	5.3	299	2	US-09-188-930-185	Sequence 189, App	220	89	5.0	309	2	US-08-479-744A-23	Sequence 23, Appli
148	93.5	5.3	2409	6	5180808-2	Patent No. 5180808	221	89	5.0	309	2	US-08-280-757B-23	Sequence 23, Appli
149	93	5.2	316	2	US-09-910-174B-24	Sequence 24, Appli	222	89	5.0	309	2	US-08-205-697A-21	Sequence 21, Appli
150	93	5.2	316	2	US-09-620-461-24	Sequence 24, Appli	223	89	5.0	309	2	US-08-702-525-21	Sequence 21, Appli
151	93	5.2	316	2	US-09-915-789A-1	Sequence 1, Appli	224	89	5.0	309	2	US-09-651-200-22	Sequence 22, Appli
152	93	5.2	561	2	US-09-192-545-2	Sequence 2, Appli	225	89	5.0	309	2	US-09-667-135-33	Sequence 33, Appli
153	92.5	5.2	299	2	US-09-188-930-331	Sequence 331, App	226	89	5.0	309	2	US-09-425-762-23	Sequence 23, Appli
154	92.5	5.2	299	2	US-09-462-270-2	Sequence 2, Appli	227	89	5.0	309	2	US-09-837-867A-21	Sequence 21, Appli
155	92.5	5.2	299	2	US-09-254-465A-1	Sequence 1, Appli	228	89	5.0	309	2	US-09-206-132-4	Sequence 4, Appli
156	92.5	5.2	299	2	US-09-312-283C-189	Sequence 189, App	229	89	5.0	309	2	US-09-441-411-13	Sequence 13, Appli
157	92.5	5.2	299	2	US-09-312-283C-331	Sequence 331, App	230	89	5.0	309	2	US-09-441-411-18	Sequence 18, Appli
158	92.5	5.2	299	2	US-09-907-794A-119	Sequence 119, App	231	89	5.0	309	2	US-09-441-411-24	Sequence 24, Appli
159	92.5	5.2	299	2	US-09-905-125A-119	Sequence 119, App	232	89	5.0	309	2	US-09-425-516-23	Sequence 23, Appli
160	92.5	5.2	299	2	US-09-902-775A-119	Sequence 119, App	233	89	5.0	309	4	PCT-US95-02576-21	Sequence 21, Appli
161	92.5	5.2	299	2	US-09-397-243D-3	Sequence 3, Appli	234	89	5.0	314	2	US-08-205-697A-13	Sequence 13, Appli
162	92.5	5.2	299	2	US-09-906-700-119	Sequence 119, App	235	89	5.0	314	2	US-08-702-525-13	Sequence 13, Appli
163	92.5	5.2	299	2	US-09-903-603A-119	Sequence 119, App	236	89	5.0	314	2	US-08-837-867A-13	Sequence 13, Appli
164	92.5	5.2	299	2	US-09-904-920A-119	Sequence 119, App	237	89	5.0	314	2	US-09-441-411-14	Sequence 14, Appli
165	92.5	5.2	299	2	US-09-909-064-119	Sequence 119, App	238	89	5.0	314	2	US-09-441-411-19	Sequence 19, Appli
166	92.5	5.2	299	2	US-09-905-381A-119	Sequence 119, App	239	89	5.0	314	4	PCT-US95-02576-13	Sequence 13, Appli
167	92.5	5.2	299	2	US-09-906-618-119	Sequence 119, App	240	89	5.0	356	2	US-09-441-411-11	Sequence 11, Appli
168	92.5	5.2	299	2	US-09-953-499-1	Sequence 1, Appli	241	89	5.0	356	2	US-09-441-411-12	Sequence 12, Appli
169	92.5	5.2	299	2	US-09-906-646-119	Sequence 119, App	242	89	5.0	356	2	US-09-441-411-16	Sequence 16, Appli
170	92.5	5.2	299	2	US-09-904-462-119	Sequence 119, App	243	89	5.0	356	2	US-09-441-411-17	Sequence 17, Appli
171	92.5	5.2	299	2	US-09-902-736A-119	Sequence 119, App	244	89	5.0	821	2	US-09-422-865-24	Sequence 24, Appli
172	92.5	5.2	299	2	US-09-906-722A-119	Sequence 119, App	245	89	5.0	821	2	US-09-538-092-972	Sequence 972, App
173	92	5.2	491	2	US-09-181-339-12	Sequence 12, Appli	246	89	5.0	821	2	US-08-836-734E-6	Sequence 6, Appli

393	83.5	4.7	450	2	US-09-904-920A-320	Sequence 320, App	466	81.5	4.6	846	1	US-08-451-883-4	Sequence 4, Appl1
394	83.5	4.7	450	2	US-09-909-064-320	Sequence 320, App	467	81.5	4.6	1441	2	US-09-949-016-10397	Sequence 10397, A
395	83.5	4.7	450	2	US-09-905-381A-320	Sequence 320, App	468	81	4.6	144	6	5169635-8	Patent No. 5169635
396	83.5	4.7	450	2	US-09-906-618-320	Sequence 320, App	469	81	4.6	252	1	US-08-414-657D-56	Sequence 56, Appl1
397	83.5	4.7	450	2	US-09-906-646-320	Sequence 320, App	470	81	4.6	287	1	US-08-414-657D-44	Sequence 48, Appl1
398	83.5	4.7	450	2	US-09-904-462-320	Sequence 320, App	471	81	4.6	304	1	US-08-414-657D-46	Sequence 46, Appl1
399	83.5	4.7	450	2	US-09-902-736A-320	Sequence 320, App	472	81	4.6	308	1	US-08-414-657D-46	Sequence 2, Appl1
400	83.5	4.7	450	2	US-09-906-722A-320	Sequence 320, App	473	81	4.6	325	1	US-08-414-657D-2	Sequence 2, Appl1
401	83.5	4.7	789	2	US-09-002-285-96	Sequence 96, Appl1	474	81	4.6	325	2	US-08-414-657D-41	Sequence 41, Appl1
402	83.5	4.7	789	2	US-09-589-477-96	Sequence 96, Appl1	475	81	4.6	325	2	US-09-135-080-2	Sequence 2, Appl1
403	83.5	4.7	789	2	US-10-099-285A-96	Sequence 96, Appl1	476	81	4.6	338	2	US-08-414-657D-60	Sequence 60, Appl1
404	83.5	4.7	1501	1	US-08-447-464-3	Sequence 3, Appl1	477	81	4.6	338	2	US-09-135-080-8	Sequence 8, Appl1
405	83.5	4.7	1501	1	US-08-716-679-3	Sequence 3, Appl1	478	81	4.6	338	2	US-09-976-594-404	Sequence 404, App
406	83	4.7	342	2	US-09-401-636-5	Sequence 5, Appl1	479	80.5	4.5	205	2	US-09-133-001C-4766	Sequence 4766, Ap
407	83	4.7	464	2	US-09-297-468-2	Sequence 2, Appl1	480	80.5	4.5	302	2	US-09-915-789A-18	Sequence 18, Appl1
408	83	4.7	757	2	US-09-818-247-2	Sequence 2, Appl1	481	80.5	4.5	313	2	US-09-701-623C-3	Sequence 3, Appl1
409	83	4.7	846	1	US-08-149-103-3	Sequence 3, Appl1	482	80.5	4.5	346	1	US-08-213-403-2	Sequence 2, Appl1
410	83	4.7	846	1	US-08-451-883-3	Sequence 3, Appl1	483	80.5	4.5	346	1	US-08-458-077-2	Sequence 2, Appl1
411	83	4.7	873	1	US-08-393-734-2	Sequence 2, Appl1	484	80.5	4.5	346	1	US-08-747-240-2	Sequence 2, Appl1
412	83	4.7	873	1	US-08-894-489-2	Sequence 2, Appl1	485	80.5	4.5	346	1	US-08-747-240-2	Sequence 2, Appl1
413	83	4.7	873	1	US-10-167-264-2	Sequence 2, Appl1	486	80.5	4.5	346	1	US-08-299-657-6	Sequence 6, Appl1
414	83	4.7	894	2	US-09-949-016-10605	Sequence 10605, A	487	80.5	4.5	346	2	US-09-039-642B-2	Sequence 2, Appl1
415	83	4.7	904	2	US-09-949-016-9528	Sequence 9528, Ap	488	80.5	4.5	522	2	US-08-635-130A-9	Sequence 9, Appl1
416	82.5	4.7	194	2	US-08-630-172-14	Sequence 14, Appl1	489	80.5	4.5	650	1	US-09-949-016-11189	Sequence 11189, A
417	82.5	4.7	194	2	US-09-375-419-14	Sequence 14, Appl1	490	80.5	4.5	650	1	US-08-121-713D-60	Sequence 60, Appl1
418	82.5	4.7	226	2	US-09-869-388-10	Sequence 10, Appl1	491	80.5	4.5	650	1	US-08-835-268-60	Sequence 60, Appl1
419	82.5	4.7	238	2	US-09-149-476-485	Sequence 485, App	492	80.5	4.5	650	1	US-09-060-632-60	Sequence 60, Appl1
420	82.5	4.7	456	2	US-09-949-016-7564	Sequence 7564, Ap	493	80.5	4.5	650	2	US-08-833-391-60	Sequence 60, Appl1
421	82.5	4.7	486	2	US-09-134-000C-5552	Sequence 5552, Ap	494	80.5	4.5	650	2	US-09-060-610-60	Sequence 60, Appl1
422	82.5	4.7	511	2	US-09-002-285-88	Sequence 88, Appl1	495	80.5	4.5	650	4	PCT-US94-10151A-60	Sequence 60, Appl1
423	82.5	4.7	511	2	US-09-589-477-88	Sequence 88, Appl1	496	80.5	4.5	721	2	US-09-390-234-20	Sequence 20, Appl1
424	82.5	4.7	511	2	US-10-099-285A-88	Sequence 88, Appl1	497	80.5	4.5	721	2	US-09-603-311-20	Sequence 20, Appl1
425	82.5	4.7	789	2	US-09-002-285-82	Sequence 82, Appl1	498	80.5	4.5	789	2	US-08-960-780-6	Sequence 6, Appl1
426	82.5	4.7	789	2	US-09-002-285-84	Sequence 84, Appl1	499	80.5	4.5	789	2	US-09-073-888-6	Sequence 6, Appl1
427	82.5	4.7	789	2	US-09-002-285-92	Sequence 92, Appl1	500	80.5	4.5	789	2	US-09-850-351A-6	Sequence 6, Appl1
428	82.5	4.7	789	2	US-09-589-477-82	Sequence 82, Appl1	501	80.5	4.5	828	1	US-08-261-304-2	Sequence 2, Appl1
429	82.5	4.7	789	2	US-09-589-477-84	Sequence 84, Appl1	502	80	4.5	227	2	US-09-869-388-6	Sequence 6, Appl1
430	82.5	4.7	789	2	US-09-589-477-92	Sequence 84, Appl1	503	80	4.5	252	1	US-08-414-657D-57	Sequence 57, Appl1
431	82.5	4.7	789	2	US-10-099-285A-82	Sequence 82, Appl1	504	80	4.5	287	1	US-08-414-657D-49	Sequence 49, Appl1
432	82.5	4.7	789	2	US-10-099-285A-84	Sequence 84, Appl1	505	80	4.5	310	1	US-08-414-657D-45	Sequence 45, Appl1
433	82.5	4.7	789	2	US-10-099-285A-82	Sequence 82, Appl1	506	80	4.5	315	1	US-08-414-657D-47	Sequence 47, Appl1
434	82.5	4.7	790	2	US-09-002-285-102	Sequence 102, App	507	80	4.5	338	1	US-08-414-657D-42	Sequence 42, Appl1
435	82.5	4.7	790	2	US-09-589-477-102	Sequence 102, App	508	80	4.5	338	1	US-08-414-657D-43	Sequence 43, Appl1
436	82.5	4.7	790	2	US-10-099-285A-102	Sequence 102, App	509	80	4.5	338	2	US-09-135-080-4	Sequence 4, Appl1
437	82.5	4.6	314	2	US-09-107-532A-4919	Sequence 4919, Ap	510	80	4.5	499	2	US-09-252-991A-3338	Sequence 23328, A
438	82	4.6	370	2	US-09-248-796A-18365	Sequence 18365, A	511	80	4.5	528	2	US-09-010-147B-20	Sequence 20, Appl1
439	82	4.6	449	2	US-09-118-319-7	Sequence 7, Appl1	512	80	4.5	528	2	US-10-188-495-71	Sequence 71, Appl1
440	82	4.6	449	2	US-09-286-691-4	Sequence 4, Appl1	513	80	4.5	529	2	US-09-383-566-31	Sequence 31, Appl1
441	82	4.6	449	2	US-09-687-147-4	Sequence 4, Appl1	514	80	4.5	529	2	US-09-823-038A-31	Sequence 12, Appl1
442	82	4.6	567	2	US-09-773-877B-20	Sequence 20, Appl1	515	80	4.5	607	1	US-08-752-307B-12	Sequence 12, Appl1
443	82	4.6	757	2	US-09-622-880B-1	Sequence 1, Appl1	516	80	4.5	607	2	US-09-707-802-12	Sequence 12, Appl1
444	82	4.6	874	1	US-08-456-647B-6	Sequence 6, Appl1	517	80	4.5	607	2	US-09-991-326-12	Sequence 12, Appl1
445	82	4.6	874	1	US-08-237-401A-6	Sequence 6, Appl1	518	80	4.5	1233	2	US-09-194-613-5	Sequence 5, Appl1
446	82	4.6	880	1	US-08-445-640-10	Sequence 10, Appl1	519	79.5	4.5	202	6	US-09-570-367C-21	Patent No. 5189147
447	82	4.6	880	1	US-08-170-558-10	Sequence 10, Appl1	520	79.5	4.5	278	2	US-09-915-524-21	Sequence 21, Appl1
448	82	4.6	880	2	US-08-447-314-10	Sequence 10, Appl1	521	79.5	4.5	278	2	US-09-934-634-21	Sequence 21, Appl1
449	82	4.6	880	2	US-08-445-461-10	Sequence 10, Appl1	522	79.5	4.5	278	2	US-09-917-278-21	Sequence 21, Appl1
450	82	4.6	880	2	US-09-223-490-10	Sequence 10, Appl1	523	79.5	4.5	278	2	US-09-917-278-21	Sequence 21, Appl1
451	82	4.6	1248	2	US-09-949-016-10595	Sequence 10595, A	524	79.5	4.5	309	2	US-09-248-796A-30432	Sequence 20432, A
452	82	4.6	1248	2	US-09-949-016-10596	Sequence 10596, A	525	79.5	4.5	309	2	US-08-821-994-84	Sequence 84, Appl1
453	81.5	4.6	309	2	US-09-667-135-6	Sequence 6, Appl1	526	79.5	4.5	335	2	US-09-489-038A-11298	Sequence 11298, A
454	81.5	4.6	309	2	US-09-910-174B-7	Sequence 7, Appl1	527	79.5	4.5	374	2	US-08-821-994-68	Sequence 68, Appl1
455	81.5	4.6	352	2	US-09-620-461-7	Sequence 7, Appl1	528	79.5	4.5	402	2	US-09-292-097-16	Sequence 16, Appl1
456	81.5	4.6	352	2	US-09-999-833A-612	Sequence 612, App	529	79.5	4.5	402	2	US-09-933-561-16	Sequence 16, Appl1
457	81.5	4.6	352	2	US-10-020-445A-612	Sequence 612, App	530	79.5	4.5	643	1	US-08-477-570-6	Sequence 6, Appl1
458	81.5	4.6	504	2	US-09-949-016-7020	Sequence 7020, App	531	79.5	4.5	769	1	US-08-477-570-8	Sequence 8, Appl1
459	81.5	4.6	504	2	US-09-991-181-119	Sequence 119, App	532	79.5	4.5	859	2	US-09-708-200-7	Sequence 7, Appl1
460	81.5	4.6	504	2	US-09-990-444-119	Sequence 119, App	533	79.5	4.5	859	2	US-09-788-657-16	Sequence 16, Appl1
461	81.5	4.6	504	2	US-09-997-333-119	Sequence 119, App	534	79.5	4.5	859	2	US-09-712-691-5	Sequence 5, Appl1
462	81.5	4.6	504	2	US-09-992-598-119	Sequence 119, App	535	79.5	4.5	859	2	US-10-641-068-16	Sequence 16, Appl1
463	81.5	4.6	511	2	US-09-949-016-10054	Sequence 10054, A	536	79	4.5	340	2	US-09-707-466C-5	Sequence 5, Appl1
464	81.5	4.6	558	2	US-09-667-135-31	Sequence 31, Appl1	537	78.5	4.4	340	2	US-09-401-636-2	Sequence 2, Appl1
465	81.5	4.6	846	1	US-08-149-103-4	Sequence 4, Appl1	538	78.5	4.4	393	1	US-08-429-742-2	Sequence 2, Appl1

539	78.5	4.4	439	2	US-09-383-586-32	Sequence 32, Appl	612	76.5	4.3	1089	2	US-08-464-436-2	Sequence 2, Appl
540	78.5	4.4	439	2	US-09-823-038A-32	Sequence 32, Appl	613	76.5	4.3	1089	2	US-09-763-987-2	Sequence 2, Appl
541	78.5	4.4	544	2	US-09-999-833A-259	Sequence 259, App	614	76.5	4.3	1089	2	US-09-866-510-4	Sequence 6, Appl
542	78.5	4.4	544	2	US-10-020-445A-259	Sequence 259, App	615	76.5	4.3	1089	2	US-09-866-510-6	Sequence 6, Appl
543	78.5	4.4	831	1	US-09-047-026A-4	Sequence 4, Appl	616	76.5	4.3	1089	2	US-09-866-510-8	Sequence 8, Appl
544	78.5	4.4	847	2	US-09-949-002-338	Sequence 328, App	617	76.5	4.3	1089	2	US-09-866-510-8	Sequence 8, Appl
545	78.5	4.4	857	2	US-09-248-796A-20522	Sequence 20522, A	618	76.5	4.3	1089	2	US-09-866-510-10	Sequence 10, Appl
546	78.5	4.4	862	2	US-09-949-002-427	Sequence 427, App	619	76.5	4.3	1089	2	US-09-919-457-90	Sequence 90, Appl
547	78	4.4	341	1	US-08-248-628A-2	Sequence 2, Appl	620	76.5	4.3	1089	2	US-09-949-016-6703	Sequence 6703, Ap
548	78	4.4	345	2	US-09-214-631-5	Sequence 5, Appl	621	76.5	4.3	1089	4	PCT-US92-00730-4	Sequence 4, Appl
549	78	4.4	588	2	US-09-949-016-10547	Sequence 10547, A	622	76.5	4.3	1089	4	PCT-US92-00862-4	Sequence 4, Appl
550	78	4.4	624	1	US-08-642-406A-22	Sequence 22, Appl	623	76.5	4.3	1125	2	US-09-949-016-10194	Sequence 10194, A
551	78	4.4	624	1	US-09-199-534-22	Sequence 22, Appl	624	76.5	4.3	1328	2	US-08-781-891-76	Sequence 76, Appl
552	78	4.4	624	2	US-09-199-534-22	Sequence 22, Appl	625	76.5	4.3	1328	2	US-09-618-166-76	Sequence 16, Appl
553	78	4.4	624	2	US-09-199-534-22	Sequence 22, Appl	626	76.5	4.3	1328	2	US-09-618-166-76	Sequence 16, Appl
554	78	4.4	624	2	US-09-199-534-22	Sequence 22, Appl	627	76.5	4.3	1328	2	US-09-618-166-76	Sequence 16, Appl
555	78	4.4	655	2	US-09-248-796A-14308	Sequence 14308, A	628	76.5	4.3	1621	2	US-09-784-358-2	Sequence 31, Appl
556	78	4.4	833	2	US-09-949-016-11496	Sequence 11496, A	629	76.5	4.3	1745	2	US-09-194-612A-31	Sequence 89, Appl
557	78	4.4	848	2	US-09-787-443-44	Sequence 44, Appl	630	76.5	4.3	1745	2	US-09-800-729-89	Sequence 89, Appl
558	78	4.4	1180	2	US-09-949-016-6577	Sequence 6577, Ap	631	76	4.3	277	1	US-09-543-681A-4527	Sequence 4527, Ap
559	77.5	4.4	321	2	US-09-254-465A-2	Sequence 2, Appl	632	76	4.3	378	1	US-08-225-477B-9	Sequence 9, Appl
560	77.5	4.4	321	2	US-09-953-499-2	Sequence 2, Appl	633	76	4.3	378	1	PCT-US95-04353-9	Sequence 9, Appl
561	77.5	4.4	321	2	US-09-999-833A-52	Sequence 52, Appl	634	76	4.3	390	2	US-08-961-564A-2	Sequence 2, Appl
562	77.5	4.4	321	2	US-10-020-445A-52	Sequence 52, Appl	635	76	4.3	390	2	US-09-050-861B-2	Sequence 2, Appl
563	77.5	4.4	477	1	US-08-432-016-3	Sequence 3, Appl	636	76	4.3	390	2	US-09-135-228B-2	Sequence 2, Appl
564	77.5	4.4	477	1	US-08-684-594-3	Sequence 3, Appl	637	76	4.3	390	2	US-09-651-150B-2	Sequence 2, Appl
565	77.5	4.4	650	2	US-09-310-463-2	Sequence 2, Appl	638	76	4.3	462	2	US-09-773-877B-18	Sequence 18, Appl
566	77.5	4.4	650	2	US-08-842-248A-2	Sequence 2, Appl	639	76	4.3	463	2	US-09-082-310-1	Sequence 1, Appl
567	77.5	4.4	650	2	US-09-949-002-390	Sequence 390, App	640	76	4.3	463	2	US-09-575-205-1	Sequence 1, Appl
568	77.5	4.4	662	1	US-08-261-304-7	Sequence 7, Appl	641	76	4.3	463	2	US-09-976-594A-721	Sequence 721, App
569	77.5	4.4	677	2	US-09-949-002-416	Sequence 416, App	642	76	4.3	567	2	US-09-773-877B-12	Sequence 12, Appl
570	77.5	4.4	735	4	PCT-US93-00031-13	Sequence 13, Appl	643	76	4.3	599	1	US-08-442-542-18	Sequence 18, Appl
571	77.5	4.4	739	2	PCT-US93-00031-15	Sequence 15, Appl	644	76	4.3	599	1	US-08-765-469-18	Sequence 18, Appl
572	77.5	4.4	739	2	US-08-482-073-6	Sequence 6, Appl	645	76	4.3	759	2	US-09-902-540-16161	Sequence 16161, A
573	77.5	4.4	739	4	PCT-US93-00031-9	Sequence 9, Appl	646	75.5	4.3	446	2	US-09-583-110-6602	Sequence 4602, Ap
574	77.5	4.4	824	2	US-09-538-092-520	Sequence 520, App	647	75.5	4.3	448	2	US-09-107-433-3945	Sequence 3945, Ap
575	77.5	4.4	824	2	US-09-949-002-448	Sequence 448, App	648	75.5	4.3	514	2	US-10-142-231-68	Sequence 68, Appl
576	77.5	4.4	1312	2	US-09-554-572-26	Sequence 26, Appl	649	75.5	4.3	530	2	US-09-949-016-9519	Sequence 9519, Ap
577	77	4.3	278	2	US-09-570-367C-2	Sequence 2, Appl	650	75.5	4.3	648	1	US-08-817-436A-2	Sequence 2, Appl
578	77	4.3	278	2	US-09-915-524-2	Sequence 2, Appl	651	75	4.2	1215	2	US-09-949-002-321	Sequence 321, App
579	77	4.3	278	2	US-09-934-634-2	Sequence 2, Appl	652	75	4.2	261	2	US-10-101-464A-691	Sequence 691, App
580	77	4.3	306	2	US-10-191-029-12	Sequence 12, Appl	653	75	4.2	303	2	US-09-509-347-7	Sequence 7, Appl
581	77	4.3	362	2	US-09-291-299A-6	Sequence 6, Appl	654	75	4.2	309	2	US-09-605-703B-2418	Sequence 2418, Ap
582	77	4.3	458	2	US-09-435-956A-1	Sequence 1, Appl	655	75	4.2	512	2	US-09-356-818A-2	Sequence 2, Appl
583	77	4.3	470	2	US-09-291-299A-1	Sequence 1, Appl	656	75	4.2	527	2	US-09-910-174B-10	Sequence 10, Appl
584	77	4.3	476	2	US-09-291-299A-3	Sequence 3, Appl	657	75	4.2	527	2	US-09-620-461-10	Sequence 10, Appl
585	77	4.3	523	2	US-08-948-564-8	Sequence 8, Appl	658	75	4.2	641	2	US-09-422-869-26	Sequence 26, Appl
586	77	4.3	581	2	US-09-270-767-42396	Sequence 42396, A	659	75	4.2	762	2	US-09-949-016-7568	Sequence 7568, Ap
587	77	4.3	651	2	US-09-270-767-44877	Sequence 44877, A	660	75	4.2	855	2	US-09-328-352-6216	Sequence 6216, Ap
588	77	4.3	1021	1	US-08-497-025-3	Sequence 3, Appl	661	75	4.2	1729	2	US-09-696-115B-2	Sequence 2, Appl
589	77	4.3	1021	1	US-09-949-002-363	Sequence 363, App	662	74.5	4.2	2137	2	US-09-134-001C-4463	Sequence 4463, Ap
590	77	4.3	1024	2	US-09-949-002-523	Sequence 523, App	663	74.5	4.2	218	2	US-09-068-655-7	Sequence 7, Appl
591	77	4.3	1033	2	US-09-252-991A-00611	Sequence 20611, A	664	74.5	4.2	230	6	5169835-13	Parent No. 5169835
592	77	4.3	4866	2	US-09-424-783-2	Sequence 2, Appl	665	74.5	4.2	338	2	US-09-688-188B-152	Sequence 152, App
593	76.5	4.3	392	2	US-09-800-729-175	Sequence 175, App	666	74.5	4.2	373	2	US-09-291-417D-152	Sequence 152, App
594	76.5	4.3	364	2	US-08-896-537A-3	Sequence 3, Appl	667	74.5	4.2	373	2	US-09-291-417D-97	Sequence 97, Appl
595	76.5	4.3	490	2	US-09-667-135-28	Sequence 28, Appl	668	74.5	4.2	374	2	US-08-821-994-69	Sequence 69, Appl
596	76.5	4.3	589	2	US-09-866-510-12	Sequence 12, Appl	669	74.5	4.2	463	1	US-08-853-659A-52	Sequence 52, Appl
597	76.5	4.3	1089	1	US-08-180-195-36	Sequence 4, Appl	670	74.5	4.2	640	2	US-09-949-016-7565	Sequence 7565, Ap
598	76.5	4.3	1089	1	US-08-168-917-4	Sequence 36, Appl	671	74.5	4.2	789	2	US-09-002-285-98	Sequence 98, Appl
599	76.5	4.3	1089	1	US-08-477-329-36	Sequence 36, Appl	672	74.5	4.2	789	2	US-09-589-477-98	Sequence 98, Appl
600	76.5	4.3	1089	1	US-08-475-458-36	Sequence 36, Appl	673	74.5	4.2	789	2	US-10-099-285A-98	Sequence 98, Appl
601	76.5	4.3	1089	1	US-08-460-510-4	Sequence 4, Appl	674	74.5	4.2	1018	1	US-08-452-052-2	Sequence 2, Appl
602	76.5	4.3	1089	1	US-08-460-510-4	Sequence 4, Appl	675	74.5	4.2	1104	1	US-10-104-047-2506	Sequence 2506, Ap
603	76.5	4.3	1089	1	US-08-980-400-36	Sequence 36, Appl	676	74.5	4.2	1148	1	US-08-313-165-58	Sequence 58, Appl
604	76.5	4.3	1089	1	US-08-462-728-2	Sequence 2, Appl	677	74.5	4.2	1571	2	US-09-082-614A-58	Sequence 58, Appl
605	76.5	4.3	1089	2	US-09-583-459A-36	Sequence 36, Appl	678	74.5	4.2	1571	2	US-08-956-991-11	Sequence 11, Appl
606	76.5	4.3	1089	2	US-09-583-459A-36	Sequence 36, Appl	679	74.5	4.2	1788	1	US-08-962-284-2	Sequence 2, Appl
607	76.5	4.3	1089	2	US-09-583-459A-36	Sequence 36, Appl	680	74.5	4.2	1910	1	US-08-956-991-2	Sequence 2, Appl
608	76.5	4.3	1089	2	US-09-583-459A-36	Sequence 36, Appl	681	74.5	4.2	1911	1	US-08-346-006B-5	Sequence 5, Appl
609	76.5	4.3	1089	2	US-09-435-059-36	Sequence 36, Appl	682	74.5	4.2	1911	1	US-08-800-825A-5	Sequence 5, Appl
610	76.5	4.3	1089	2	US-08-461-917-2	Sequence 2, Appl	683	74.5	4.2	1911	1	US-09-158-657-5	Sequence 5, Appl
611	76.5	4.3	1089	2	US-08-464-436-2	Sequence 2, Appl	684	74.5	4.2	1911	1	US-09-158-657-5	Sequence 5, Appl

685	74.5	4.2	1911	4	PCT-US94-10166-5	Sequence 5, Appli	758	72.5	4.1	293	6	5189147-3	Patent No. 5189147
686	74.5	4.2	4654	2	US-08-476-515A-84	Sequence 84, Appl	759	72.5	4.1	331	1	US-08-364-081-3	Sequence 3, Appli
687	74.5	4.2	4655	2	US-08-652-877-84	Sequence 86, Appl	760	72.5	4.1	331	1	US-08-630-552-3	Sequence 3, Appli
688	74.5	4.2	4655	2	US-08-652-877-86	Sequence 86, Appl	761	72.5	4.1	331	4	PCT-US95-16558-3	Sequence 3, Appli
689	74.5	4.2	4655	2	US-08-652-877-88	Sequence 89, Appl	762	72.5	4.1	347	2	US-09-667-135-4	Sequence 4, Appli
690	74.5	4.2	4655	2	US-08-652-877-90	Sequence 90, Appl	763	72.5	4.1	354	6	5169835-4	Patent No. 5169835
691	74	4.2	342	2	US-09-401-636-8	Sequence 8, Appli	764	72.5	4.1	370	2	US-08-821-994-70	Sequence 70, Appl
692	74	4.2	343	2	US-09-454-034-8	Sequence 8, Appli	765	72.5	4.1	370	2	US-08-979-424-1	Sequence 1, Appli
693	74	4.2	387	2	US-09-175-928-2	Sequence 2, Appli	766	72.5	4.1	390	2	US-09-907-794A-39	Sequence 39, Appl
694	74	4.2	451	2	US-09-107-532A-6652	Sequence 6652, Ap	767	72.5	4.1	390	2	US-09-905-125A-39	Sequence 39, Appl
695	74	4.2	543	2	US-09-042-709A-18	Sequence 18, Appl	768	72.5	4.1	390	2	US-09-902-775A-39	Sequence 39, Appl
696	74	4.2	548	2	US-08-247-902A-2	Sequence 2, Appli	769	72.5	4.1	390	2	US-09-906-700-39	Sequence 39, Appl
697	74	4.2	548	4	PCT-US93-10541-2	Sequence 2, Appli	770	72.5	4.1	390	2	US-09-903-603A-39	Sequence 39, Appl
698	74	4.2	862	2	US-09-949-016-10140	Sequence 10140, A	771	72.5	4.1	390	2	US-09-904-620A-39	Sequence 39, Appl
699	74	4.2	705	2	US-08-556-422A-2	Sequence 2, Appli	772	72.5	4.1	390	2	US-09-909-064-39	Sequence 39, Appl
700	74	4.2	1027	2	US-09-162-021B-2	Sequence 2, Appli	773	72.5	4.1	390	2	US-09-905-381A-39	Sequence 39, Appl
701	74	4.2	1027	2	US-10-268-051-8	Sequence 8, Appli	774	72.5	4.1	390	2	US-09-906-618-39	Sequence 39, Appl
702	74	4.2	1027	2	US-10-125-772-2	Sequence 2, Appli	775	72.5	4.1	390	2	US-09-906-646-39	Sequence 39, Appl
703	74	4.2	1165	2	US-09-487-558B-76	Sequence 76, Appl	776	72.5	4.1	390	2	US-09-904-462-39	Sequence 39, Appl
704	74	4.2	1194	2	US-10-191-029-10	Sequence 10, Appl	777	72.5	4.1	390	2	US-09-904-462-39	Sequence 39, Appl
705	74	4.2	1333	1	US-08-447-411-76	Sequence 76, Appl	778	72.5	4.1	390	2	US-09-904-462-39	Sequence 39, Appl
706	74	4.2	1333	1	US-08-662-227-34	Sequence 34, Appl	779	72.5	4.1	424	6	US-09-906-722A-39	Sequence 39, Appl
707	74	4.2	1333	2	US-09-017-947-34	Sequence 34, Appl	780	72.5	4.1	489	2	US-09-134-001C-4902	Sequence 4902, Ap
708	74	4.2	1333	2	US-09-925-442-34	Sequence 34, Appl	781	72.5	4.1	521	1	US-08-504-048-9	Sequence 9, Appli
709	74	4.2	1709	2	US-09-949-016-10503	Sequence 10503, A	782	72.5	4.1	526	1	US-08-471-570-4	Sequence 4, Appli
710	73.5	4.1	217	2	US-09-134-001C-5638	Sequence 5638, Ap	783	72.5	4.1	560	2	US-09-071-035-220	Sequence 220, App
711	73.5	4.1	238	2	US-08-978-289-10	Sequence 10, Appl	784	72.5	4.1	560	2	US-10-206-576-220	Sequence 220, App
712	73.5	4.1	321	2	US-09-171-461-22	Sequence 22, Appl	785	72.5	4.1	605	1	US-08-752-307B-8	Sequence 8, Appli
713	73.5	4.1	321	2	US-09-970-711-22	Sequence 22, Appl	786	72.5	4.1	605	2	US-09-707-802-8	Sequence 8, Appli
714	73.5	4.1	332	2	US-09-248-796A-18143	Sequence 18143, A	787	72.5	4.1	605	2	US-09-991-326-8	Sequence 8, Appli
715	73.5	4.1	344	2	US-09-700-397-3	Sequence 3, Appli	788	72.5	4.1	627	2	US-09-071-035-218	Sequence 218, App
716	73.5	4.1	344	2	US-09-999-833A-523	Sequence 523, App	789	72.5	4.1	627	2	US-10-206-576-218	Sequence 218, App
717	73.5	4.1	344	2	US-10-020-445A-523	Sequence 523, App	790	72.5	4.1	635	2	US-10-101-464A-932	Sequence 93, App
718	73.5	4.1	348	2	US-10-104-047-2468	Sequence 2468, Ap	791	72.5	4.1	652	1	US-08-471-570-10	Sequence 10, Appl
719	73.5	4.1	513	2	US-09-910-174B-18	Sequence 18, Appl	792	72.5	4.1	659	2	US-09-134-000C-6124	Sequence 6124, Ap
720	73.5	4.1	513	2	US-09-620-461-18	Sequence 18, Appl	793	72.5	4.1	759	2	US-09-002-285-86	Sequence 86, Appl
721	73.5	4.1	631	2	US-09-248-796A-19450	Sequence 19450, A	794	72.5	4.1	759	2	US-09-589-477-86	Sequence 86, Appl
722	73.5	4.1	699	2	US-09-134-001C-4054	Sequence 4054, Ap	795	72.5	4.1	759	2	US-10-099-285A-86	Sequence 86, Appl
723	73.5	4.1	716	2	US-09-171-945-125	Sequence 125, App	796	72.5	4.1	768	2	US-09-489-039A-12897	Sequence 12897, A
724	73.5	4.1	716	2	US-09-910-059-115	Sequence 125, App	797	72.5	4.1	790	2	US-09-543-681A-5459	Sequence 5459, Ap
725	73.5	4.1	842	2	US-09-902-540-11810	Sequence 11810, A	798	72.5	4.1	913	2	US-09-140-378A-2	Sequence 2, Appli
726	73.5	4.1	913	1	US-08-445-640-4	Sequence 4, Appli	799	72.5	4.1	919	1	US-08-336-343A-2	Sequence 2, Appli
727	73.5	4.1	913	2	US-08-170-558-4	Sequence 4, Appli	800	72.5	4.1	919	2	US-09-551-188-2	Sequence 2, Appli
728	73.5	4.1	913	2	US-08-447-314-4	Sequence 4, Appli	801	72.5	4.1	937	2	US-09-949-016-8366	Sequence 8366, Ap
729	73.5	4.1	913	2	US-08-445-461-4	Sequence 4, Appli	802	72.5	4.1	937	2	US-09-949-016-8367	Sequence 8367, Ap
730	73.5	4.1	913	2	US-09-223-490-4	Sequence 4, Appli	803	72.5	4.1	937	2	US-09-949-016-8368	Sequence 8368, Ap
731	73.5	4.1	1000	2	US-09-193-562D-30	Sequence 30, Appl	804	72.5	4.1	1434	1	US-08-540-406-10	Sequence 10, Appl
732	73.5	4.1	1000	2	US-10-053-412B-30	Sequence 30, Appl	805	72.5	4.1	1434	2	US-08-656-055-10	Sequence 10, Appl
733	73.5	4.1	4544	1	US-08-469-486-52	Sequence 52, Appl	806	72.5	4.1	1434	2	US-08-954-668-10	Sequence 10, Appl
734	73.5	4.1	4544	1	US-08-469-658-52	Sequence 52, Appl	807	72.5	4.1	1434	2	US-09-918-658-10	Sequence 10, Appl
735	73.5	4.1	1112	2	US-08-545-809A-136	Sequence 136, App	808	72.5	4.1	1434	2	US-09-724-631-10	Sequence 10, Appl
736	73	4.1	115	2	US-09-515-697-136	Sequence 136, App	809	72.5	4.1	1434	2	US-08-954-701A-10	Sequence 10, Appl
737	73	4.1	155	2	US-09-270-767-57684	Sequence 57684, A	810	72.5	4.1	1434	2	US-09-754-032-10	Sequence 10, Appl
738	73	4.1	175	2	US-10-144-929-106	Sequence 106, App	811	72.5	4.1	1434	2	US-08-916-140-10	Sequence 10, Appl
739	73	4.1	250	2	US-09-270-767-42724	Sequence 42724, A	812	72.5	4.1	1434	4	PCT-US95-13233-10	Sequence 10, Appl
740	73	4.1	270	2	US-09-569-611C-37	Sequence 37, Appl	813	72	4.1	222	2	US-09-248-796A-00974	Sequence 20974, A
741	73	4.1	308	2	US-09-248-796A-14626	Sequence 14626, A	814	72	4.1	311	2	US-09-252-991A-28792	Sequence 128792, A
742	73	4.1	373	2	US-09-823-038A-60	Sequence 60, Appl	815	72	4.1	328	1	US-09-489-039A-13216	Sequence 13216, A
743	73	4.1	389	2	US-08-724-378D-3	Sequence 3, Appli	816	72	4.1	348	1	US-09-031-485-28	Sequence 28, Appl
744	73	4.1	459	1	US-08-157-101A-7	Sequence 7, Appli	817	72	4.1	348	1	US-08-847-429A-28	Sequence 28, Appl
745	73	4.1	501	1	US-08-408-095-31	Sequence 31, Appli	818	72	4.1	348	2	US-09-065-474-28	Sequence 28, Appl
746	73	4.1	504	2	US-08-868-373-6	Sequence 6, Appli	819	72	4.1	348	2	US-09-557-034-28	Sequence 28, Appl
747	73	4.1	548	2	US-09-398-395A-12	Sequence 12, Appl	820	72	4.1	358	2	US-09-265-585C-118	Sequence 118, App
748	73	4.1	548	2	US-09-887-586A-12	Sequence 12, Appl	821	72	4.1	378	2	US-09-265-585C-109	Sequence 109, App
749	73	4.1	548	2	US-09-895-752-12	Sequence 12, Appl	822	72	4.1	378	2	US-09-186-276B-46	Sequence 46, Appl
750	73	4.1	548	2	US-09-893-820-12	Sequence 12, Appl	823	72	4.1	379	2	US-08-842-445-46	Sequence 46, Appl
751	73	4.1	548	2	US-09-903-012B-12	Sequence 12, Appl	824	72	4.1	379	2	US-09-186-188B-46	Sequence 46, Appl
752	73	4.1	548	2	US-09-900-797-12	Sequence 12, Appl	825	72	4.1	394	2	US-09-265-585C-16	Sequence 16, Appl
753	73	4.1	623	2	US-09-949-016-11206	Sequence 11206, A	826	72	4.1	427	2	US-09-949-016-6716	Sequence 6716, Ap
754	73	4.1	646	2	US-09-653-961-2	Sequence 22, Appli	827	72	4.1	452	2	US-09-949-016-9842	Sequence 9842, Ap
755	73	4.1	651	2	US-08-985-950-22	Sequence 22, Appl	828	72	4.1	456	1	US-09-773-877B-16	Sequence 16, Appli
756	73	4.1	651	2	US-09-546-049-22	Sequence 22, Appl	829	72	4.1	456	1	US-08-435-933-6	Sequence 6, Appli
757	72.5	4.1	283	2	US-09-248-796A-19610	Sequence 19610, A	830	72	4.1	456	4	PCT-US96-06035-6	Sequence 6, Appli

831	72	4.1	3	497	2	US-08-709-731A-29	Sequence 29, Appl	904	71	4.0	107	1	US-08-425-336-125	Sequence 125, App
832	72	4.1	514	514	2	US-09-949-016-11380	Sequence 11380, A	905	71	4.0	107	1	US-08-488-113B-125	Sequence 125, App
833	72	4.1	517	2	US-09-723-368-4	Sequence 4, Appl1	906	71	4.0	107	1	US-08-477-484B-125	Sequence 125, App	
834	72	4.1	528	2	US-09-710-279-1930	Sequence 1930, Ap	907	71	4.0	107	1	US-08-107-669D-65	Sequence 65, Appl	
835	72	4.1	546	2	US-09-303-518D-58	Sequence 58, Appl	908	71	4.0	107	1	US-08-472-768A-87	Sequence 87, Appl	
836	72	4.1	548	2	US-09-398-395A-2	Sequence 2, Appl1	909	71	4.0	107	1	US-08-477-531B-65	Sequence 65, Appl	
837	72	4.1	548	2	US-09-887-758A-2	Sequence 2, Appl1	910	71	4.0	107	1	US-08-646-360-125	Sequence 125, App	
838	72	4.1	548	2	US-09-895-752-2	Sequence 2, Appl1	911	71	4.0	107	1	US-08-082-842A-87	Sequence 87, Appl	
839	72	4.1	548	2	US-09-903-012B-2	Sequence 2, Appl1	912	71	4.0	107	2	US-08-839-765-125	Sequence 125, App	
840	72	4.1	548	2	US-09-900-797-2	Sequence 2, Appl1	913	71	4.0	107	2	US-09-136-389-125	Sequence 125, App	
841	72	4.1	548	2	US-09-893-820-2	Sequence 2, Appl1	914	71	4.0	107	2	US-09-610-838-125	Sequence 125, App	
842	72	4.1	557	2	US-09-773-877B-14	Sequence 14, Appl1	915	71	4.0	107	2	US-09-711-485-125	Sequence 125, App	
843	72	4.1	633	2	US-09-248-796A-20407	Sequence 20407, A	916	71	4.0	233	2	US-09-198-452A-244	Sequence 244, App	
844	72	4.1	646	2	US-09-949-016-6728	Sequence 6728, Ap	917	71	4.0	233	2	US-09-438-185A-236	Sequence 236, App	
845	72	4.1	646	2	US-09-653-961-4	Sequence 4, Appl1	918	71	4.0	236	2	US-09-049-672A-7	Sequence 7, Appl1	
846	72	4.1	670	2	US-09-575-081B-27	Sequence 27, Appl1	919	71	4.0	240	1	US-08-488-113B-147	Sequence 147, App	
847	72	4.1	670	2	US-09-949-016-6584	Sequence 6584, Ap	920	71	4.0	240	1	US-08-488-113B-148	Sequence 147, App	
848	72	4.1	670	2	US-09-949-016-6590	Sequence 6590, Ap	921	71	4.0	240	1	US-08-477-484B-147	Sequence 147, App	
849	72	4.1	679	2	US-09-949-016-8034	Sequence 8034, Ap	922	71	4.0	240	1	US-08-477-484B-148	Sequence 148, App	
850	72	4.1	679	2	US-09-949-016-8035	Sequence 8035, Ap	923	71	4.0	240	1	US-08-646-360-147	Sequence 148, App	
851	72	4.1	754	1	US-08-525-864A-2	Sequence 2, Appl1	924	71	4.0	240	1	US-08-646-360-148	Sequence 148, App	
852	72	4.1	852	1	US-09-319-588C-18	Sequence 18, Appl1	925	71	4.0	240	2	US-08-839-765-147	Sequence 147, App	
853	72	4.1	1297	2	US-09-540-245A-17	Sequence 17, Appl1	926	71	4.0	240	2	US-08-839-765-148	Sequence 148, App	
854	72	4.1	1297	2	US-10-289-776-17	Sequence 17, Appl1	927	71	4.0	240	2	US-09-136-389-147	Sequence 147, App	
855	72	4.1	1456	1	US-08-803-973-2	Sequence 2, Appl1	928	71	4.0	240	2	US-09-136-389-148	Sequence 148, App	
856	72	4.1	1456	1	US-08-803-973-2	Sequence 2, Appl1	929	71	4.0	240	2	US-09-610-838-147	Sequence 147, App	
857	72	4.1	1745	1	US-09-031-485-33	Sequence 33, Appl1	930	71	4.0	240	2	US-09-610-838-148	Sequence 148, App	
858	72	4.1	1745	1	US-08-847-429A-33	Sequence 33, Appl1	931	71	4.0	240	2	US-09-711-485-147	Sequence 147, App	
859	72	4.1	1745	2	US-09-065-474-33	Sequence 33, Appl1	932	71	4.0	240	2	US-09-711-485-148	Sequence 148, App	
860	72	4.1	1745	2	US-09-557-034-33	Sequence 33, Appl1	933	71	4.0	379	2	US-09-543-681A-7089	Sequence 7089, App	
861	72	4.1	2383	2	US-09-492-709A-302	Sequence 302, App	934	71	4.0	384	2	US-08-504-617-2	Sequence 2, Appl1	
862	72	4.1	2753	2	US-09-949-016-7659	Sequence 7659, Ap	935	71	4.0	475	2	US-08-657-749D-11	Sequence 11, Appl1	
863	72	4.1	2753	2	US-09-949-016-7660	Sequence 7660, Ap	936	71	4.0	615	2	US-09-297-937C-9	Sequence 9, Appl1	
864	72	4.1	2780	2	US-10-220-587-2	Sequence 2, Appl1	937	71	4.0	621	2	US-09-248-796A-14463	Sequence 14463, A	
865	72	4.1	4872	2	US-09-424-783-3	Sequence 3, Appl1	938	71	4.0	647	2	US-08-753-007A-32	Sequence 32, Appl1	
866	72	4.0	206	2	US-08-821-994-77	Sequence 77, Appl1	939	71	4.0	647	2	US-09-398-496-32	Sequence 32, Appl1	
867	71.5	4.0	241	2	US-09-248-796A-17942	Sequence 17942, A	940	71	4.0	649	2	US-10-188-495-63	Sequence 63, Appl1	
868	71.5	4.0	248	6	5169835-15	Sequence 375, App	941	71	4.0	661	1	US-08-232-538-12	Sequence 12, Appl1	
869	71.5	4.0	276	2	US-09-949-002-375	Sequence 5, Appl1	942	71	4.0	661	1	US-08-786-164-12	Sequence 12, Appl1	
870	71.5	4.0	327	2	US-09-173-581-5	Sequence 5, Appl1	943	71	4.0	671	2	US-10-188-495-61	Sequence 61, Appl1	
871	71.5	4.0	327	2	US-09-420-915-5	Sequence 5, Appl1	944	71	4.0	687	1	US-08-232-538-6	Sequence 6, Appl1	
872	71.5	4.0	333	2	US-09-949-002-502	Sequence 502, App	945	71	4.0	687	1	US-08-786-164-6	Sequence 6, Appl1	
873	71.5	4.0	384	2	US-09-552-322-2	Sequence 2, Appl1	946	71	4.0	687	2	US-09-427-353-2	Sequence 2, Appl1	
874	71.5	4.0	403	2	US-09-638-649-5	Sequence 5, Appl1	947	71	4.0	687	2	US-10-104-047-2982	Sequence 2982, App	
875	71.5	4.0	403	2	US-09-638-648-5	Sequence 5, Appl1	948	71	4.0	731	2	US-09-107-532A-6999	Sequence 6999, App	
876	71.5	4.0	456	2	US-09-248-796A-23791	Sequence 23791, A	949	71	4.0	758	1	US-08-874-678-1	Sequence 1, Appl1	
877	71.5	4.0	462	2	US-09-166-350-18	Sequence 18, Appl1	950	71	4.0	758	1	US-08-643-839-1	Sequence 1, Appl1	
878	71.5	4.0	523	2	US-09-910-174B-11	Sequence 11, Appl1	951	71	4.0	758	2	US-09-051-363-24	Sequence 24, Appl1	
879	71.5	4.0	523	2	US-09-620-461-11	Sequence 11, Appl1	952	71	4.0	758	2	US-09-348-886-1	Sequence 1, Appl1	
880	71.5	4.0	608	2	US-09-095-385-4	Sequence 4, Appl1	953	71	4.0	758	2	US-10-105-901A-1	Sequence 1, Appl1	
881	71.5	4.0	624	2	US-09-949-016-10587	Sequence 10587, A	954	71	4.0	780	1	US-08-232-538-14	Sequence 14, Appl1	
882	71.5	4.0	746	2	US-08-434-000A-4	Sequence 4, Appl1	955	71	4.0	780	1	US-08-786-164-14	Sequence 14, Appl1	
883	71.5	4.0	746	2	US-09-312-157-4	Sequence 4, Appl1	956	71	4.0	821	1	US-08-451-832A-13	Sequence 13, Appl1	
884	71.5	4.0	746	2	US-09-717-888-4	Sequence 4, Appl1	957	71	4.0	821	2	US-08-323-430-13	Sequence 13, Appl1	
885	71.5	4.0	764	2	US-09-949-016-6254	Sequence 6254, Ap	958	71	4.0	905	4	PCT-US96-06221-2	Sequence 2, Appl1	
886	71.5	4.0	764	2	US-09-818-247-1	Sequence 1, Appl1	959	71	4.0	905	2	US-09-651-656-13	Sequence 13, Appl1	
887	71.5	4.0	816	2	US-09-949-016-8119	Sequence 8119, Ap	960	71	4.0	906	2	US-09-650-855-13	Sequence 13, Appl1	
888	71.5	4.0	919	1	US-08-788-674-4	Sequence 4, Appl1	961	71	4.0	916	2	US-09-919-457-64	Sequence 64, App	
889	71.5	4.0	941	2	US-09-949-016-6062	Sequence 6062, Ap	962	71	4.0	930	2	US-09-134-001C-5314	Sequence 5314, App	
890	71.5	4.0	1006	2	US-09-949-016-10730	Sequence 10730, A	963	71	4.0	930	2	US-09-386-962C-10	Sequence 10, Appl1	
891	71.5	4.0	1115	2	US-10-012-231A-58	Sequence 58, Appl1	964	71	4.0	975	2	US-09-695-481-4	Sequence 4, Appl1	
892	71.5	4.0	1115	2	US-10-015-389A-58	Sequence 58, Appl1	965	71	4.0	1018	1	US-08-408-093-6	Sequence 6, Appl1	
893	71.5	4.0	1115	2	US-10-006-768A-58	Sequence 58, Appl1	966	71	4.0	1018	1	US-08-408-420A-6	Sequence 6, Appl1	
894	71.5	4.0	1115	2	US-10-015-671A-58	Sequence 58, Appl1	967	71	4.0	1018	1	US-08-714-901-6	Sequence 6, Appl1	
895	71.5	4.0	1115	2	US-10-015-393A-58	Sequence 58, Appl1	968	71	4.0	1018	1	US-08-040-741-6	Sequence 6, Appl1	
896	71.5	4.0	1115	2	US-10-011-833A-58	Sequence 58, Appl1	969	71	4.0	1044	2	US-09-949-016-10321	Sequence 10321, A	
897	71.5	4.0	1115	2	US-10-006-041A-58	Sequence 58, Appl1	970	71	4.0	1072	2	US-09-538-092-533	Sequence 53, App	
898	71.5	4.0	1115	2	US-10-012-064A-58	Sequence 58, Appl1	971	71	4.0	1286	2	US-09-297-937C-13	Sequence 13, Appl1	
899	71.5	4.0	1255	2	US-09-902-560A-12628	Sequence 12628, A	972	71	4.0	1338	2	US-08-750-141A-3	Sequence 3, Appl1	
900	71.5	4.0	1405	2	US-09-248-796A-18103	Sequence 18103, A	973	71	4.0	1338	2	US-09-119-014D-6	Sequence 6, Appl1	
901	71.5	4.0	2468	2	US-09-976-594-726	Sequence 726, App	974	71	4.0	1362	1	US-08-874-678-3	Sequence 33, Appl1	
902	71.5	4.0	2468	2	US-09-538-092-1135	Sequence 1135, App	975	71	4.0	1362	1	US-08-643-839-33	Sequence 33, Appl1	
903	71.5	4.0	2522	2	US-09-949-016-10237	Sequence 10237, A	976	71	4.0	1362	2	US-09-348-886-33	Sequence 33, Appl1	

977	71	4.0	1362	2	US-10-105-901A-33	Sequence 33, Appl	1050	70	4.0	320	2	US-09-370-700-14	Sequence 14, Appl
978	71	4.0	1481	1	US-08-616-844-40	Sequence 40, Appl	1051	70	4.0	320	2	US-09-603-207-11	Sequence 11, Appl
979	71	4.0	1481	1	US-08-599-654-40	Sequence 40, Appl	1052	70	4.0	338	1	US-08-442-043A-17	Sequence 17, Appl
980	71	4.0	1481	2	US-08-944-868A-40	Sequence 40, Appl	1053	70	4.0	338	1	US-08-441-893A-17	Sequence 17, Appl
981	71	4.0	1481	2	US-08-944-423A-40	Sequence 40, Appl	1054	70	4.0	347	1	US-07-940-861-13	Sequence 43, Appl
982	71	4.0	1481	2	US-08-944-496-40	Sequence 40, Appl	1055	70	4.0	347	1	US-08-459-512-43	Sequence 43, Appl
983	71	4.0	4391	2	US-10-006-011A-2	Sequence 2, Appl	1056	70	4.0	347	1	US-08-459-657-43	Sequence 43, Appl
984	70.5	4.0	183	2	US-09-621-976-3942	Sequence 3942, Ap	1057	70	4.0	347	1	US-08-460-132-43	Sequence 43, Appl
985	70.5	4.0	184	2	US-09-303-518D-774	Sequence 774, App	1058	70	4.0	347	1	US-08-466-465-8	Sequence 8, Appl
986	70.5	4.0	223	2	US-09-303-518D-776	Sequence 776, App	1059	70	4.0	347	2	US-09-730-465-8	Sequence 8, Appl
987	70.5	4.0	223	2	US-09-303-518D-778	Sequence 778, App	1060	70	4.0	347	4	PCT-US92-02050-43	Sequence 43, Appl
988	70.5	4.0	241	2	US-09-915-789A-11	Sequence 11, Appl	1061	70	4.0	363	2	US-09-949-016-11040	Sequence 11040, A
989	70.5	4.0	261	2	US-09-899-634C-2	Sequence 452, App	1062	70	4.0	412	2	US-09-543-681A-6782	Sequence 6782, Ap
990	70.5	4.0	314	2	US-09-438-185A-452	Sequence 15329, A	1063	70	4.0	469	2	US-08-753-007A-8	Sequence 8, Appl
991	70.5	4.0	334	2	US-09-248-796A-15329	Sequence 1, Appl	1064	70	4.0	469	2	US-09-398-496-8	Sequence 8, Appl
992	70.5	4.0	338	2	US-08-922-957-1	Sequence 3, Appl	1065	70	4.0	523	2	US-09-489-039A-9610	Sequence 9610, Ap
993	70.5	4.0	343	2	US-08-922-957-3	Sequence 3, Appl	1066	70	4.0	548	2	US-09-248-796A-17555	Sequence 17555, A
994	70.5	4.0	348	2	US-09-134-000C-6363	Sequence 6363, Ap	1067	70	4.0	548	2	US-09-398-395A-6	Sequence 4, Appl
995	70.5	4.0	371	2	US-09-248-796A-16428	Sequence 16428, A	1068	70	4.0	548	2	US-09-398-395A-8	Sequence 8, Appl
996	70.5	4.0	374	2	US-09-248-796A-15744	Sequence 15744, A	1069	70	4.0	548	2	US-09-398-395A-10	Sequence 10, Appl
997	70.5	4.0	466	2	US-09-134-001C-3526	Sequence 3526, Ap	1070	70	4.0	548	2	US-09-887-586A-4	Sequence 4, Appl
998	70.5	4.0	467	2	US-08-821-994-83	Sequence 83, Appl	1071	70	4.0	548	2	US-09-887-586A-6	Sequence 6, Appl
999	70.5	4.0	472	2	US-08-821-994-83	Sequence 1352, Ap	1072	70	4.0	548	2	US-09-887-586A-8	Sequence 8, Appl
1000	70.5	4.0	491	2	US-09-134-001C-4727	Sequence 4727, Ap	1073	70	4.0	548	2	US-09-887-586A-10	Sequence 10, Appl
1001	70.5	4.0	495	2	US-10-122-706-6	Sequence 6, Appl	1074	70	4.0	548	2	US-09-895-752-6	Sequence 6, Appl
1002	70.5	4.0	495	2	US-10-154-515A-6	Sequence 6, Appl	1075	70	4.0	548	2	US-09-895-752-8	Sequence 8, Appl
1003	70.5	4.0	502	2	US-09-489-039A-8035	Sequence 8035, Ap	1076	70	4.0	548	2	US-09-895-752-10	Sequence 10, Appl
1004	70.5	4.0	533	1	US-07-820-881A-2	Sequence 2, Appl	1077	70	4.0	548	2	US-09-903-012B-4	Sequence 4, Appl
1005	70.5	4.0	533	2	US-09-470-881-3	Sequence 3, Appl	1078	70	4.0	548	2	US-09-903-012B-6	Sequence 6, Appl
1006	70.5	4.0	533	4	PCT-US93-00445-2	Sequence 2, Appl	1079	70	4.0	548	2	US-09-903-012B-8	Sequence 8, Appl
1007	70.5	4.0	579	2	US-09-173-151A-4	Sequence 2, Appl	1080	70	4.0	548	2	US-09-903-012B-10	Sequence 10, Appl
1008	70.5	4.0	610	2	US-09-976-594-947	Sequence 947, App	1081	70	4.0	548	2	US-09-903-012B-12	Sequence 12, Appl
1009	70.5	4.0	617	2	US-09-188-930-303	Sequence 303, App	1082	70	4.0	548	2	US-09-900-797-4	Sequence 4, Appl
1010	70.5	4.0	617	2	US-09-312-283C-303	Sequence 303, App	1083	70	4.0	548	2	US-09-900-797-6	Sequence 6, Appl
1011	70.5	4.0	644	2	US-09-949-016-11714	Sequence 11714, A	1084	70	4.0	548	2	US-09-900-797-8	Sequence 8, Appl
1012	70.5	4.0	668	1	US-08-232-538-13	Sequence 13, Appl	1085	70	4.0	548	2	US-09-900-797-10	Sequence 10, Appl
1013	70.5	4.0	668	1	US-08-786-164-13	Sequence 13, Appl	1086	70	4.0	548	2	US-09-893-820-6	Sequence 6, Appl
1014	70.5	4.0	686	2	US-09-173-151A-4	Sequence 4, Appl	1087	70	4.0	548	2	US-09-893-820-8	Sequence 8, Appl
1015	70.5	4.0	724	2	US-10-104-047-2224	Sequence 2224, Ap	1088	70	4.0	548	2	US-09-893-820-10	Sequence 10, Appl
1016	70.5	4.0	760	2	US-09-248-796A-17568	Sequence 17568, A	1089	70	4.0	548	2	US-09-893-820-12	Sequence 12, Appl
1017	70.5	4.0	764	2	US-09-142-958B-14	Sequence 14, Appl	1090	70	4.0	550	1	US-08-443-639-8	Sequence 8, Appl
1018	70.5	4.0	767	2	US-08-874-678-2	Sequence 2, Appl	1091	70	4.0	550	2	US-08-577-483-8	Sequence 8, Appl
1019	70.5	4.0	767	2	US-08-643-839-2	Sequence 2, Appl	1092	70	4.0	550	2	US-09-435-380-8	Sequence 8, Appl
1020	70.5	4.0	767	2	US-09-348-886-2	Sequence 2, Appl	1093	70	4.0	550	2	US-09-303-064-53	Sequence 53, Appl
1021	70.5	4.0	767	2	US-10-105-901A-2	Sequence 2, Appl	1094	70	4.0	551	2	US-09-086-503-53	Sequence 53, Appl
1022	70.5	4.0	788	1	US-08-232-538-15	Sequence 15, Appl	1095	70	4.0	576	1	US-07-821-716-4	Sequence 4, Appl
1023	70.5	4.0	788	1	US-08-786-164-15	Sequence 15, Appl	1096	70	4.0	576	1	US-08-381-603-4	Sequence 4, Appl
1024	70.5	4.0	915	2	US-10-282-162-52	Sequence 52, Appl	1097	70	4.0	576	2	US-08-924-376-4	Sequence 4, Appl
1025	70.5	4.0	940	2	US-09-198-452A-500	Sequence 500, Appl	1098	70	4.0	576	2	US-08-685-212-4	Sequence 2, Appl
1026	70.5	4.0	940	2	US-09-438-185A-468	Sequence 468, App	1099	70	4.0	576	2	US-09-173-151A-30	Sequence 30, Appl
1027	70.5	4.0	983	2	US-09-412-554A-2	Sequence 2, Appl	1100	70	4.0	576	2	US-08-466-932A-4	Sequence 4, Appl
1028	70.5	4.0	1088	1	US-08-485-588-6	Sequence 6, Appl	1101	70	4.0	576	4	PCT-US94-02414-4	Sequence 4, Appl
1029	70.5	4.0	1088	1	US-08-484-751-6	Sequence 6, Appl	1102	70	4.0	576	4	PCT-US96-08899-4	Sequence 4, Appl
1030	70.5	4.0	1088	1	US-08-480-844-8	Sequence 8, Appl	1103	70	4.0	582	2	US-09-147-405B-13	Sequence 13, Appl
1031	70.5	4.0	1088	1	US-08-943-986-6	Sequence 6, Appl	1104	70	4.0	590	2	US-10-104-047-3415	Sequence 3415, Ap
1032	70.5	4.0	1088	2	US-08-353-784-6	Sequence 6, Appl	1105	70	4.0	593	2	US-07-757-342D-8	Sequence 8, Appl
1033	70.5	4.0	1088	2	US-08-484-719B-6	Sequence 6, Appl	1106	70	4.0	611	2	US-07-757-342D-11	Sequence 11, Appl
1034	70.5	4.0	1088	2	US-08-484-159-6	Sequence 6, Appl	1107	70	4.0	611	2	US-09-461-657B-8	Sequence 8, Appl
1035	70.5	4.0	1356	1	US-08-810-116-8	Sequence 8, Appl	1108	70	4.0	625	2	US-09-461-657B-8	Sequence 8, Appl
1036	70.5	4.0	1356	1	US-07-930-548A-8	Sequence 2, Appl	1109	70	4.0	625	2	US-09-134-001C-4504	Sequence 4504, Ap
1037	70.5	4.0	1356	2	US-09-930-707A-2	Sequence 2, Appl	1110	70	4.0	636	2	US-10-101-464A-827	Sequence 827, App
1038	70.5	4.0	1356	2	US-09-483-539-9	Sequence 2, Appl	1111	70	4.0	636	2	US-07-757-342D-7	Sequence 7, Appl
1039	70.5	4.0	1356	2	US-09-949-016-6198	Sequence 6198, Ap	1112	70	4.0	636	2	US-09-461-657B-7	Sequence 7, Appl
1040	70.5	4.0	1356	2	US-10-100-405A-2	Sequence 2, Appl	1113	70	4.0	637	2	US-09-569-611C-35	Sequence 35, Appl
1041	70.5	4.0	1356	2	US-09-949-016-9853	Sequence 9853, Ap	1114	70	4.0	652	2	US-09-310-463-4	Sequence 4, Appl
1042	70.5	4.0	126	2	US-09-240-274-146	Sequence 146, App	1115	70	4.0	652	2	US-08-842-248A-4	Sequence 4, Appl
1043	70	4.0	126	2	US-09-848-798-146	Sequence 146, App	1116	70	4.0	687	4	PCT-US91-09784-2	Sequence 2, Appl
1044	70	4.0	167	2	US-08-821-994-43	Sequence 43, Appl	1117	70	4.0	783	2	US-08-780-562-7	Sequence 7, Appl
1045	70	4.0	167	2	US-08-821-994-43	Sequence 43, Appl	1118	70	4.0	837	1	US-07-923-976-2	Sequence 2, Appl
1046	70	4.0	282	2	US-09-602-787A-162	Sequence 162, App	1119	70	4.0	894	2	US-08-599-455B-2	Sequence 2, Appl
1047	70	4.0	282	2	US-09-602-787A-164	Sequence 164, App	1120	70	4.0	894	2	US-09-069-781B-2	Sequence 12, Appl
1048	70	4.0	313	2	US-09-252-991A-32836	Sequence 32836, A	1121	70	4.0	894	2	US-08-618-957A-12	Sequence 12, Appl
1049	70	4.0	320	2	US-09-036-987A-14	Sequence 14, Appl	1122	70	4.0	894	2	US-09-137-132-2	Sequence 2, Appl

1123	70	4.0	894	2	US-08-864-564A-2	Sequence 2, Appl1	1196	69	3.9	355	2	US-08-875-811-41	Sequence 41, Appl1
1124	70	4.0	894	2	US-09-094-410-2	Sequence 2, Appl1	1197	69	3.9	355	2	US-08-875-811-49	Sequence 49, Appl1
1125	70	4.0	894	2	US-08-708-123D-2	Sequence 2, Appl1	1198	69	3.9	355	2	US-08-875-811-64	Sequence 64, Appl1
1126	70	4.0	894	2	US-08-583-153A-2	Sequence 2, Appl1	1199	69	3.9	357	2	US-09-949-016-9074	Sequence 9074, Ap
1127	70	4.0	894	2	US-08-570-142D-2	Sequence 2, Appl1	1200	69	3.9	358	2	US-08-875-811-45	Sequence 45, Appl1
1128	70	4.0	894	2	US-08-638-524B-2	Sequence 2, Appl1	1201	69	3.9	358	2	US-08-875-811-51	Sequence 51, Appl1
1129	70	4.0	894	2	US-10-095-929-12	Sequence 12, Appl1	1202	69	3.9	360	2	US-08-875-811-47	Sequence 47, Appl1
1130	70	4.0	944	2	US-09-449-285A-2	Sequence 2, Appl1	1203	69	3.9	373	2	US-08-875-811-43	Sequence 43, Appl1
1131	70	4.0	944	2	US-09-964-238-2	Sequence 2, Appl1	1204	69	3.9	383	2	US-09-079-030-82	Sequence 82, Appl1
1132	70	4.0	950	2	US-09-449-285A-4	Sequence 4, Appl1	1205	69	3.9	408	2	US-09-248-796A-17517	Sequence 17517, A
1133	70	4.0	950	2	US-09-964-238-4	Sequence 4, Appl1	1206	69	3.9	467	2	US-08-030-175-42	Sequence 42, Appl1
1134	70	4.0	1092	2	US-09-147-405B-15	Sequence 15, Appl1	1207	69	3.9	468	1	US-08-220-151-16	Sequence 16, Appl1
1135	70	4.0	1162	1	US-08-599-455B-43	Sequence 43, Appl1	1208	69	3.9	468	1	US-08-413-118-16	Sequence 16, Appl1
1136	70	4.0	1162	2	US-09-069-781B-43	Sequence 43, Appl1	1209	69	3.9	468	2	US-08-473-446-15	Sequence 124, App
1137	70	4.0	1162	2	US-09-137-132-43	Sequence 43, Appl1	1210	69	3.9	514	2	US-09-800-729-14	Sequence 124, App
1138	70	4.0	1162	2	US-08-864-564A-43	Sequence 43, Appl1	1211	69	3.9	519	2	US-08-996-338-21	Sequence 21, Appl1
1139	70	4.0	1162	2	US-09-094-410-43	Sequence 43, Appl1	1212	69	3.9	519	2	US-09-556-972-21	Sequence 21, Appl1
1140	70	4.0	1162	2	US-08-708-123D-43	Sequence 43, Appl1	1213	69	3.9	523	2	US-08-606-505B-67	Sequence 67, Appl1
1141	70	4.0	1162	2	US-08-638-524B-43	Sequence 43, Appl1	1214	69	3.9	523	2	US-09-616-990-67	Sequence 67, Appl1
1142	70	4.0	1114	2	US-09-949-016-6885	Sequence 6885, Ap	1215	69	3.9	537	1	US-08-604-333-4	Sequence 4, Appl1
1143	70	4.0	1318	2	US-09-949-016-7130	Sequence 7130, Ap	1216	69	3.9	537	2	US-09-110-618-4	Sequence 4, Appl1
1144	70	4.0	1461	2	US-09-976-594-531	Sequence 531, App	1217	69	3.9	537	2	US-09-173-151A-29	Sequence 29, Appl1
1145	70	4.0	2183	2	US-08-746-111-5	Sequence 5, Appl1	1218	69	3.9	537	2	US-09-578-178-4	Sequence 4, Appl1
1146	69.5	3.9	223	2	US-09-303-518D-780	Sequence 780, App	1219	69	3.9	537	2	US-09-577-806-4	Sequence 4, Appl1
1147	69.5	3.9	307	2	US-09-540-236-2790	Sequence 2790, Ap	1220	69	3.9	537	2	US-09-621-502-8	Sequence 8, Appl1
1148	69.5	3.9	314	1	US-08-353-476-71	Sequence 71, Appl1	1221	69	3.9	542	1	US-08-140-729A-5	Sequence 5, Appl1
1149	69.5	3.9	324	1	US-09-328-352-4577	Sequence 4577, Ap	1222	69	3.9	542	1	US-08-546-666-5	Sequence 5, Appl1
1150	69.5	3.9	328	4	US-08-225-477B-5	Sequence 5, Appl1	1223	69	3.9	542	1	US-08-916-745-5	Sequence 5, Appl1
1151	69.5	3.9	328	4	PCT-US95-04353-5	Sequence 5, Appl1	1224	69	3.9	542	1	US-08-663-808-4	Sequence 4, Appl1
1152	69.5	3.9	333	1	US-08-436-463-6	Sequence 6, Appl1	1225	69	3.9	542	1	US-09-042-929-5	Sequence 5, Appl1
1153	69.5	3.9	333	1	US-08-024-253-6	Sequence 6, Appl1	1226	69	3.9	542	1	US-08-546-661-5	Sequence 5, Appl1
1154	69.5	3.9	333	1	US-09-134-000C-5207	Sequence 5207, Ap	1227	69	3.9	542	2	US-09-042-960-5	Sequence 5, Appl1
1155	69.5	3.9	334	1	US-08-646-981-16	Sequence 16, Appl1	1228	69	3.9	542	2	US-09-198-650-5	Sequence 4, Appl1
1156	69.5	3.9	447	2	US-09-198-452A-972	Sequence 972, App	1229	69	3.9	542	2	US-09-332-740-4	Sequence 4, Appl1
1157	69.5	3.9	456	2	US-09-438-185A-901	Sequence 901, App	1230	69	3.9	542	2	US-09-042-993-5	Sequence 5, Appl1
1158	69.5	3.9	484	2	US-09-248-796A-15483	Sequence 15483, A	1231	69	3.9	542	2	US-09-188-496-4	Sequence 4, Appl1
1159	69.5	3.9	496	2	US-10-104-047-3006	Sequence 3006, Ap	1232	69	3.9	542	2	US-09-042-937-5	Sequence 4, Appl1
1160	69.5	3.9	499	2	US-09-049-672A-1	Sequence 1, Appl1	1233	69	3.9	542	2	US-09-368-282-4	Sequence 4, Appl1
1161	69.5	3.9	503	2	US-09-487-558B-424	Sequence 424, App	1234	69	3.9	542	2	US-09-566-708A-4	Sequence 4, Appl1
1162	69.5	3.9	506	2	US-08-888-998-2	Sequence 2, Appl1	1235	69	3.9	542	2	US-09-042-709A-5	Sequence 5, Appl1
1163	69.5	3.9	506	2	US-09-362-633-2	Sequence 2, Appl1	1236	69	3.9	542	2	US-09-227-614-5	Sequence 5, Appl1
1164	69.5	3.9	506	2	US-09-877-476-2	Sequence 2, Appl1	1237	69	3.9	542	2	US-09-949-016-6462	Sequence 6462, Ap
1165	69.5	3.9	506	2	US-09-877-476-28	Sequence 28, Appl1	1238	69	3.9	543	2	US-09-949-016-10085	Sequence 10085, A
1166	69.5	3.9	506	2	US-09-877-476-36	Sequence 36, Appl1	1239	69	3.9	561	2	US-09-198-452A-744	Sequence 744, App
1167	69.5	3.9	512	2	US-09-248-796A-14219	Sequence 14219, A	1240	69	3.9	584	2	US-09-911-909B-14	Sequence 14, Appl1
1168	69.5	3.9	548	2	US-09-538-092-1058	Sequence 1058, Ap	1241	69	3.9	627	2	US-09-303-518B-456	Sequence 456, App
1169	69.5	3.9	555	2	US-09-328-352-5873	Sequence 5873, Ap	1242	69	3.9	657	2	US-08-508-761B-2	Sequence 2, Appl1
1170	69.5	3.9	559	2	US-09-949-016-9137	Sequence 9137, Ap	1243	69	3.9	673	2	US-09-196-387-8	Sequence 8, Appl1
1171	69.5	3.9	677	2	US-09-270-767-58094	Sequence 58094, A	1244	69	3.9	673	2	US-09-841-835-8	Sequence 8, Appl1
1172	69.5	3.9	697	2	US-09-486-072-3	Sequence 3, Appl1	1245	69	3.9	688	2	US-09-071-035-464	Sequence 464, App
1173	69.5	3.9	742	2	US-09-494-297A-4	Sequence 4, Appl1	1246	69	3.9	688	2	US-10-206-576-464	Sequence 464, App
1174	69.5	3.9	804	2	US-08-981-446B-3	Sequence 3, Appl1	1247	69	3.9	712	2	US-09-949-016-10600	Sequence 10600, A
1175	69.5	3.9	847	2	US-09-270-767-42783	Sequence 42783, A	1248	69	3.9	745	2	US-09-949-016-9976	Sequence 9976, Ap
1176	69.5	3.9	898	2	US-09-949-016-10987	Sequence 10987, A	1249	69	3.9	821	2	US-09-308-345A-8	Sequence 48, Appl1
1177	69.5	3.9	948	2	US-10-363-937-13	Sequence 13, Appl1	1250	69	3.9	851	2	US-09-543-681A-7277	Sequence 7277, Ap
1178	69.5	3.9	1033	2	US-10-029-347-4	Sequence 4, Appl1	1251	69	3.9	919	2	US-09-949-016-6954	Sequence 6954, A
1179	69.5	3.9	1172	2	US-09-712-363-176	Sequence 176, App	1252	69	3.9	924	2	US-09-438-185A-704	Sequence 704, App
1180	69.5	3.9	1260	2	US-08-506-295B-21	Sequence 21, Appl1	1253	69	3.9	928	2	US-10-104-047-2435	Sequence 2435, Ap
1181	69.5	3.9	1222	2	US-09-194-612A-1	Sequence 1, Appl1	1254	69	3.9	949	2	US-09-196-387-10	Sequence 10, Appl1
1182	69.5	3.9	1722	2	US-09-949-002-5341	Sequence 341, App	1255	69	3.9	949	2	US-09-841-835-10	Sequence 10, Appl1
1183	69.5	3.9	1740	2	US-09-949-002-535	Sequence 535, App	1256	69	3.9	1068	2	US-09-215-694-7	Sequence 7, Appl1
1184	69.5	3.9	108	1	US-08-378-939-30	Sequence 30, Appl1	1257	69	3.9	1257	2	US-10-109-310-7	Sequence 2, Appl1
1185	69	3.9	127	2	US-08-136-315-4	Sequence 4, Appl1	1258	69	3.9	1327	2	US-09-196-387-2	Sequence 2, Appl1
1186	69	3.9	127	2	US-09-767-888-4	Sequence 4, Appl1	1259	69	3.9	1327	2	US-09-841-835-2	Sequence 2, Appl1
1187	69	3.9	156	2	US-08-821-994-42	Sequence 42, Appl1	1260	69	3.9	1327	2	US-09-971-115A-8	Sequence 8, Appl1
1188	69	3.9	243	2	US-09-107-532A-6856	Sequence 6856, Ap	1261	69	3.9	2032	2	US-09-071-035-458	Sequence 458, App
1189	69	3.9	269	1	US-08-727-311-3	Sequence 3, Appl1	1262	69	3.9	2032	2	US-09-071-035-462	Sequence 462, App
1190	69	3.9	329	2	US-09-651-200-18	Sequence 18, Appl1	1263	69	3.9	2032	2	US-09-071-035-466	Sequence 466, App
1191	69	3.9	329	2	US-09-303-040-6	Sequence 6, Appl1	1264	69	3.9	2032	2	US-10-206-576-458	Sequence 458, App
1192	69	3.9	329	2	US-09-710-279-414	Sequence 414, App	1265	69	3.9	2032	2	US-10-206-576-462	Sequence 462, App
1193	69	3.9	331	2	US-09-134-001C-5258	Sequence 5258, Ap	1266	69	3.9	2032	2	US-10-206-576-466	Sequence 466, App
1194	69	3.9	332	2	US-09-646-561-26	Sequence 26, Appl1	1267	69	3.9	2054	2	US-09-134-000C-6612	Sequence 6612, Ap
1195	69	3.9	335	2	US-09-902-540-11829	Sequence 11829, A	1268	69	3.9	3892	2	US-09-328-352-5503	Sequence 5503, Ap

1269	69	3.9	4536	2	US-09-180-422B-27	Sequence 27, Appl	1342	68.5	3.9	714	2	US-09-107-532A-4039	Sequence 4039, Ap
1270	69	3.9	4536	2	US-09-079-030-1	Sequence 1, Appl	1343	68.5	3.9	822	2	US-09-252-993A-29534	Sequence 29534, A
1271	69	3.9	4563	2	US-09-108-006C-1	Sequence 1, Appl	1344	68.5	3.9	824	2	US-09-248-796A-20885	Sequence 20885, A
1272	69	3.9	4563	2	US-09-538-092-842	Sequence 842, App	1345	68.5	3.9	879	2	US-09-248-796A-16729	Sequence 16729, A
1273	68.5	3.9	105	1	US-08-820-754-22	Sequence 22, Appl	1346	68.5	3.9	906	2	US-09-417-039-11	Sequence 11, Appl
1274	68.5	3.9	105	1	US-08-956-652-22	Sequence 22, Appl	1347	68.5	3.9	910	2	US-09-134-000C-4288	Sequence 4288, Ap
1275	68.5	3.9	105	2	US-08-956-869-22	Sequence 22, Appl	1348	68.5	3.9	972	2	US-08-750-111A-2	Sequence 2, Appl
1276	68.5	3.9	105	2	US-08-948-547-22	Sequence 22, Appl	1349	68.5	3.9	972	2	US-09-944-807-10	Sequence 10, Appl
1277	68.5	3.9	105	2	US-08-212-185-22	Sequence 22, Appl	1350	68.5	3.9	1188	1	US-10-011-146-3	Sequence 3, Appl
1278	68.5	3.9	212	2	US-09-640-211A-796	Sequence 796, App	1351	68.5	3.9	1248	1	US-09-080-897-2	Sequence 2, Appl
1279	68.5	3.9	217	2	US-09-291-299A-7	Sequence 7, Appl	1352	68.5	3.9	1248	2	US-09-323-735-2	Sequence 2, Appl
1280	68.5	3.9	234	6	US-09-770-916-4	Patent No. 5189147	1353	68.5	3.9	1253	2	US-08-506-296B-14	Sequence 14, Appl
1281	68.5	3.9	234	2	US-09-997-165-2	Sequence 4, Appl	1354	68.5	3.9	1315	2	US-08-899-355-3	Sequence 3, Appl
1282	68.5	3.9	240	2	US-09-270-767-43805	Sequence 43805, A	1355	68.5	3.9	1453	1	US-08-308-872B-6	Sequence 6, Appl
1283	68.5	3.9	256	2	US-09-270-767-43173	Sequence 37173, A	1356	68.5	3.9	1686	2	US-09-355-160D-2	Sequence 2, Appl
1284	68.5	3.9	256	2	US-09-270-767-52390	Sequence 52390, A	1357	68.5	3.9	1686	2	US-10-092-219-2	Sequence 2, Appl
1285	68.5	3.9	296	2	US-09-492-709A-307	Sequence 307, App	1358	68.5	3.9	1787	2	US-09-543-681A-5402	Sequence 5402, Ap
1286	68.5	3.9	306	2	US-09-171-945-95	Sequence 95, Appl	1359	68.5	3.9	242	2	US-09-478-614-20	Sequence 20, Appl
1287	68.5	3.9	306	2	US-09-910-059-95	Sequence 95, Appl	1360	68.5	3.9	254	2	US-09-240-915-7	Sequence 7, Appl
1288	68.5	3.9	310	1	US-08-078-683A-3	Sequence 3, Appl	1361	68.5	3.9	254	2	US-09-591-435-7	Sequence 7, Appl
1289	68.5	3.9	310	1	US-08-488-199-4	Sequence 4, Appl	1362	68.5	3.9	304	2	US-10-098-600B-7	Sequence 7, Appl
1290	68.5	3.9	310	1	US-08-471-970A-3	Sequence 3, Appl	1363	68.5	3.9	345	2	US-09-328-352-5720	Sequence 5720, Ap
1291	68.5	3.9	310	2	US-09-723-677B-3	Sequence 3, Appl	1364	68.5	3.9	345	2	US-08-618-408B-2	Sequence 2, Appl
1292	68.5	3.9	310	2	US-09-949-016-6296	Sequence 6296, Ap	1365	68.5	3.9	355	2	US-09-948-016-9073	Sequence 7, Appl
1293	68.5	3.9	313	2	US-09-700-397-4	Sequence 4, Appl	1366	68.5	3.9	371	2	US-08-872-979-7	Sequence 7, Appl
1294	68.5	3.9	322	2	US-09-134-000C-6292	Sequence 6292, Ap	1367	68.5	3.9	389	2	US-09-949-016-9073	Sequence 9073, Ap
1295	68.5	3.9	362	2	US-09-949-016-9134	Sequence 9134, Ap	1368	68.5	3.9	407	2	US-08-753-007A-6	Sequence 6, Appl
1296	68.5	3.9	376	2	US-09-270-767-42614	Sequence 42614, A	1369	68.5	3.9	423	2	US-09-398-496-6	Sequence 6, Appl
1297	68.5	3.9	388	1	US-08-429-742-4	Sequence 4, Appl	1370	68.5	3.9	467	2	US-09-778-510-22	Sequence 22, Appl
1298	68.5	3.9	421	2	US-09-902-540-14796	Sequence 14796, A	1371	68.5	3.9	479	2	US-08-030-1175-41	Sequence 41, Appl
1299	68.5	3.9	457	2	US-08-328-500-9	Sequence 9, Appl	1372	68.5	3.9	479	2	US-10-104-047-3482	Sequence 3482, Ap
1300	68.5	3.9	458	2	US-09-039-555B-15	Sequence 15, Appl	1373	68.5	3.9	479	1	US-08-665-220-2	Sequence 2, Appl
1301	68.5	3.9	462	1	US-08-417-495-5	Sequence 5, Appl	1374	68.5	3.9	479	2	US-09-291-692-2	Sequence 2, Appl
1302	68.5	3.9	462	1	US-08-284-391B-5	Sequence 5, Appl	1375	68.5	3.9	479	2	US-09-561-756-33	Sequence 33, Appl
1303	68.5	3.9	462	2	US-09-218-950-5	Sequence 5, Appl	1376	68.5	3.9	479	2	US-09-954-697-33	Sequence 33, Appl
1304	68.5	3.9	462	2	US-08-394-388A-5	Sequence 5, Appl	1377	68.5	3.9	479	2	US-09-009-893A-4	Sequence 4, Appl
1305	68.5	3.9	462	4	PCT-US92-01785-5	Sequence 5, Appl	1378	68.5	3.9	479	2	US-09-489-155-4	Sequence 4, Appl
1306	68.5	3.9	462	4	PCT-US95-00454-5	Sequence 5, Appl	1379	68.5	3.9	479	2	US-09-952-768-2	Sequence 2, Appl
1307	68.5	3.9	482	4	PCT-US95-00454-5	Sequence 5, Appl	1380	68.5	3.9	479	2	US-10-668-955-2	Sequence 2, Appl
1308	68.5	3.9	482	2	US-09-248-796A-17755	Sequence 17755, A	1381	68.5	3.9	479	2	US-09-949-002-317	Sequence 317, App
1309	68.5	3.9	503	2	US-09-920-262A-9	Sequence 9, Appl	1382	68.5	3.9	479	2	US-09-949-002-317	Sequence 559, App
1310	68.5	3.9	504	2	US-10-029-180-6	Sequence 6, Appl	1383	68.5	3.9	482	2	US-09-962-834A-2	Sequence 2, Appl
1311	68.5	3.9	508	2	US-10-104-047-3233	Sequence 3233, Ap	1384	68.5	3.9	521	2	US-09-962-834A-2	Sequence 103, Appl
1312	68.5	3.9	522	2	US-09-270-767-43072	Sequence 43072, A	1385	68.5	3.9	521	2	US-09-851-873-103	Sequence 2, Appl
1313	68.5	3.9	538	2	US-08-994-076-2	Sequence 2, Appl	1386	68.5	3.9	542	1	US-08-948-569A-2	Sequence 2, Appl
1314	68.5	3.9	538	2	US-09-643-476-2	Sequence 2, Appl	1387	68.5	3.9	542	1	US-09-188-469-2	Sequence 2, Appl
1315	68.5	3.9	542	1	US-08-246-583-3	Sequence 3, Appl	1388	68.5	3.9	542	1	US-09-397-238A-2	Sequence 34, Appl
1316	68.5	3.9	542	2	US-09-638-791A-5	Sequence 5, Appl	1389	68.5	3.9	542	2	US-09-889-463A-4	Sequence 15, Appl
1317	68.5	3.9	542	2	US-09-538-092-672	Sequence 672, App	1390	68.5	3.9	542	2	US-09-345-473B-15	Sequence 16, Appl
1318	68.5	3.9	542	2	US-08-444-994-12	Sequence 12, Appl	1391	68.5	3.9	645	2	US-09-345-473B-15	Sequence 15, Appl
1319	68.5	3.9	589	2	US-08-991-862-2	Sequence 2, Appl	1392	68.5	3.9	645	2	US-09-862-027-16	Sequence 16, Appl
1320	68.5	3.9	589	2	US-09-813-156-2	Sequence 2, Appl	1393	68.5	3.9	645	2	US-09-862-027-16	Sequence 16, Appl
1321	68.5	3.9	589	2	US-09-456-886-2	Sequence 2, Appl	1394	68.5	3.9	721	2	US-09-541-094-12	Sequence 12, Appl
1322	68.5	3.9	589	2	US-09-824-647-2	Sequence 2, Appl	1395	68.5	3.9	721	2	US-09-945-258-12	Sequence 12, Appl
1323	68.5	3.9	589	2	US-09-880-842-2	Sequence 2, Appl	1396	68.5	3.9	721	2	US-09-328-352-5942	Sequence 5942, Ap
1324	68.5	3.9	613	2	US-09-171-945-113	Sequence 113, App	1397	68.5	3.9	761	2	US-09-364-970-5	Sequence 5, Appl
1325	68.5	3.9	613	2	US-09-510-059-113	Sequence 113, App	1398	68.5	3.9	770	2	US-09-738-946-8	Sequence 8, Appl
1326	68.5	3.9	628	2	US-10-101-464A-917	Sequence 917, App	1399	68.5	3.9	781	2	US-09-332-643-48	Sequence 48, Appl
1327	68.5	3.9	636	2	US-09-907-794A-175	Sequence 175, App	1400	68.5	3.9	793	1	US-08-332-643-48	Sequence 54, Appl
1328	68.5	3.9	636	2	US-09-905-125A-175	Sequence 175, App	1401	68.5	3.9	793	1	US-08-332-638-54	Sequence 54, Appl
1329	68.5	3.9	636	2	US-09-902-775A-175	Sequence 175, App	1402	68.5	3.9	814	1	US-08-233-788A-42	Sequence 42, Appl
1330	68.5	3.9	636	2	US-09-906-700-175	Sequence 175, App	1403	68.5	3.9	814	1	US-08-233-788A-42	Sequence 18931, A
1331	68.5	3.9	636	2	US-09-903-603A-175	Sequence 175, App	1404	68.5	3.9	883	3	US-09-248-796A-18931	Sequence 2, Appl
1332	68.5	3.9	636	2	US-09-904-920A-175	Sequence 175, App	1405	68.5	3.9	912	4	PCT-US95-03747-2	Sequence 8, Appl
1333	68.5	3.9	636	2	US-09-905-381A-175	Sequence 175, App	1406	68.5	3.9	1087	1	US-08-570-311-8	Sequence 8, Appl
1334	68.5	3.9	636	2	US-09-905-381A-175	Sequence 175, App	1407	68.5	3.9	1087	1	US-08-353-485-8	Sequence 36, Appl
1335	68.5	3.9	636	2	US-09-906-618-175	Sequence 175, App	1408	68.5	3.9	1174	2	US-08-446-345-36	Sequence 7163, Ap
1336	68.5	3.9	636	2	US-09-906-646-175	Sequence 175, App	1409	68.5	3.9	1174	2	US-09-949-016-7163	Sequence 7, Appl
1337	68.5	3.9	636	2	US-09-904-462-175	Sequence 175, App	1410	68.5	3.9	1185	2	US-09-964-956-7	Sequence 2, Appl
1338	68.5	3.9	636	2	US-09-902-736A-175	Sequence 175, App	1411	68.5	3.9	1232	2	US-09-770-170-2	Sequence 27, Appl
1339	68.5	3.9	636	2	US-09-906-722A-175	Sequence 175, App	1412	68.5	3.9	1358	1	US-08-570-311-27	Sequence 27, Appl
1340	68.5	3.9	677	2	US-09-270-767-45699	Sequence 45699, A	1413	68.5	3.9	1752	2	US-09-865-621A-2	Sequence 25, Appl
1341	68.5	3.9	679	2	US-09-949-016-7266	Sequence 7266, Ap	1414	68.5	3.9	2232	2	US-09-091-219-25	Sequence 25, Appl

1415	68	3.8	2232	2	US-09-660-541-25	Sequence 25, Appl
1416	68	3.8	2247	2	US-09-091-219-2	Sequence 2, Appl1
1417	68	3.8	2247	2	US-09-660-541-2	Sequence 2, Appl1
1418	68	3.8	2277	1	US-09-543-681A-6124	Sequence 6124, Ap
1419	67.5	3.8	131	1	US-08-328-152A-1	Sequence 1, Appl1
1420	67.5	3.8	185	2	US-10-101-464A-640	Sequence 640, App
1421	67.5	3.8	201	2	US-09-015-734-12	Sequence 12, Appl
1422	67.5	3.8	201	2	US-09-515-311-12	Sequence 12, Appl
1423	67.5	3.8	201	2	US-10-434-817-12	Sequence 12, Appl
1424	67.5	3.8	205	2	US-09-462-270-4	Sequence 4, Appl1
1425	67.5	3.8	253	2	US-09-320-424-11	Sequence 11, Appl
1426	67.5	3.8	253	2	US-09-825-563-11	Sequence 11, Appl
1427	67.5	3.8	255	2	US-09-015-734-2	Sequence 2, Appl1
1428	67.5	3.8	255	2	US-09-515-311-2	Sequence 2, Appl1
1429	67.5	3.8	255	2	US-10-434-817-2	Sequence 2, Appl1
1430	67.5	3.8	271	1	US-08-400-115-4	Sequence 4, Appl1
1431	67.5	3.8	287	2	US-09-252-991A-21133	Sequence 21133, A
1432	67.5	3.8	315	2	US-09-462-846-7	Sequence 7, Appl1
1433	67.5	3.8	322	2	US-09-667-135-2	Sequence 2, Appl1
1434	67.5	3.8	322	2	US-09-910-1748-29	Sequence 29, Appl
1435	67.5	3.8	322	2	US-09-620-461-29	Sequence 29, Appl
1436	67.5	3.8	328	2	US-09-270-767-45597	Sequence 45597, A
1437	67.5	3.8	329	2	US-10-104-047-3709	Sequence 3709, Ap
1438	67.5	3.8	335	2	US-09-543-681A-5733	Sequence 5733, Ap
1439	67.5	3.8	337	2	US-08-442-043A-18	Sequence 18, Appl
1440	67.5	3.8	337	2	US-09-560-639-6	Sequence 6, Appl1
1441	67.5	3.8	337	2	US-08-441-893A-18	Sequence 18, Appl
1442	67.5	3.8	342	2	US-09-032-337-41	Sequence 41, Appl
1443	67.5	3.8	352	2	US-09-252-991A-23825	Sequence 23825, A
1444	67.5	3.8	375	2	US-09-828-995B-32	Sequence 32, Appl
1445	67.5	3.8	383	1	US-08-609-572-2	Sequence 2, Appl1
1446	67.5	3.8	383	1	US-08-841-751-2	Sequence 2, Appl1
1447	67.5	3.8	383	2	US-08-846-340-2	Sequence 2, Appl1
1448	67.5	3.8	383	2	US-08-846-344-2	Sequence 2, Appl1
1449	67.5	3.8	383	2	US-09-301-808-2	Sequence 2, Appl1
1450	67.5	3.8	383	2	US-09-902-540-11160	Sequence 11160, A
1451	67.5	3.8	454	2	US-09-771-161A-95	Sequence 95, Appl
1452	67.5	3.8	458	2	US-10-070-778-2	Sequence 2, Appl1
1453	67.5	3.8	458	6	5223394-7	Patent No. 5223394
1454	67.5	3.8	462	2	US-09-949-016-8272	Sequence 8272, Ap
1455	67.5	3.8	530	2	US-09-444-711A-4	Sequence 4, Appl1
1456	67.5	3.8	536	1	US-07-820-011A-4	Sequence 4, Appl1
1457	67.5	3.8	536	2	US-08-426-509A-13	Sequence 13, Appl
1458	67.5	3.8	536	2	US-08-232-545-13	Sequence 13, Appl
1459	67.5	3.8	536	2	US-09-444-711A-2	Sequence 2, Appl1
1460	67.5	3.8	536	2	US-09-829-266-10	Sequence 10, Appl
1461	67.5	3.8	536	2	US-09-977-261-13	Sequence 13, Appl
1462	67.5	3.8	536	4	PCT-US93-00445-4	Sequence 4, Appl1
1463	67.5	3.8	536	4	PCT-US95-05008-13	Sequence 13, Appl
1464	67.5	3.8	537	2	US-09-949-016-10282	Sequence 10282, A
1465	67.5	3.8	567	2	US-09-560-639-7	Sequence 7, Appl1
1466	67.5	3.8	567	2	US-09-173-151A-24	Sequence 24, Appl1
1467	67.5	3.8	567	2	US-09-032-337-39	Sequence 39, Appl
1468	67.5	3.8	591	1	US-08-188-582-7	Sequence 7, Appl1
1469	67.5	3.8	591	1	US-08-646-715-7	Sequence 7, Appl1
1470	67.5	3.8	621	2	US-09-198-452A-361	Sequence 361, App
1471	67.5	3.8	625	2	US-09-438-185A-346	Sequence 346, App
1472	67.5	3.8	630	1	US-08-752-307B-14	Sequence 14, Appl
1473	67.5	3.8	630	2	US-09-707-802-14	Sequence 14, Appl
1474	67.5	3.8	630	2	US-09-991-326-14	Sequence 14, Appl
1475	67.5	3.8	680	1	US-08-164-839-70	Sequence 70, Appl
1476	67.5	3.8	680	1	US-08-583-799-70	Sequence 70, Appl
1477	67.5	3.8	687	1	US-08-164-839-31	Sequence 31, Appl
1478	67.5	3.8	687	1	US-08-583-799-31	Sequence 31, Appl
1479	67.5	3.8	687	1	US-08-583-799-33	Sequence 33, Appl
1480	67.5	3.8	688	1	US-08-164-839-70	Sequence 70, Appl
1481	67.5	3.8	688	1	US-08-583-799-70	Sequence 70, Appl
1482	67.5	3.8	688	1	US-08-583-799-72	Sequence 72, Appl
1483	67.5	3.8	777	2	US-09-270-767-45498	Sequence 45498, A
1484	67.5	3.8	837	2	US-09-949-016-6515	Sequence 6515, Ap
1485	67.5	3.8	893	1	US-08-706-702-3	Sequence 3, Appl1
1486	67.5	3.8	893	2	US-08-706-706-3	Sequence 3, Appl1
1487	67.5	3.8	893	2	US-09-238-471-3	Sequence 3, Appl1
1488	67.5	3.8	956	1	US-08-185-232A-2	Sequence 2, Appl1
1489	67.5	3.8	956	1	US-08-416-523-2	Sequence 2, Appl1
1490	67.5	3.8	956	2	US-08-789-478-2	Sequence 2, Appl1
1491	67.5	3.8	1070	2	US-09-961-403-3	Sequence 3, Appl1
1492	67.5	3.8	1095	2	US-09-107-532A-3855	Sequence 3855, Ap
1493	67.5	3.8	1527	2	US-09-695-795A-4	Sequence 4, Appl1
1494	67.5	3.8	1606	2	US-09-948-016-7371	Sequence 7371, Ap
1495	67.5	3.8	2385	2	US-09-543-681A-6304	Sequence 6304, Ap
1496	67	3.8	90	2	US-09-540-236-3200	Sequence 3200, Ap
1497	67	3.8	100	2	US-09-245-041-126	Sequence 126, App
1498	67	3.8	100	2	US-09-358-055B-127	Sequence 127, App
1499	67	3.8	100	2	US-09-893-238-126	Sequence 126, App
1500	67	3.8	107	1	US-08-425-336-123	Sequence 123, App
ALIGNMENTS						
RESULT 1						
US-09-991-181-253						
; Sequence 253, Application US/09991181						
; Patent No. 6913919						
GENERAL INFORMATION:						
; APPLICANT: Ashkenazi, Avi J.						
; APPLICANT: Baker, Kevin P.						
; APPLICANT: Bolstein, David						
; APPLICANT: Desnoyers, Luc						
; APPLICANT: Eaton, Dan L.						
; APPLICANT: Ferrara, Napoleone						
; APPLICANT: Fong, Sherman						
; APPLICANT: Gerber, Hanspeter						
; APPLICANT: Gerlitsen, Mary E.						
; APPLICANT: Goddard, Audrey						
; APPLICANT: Godowski, Paul J.						
; APPLICANT: Grimaldi, J Christopher						
; APPLICANT: Gurney, Auebin L.						
; APPLICANT: Kljavin, Ivar J.						
; APPLICANT: Napier, Mary A.						
; APPLICANT: Pan, James						
; APPLICANT: Paoni, Nicholas F.						
; APPLICANT: Roy, Margaret Ann						
; APPLICANT: Stewart, Timothy A.						
; APPLICANT: Tumas, Daniel						
; APPLICANT: Watanabe, Colin K.						
; APPLICANT: Williams, P. Mickey						
; APPLICANT: Wood, William I.						
; APPLICANT: Zhang, Zemin						
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic						
FILE REFERENCE: P2730PIC53						
CURRENT APPLICATION NUMBER: US/09/991,181						
CURRENT FILING DATE: 2001-11-16						
PRIOR APPLICATION NUMBER: 60/049787						
PRIOR FILING DATE: 1997-06-16						
PRIOR APPLICATION NUMBER: 60/062250						
PRIOR FILING DATE: 1997-10-17						
PRIOR APPLICATION NUMBER: 60/065186						
PRIOR FILING DATE: 1997-11-12						
PRIOR APPLICATION NUMBER: 60/065311						
PRIOR FILING DATE: 1997-11-13						
PRIOR APPLICATION NUMBER: 60/066770						
PRIOR FILING DATE: 1997-11-24						
PRIOR APPLICATION NUMBER: 60/075945						
PRIOR FILING DATE: 1998-02-25						
PRIOR APPLICATION NUMBER: 60/078910						
PRIOR FILING DATE: 1998-03-20						
PRIOR APPLICATION NUMBER: 60/083322						
PRIOR FILING DATE: 1998-04-28						
PRIOR APPLICATION NUMBER: 60/084600						
PRIOR FILING DATE: 1998-05-07						
PRIOR APPLICATION NUMBER: 60/087106						
PRIOR FILING DATE: 1998-05-28						
PRIOR APPLICATION NUMBER: 60/087607						

1	PRIOR FILING DATE: 1998-06-02	1	PRIOR APPLICATION NUMBER: 60/089307
2	PRIOR APPLICATION NUMBER: 60/087609	2	PRIOR FILING DATE: 1998-06-18
3	PRIOR FILING DATE: 1998-06-02	3	PRIOR APPLICATION NUMBER: 60/089908
4	PRIOR APPLICATION NUMBER: 60/087759	4	PRIOR FILING DATE: 1998-06-18
5	PRIOR FILING DATE: 1998-06-02	5	PRIOR APPLICATION NUMBER: 60/089947
6	PRIOR APPLICATION NUMBER: 60/087827	6	PRIOR FILING DATE: 1998-06-19
7	PRIOR FILING DATE: 1998-06-03	7	PRIOR APPLICATION NUMBER: 60/089948
8	PRIOR APPLICATION NUMBER: 60/088021	8	PRIOR FILING DATE: 1998-06-19
9	PRIOR FILING DATE: 1998-06-04	9	PRIOR APPLICATION NUMBER: 60/089952
10	PRIOR APPLICATION NUMBER: 60/088025	10	PRIOR FILING DATE: 1998-06-19
11	PRIOR FILING DATE: 1998-06-04	11	PRIOR APPLICATION NUMBER: 60/090246
12	PRIOR APPLICATION NUMBER: 60/088026	12	PRIOR FILING DATE: 1998-06-22
13	PRIOR FILING DATE: 1998-06-04	13	PRIOR APPLICATION NUMBER: 60/090252
14	PRIOR APPLICATION NUMBER: 60/088028	14	PRIOR FILING DATE: 1998-06-22
15	PRIOR FILING DATE: 1998-06-04	15	PRIOR APPLICATION NUMBER: 60/090254
16	PRIOR APPLICATION NUMBER: 60/088029	16	PRIOR FILING DATE: 1998-06-22
17	PRIOR FILING DATE: 1998-06-04	17	PRIOR APPLICATION NUMBER: 60/090349
18	PRIOR APPLICATION NUMBER: 60/088030	18	PRIOR FILING DATE: 1998-06-23
19	PRIOR FILING DATE: 1998-06-04	19	PRIOR APPLICATION NUMBER: 60/090355
20	PRIOR APPLICATION NUMBER: 60/088033	20	PRIOR FILING DATE: 1998-06-23
21	PRIOR FILING DATE: 1998-06-04	21	PRIOR APPLICATION NUMBER: 60/090429
22	PRIOR APPLICATION NUMBER: 60/088326	22	PRIOR FILING DATE: 1998-06-24
23	PRIOR FILING DATE: 1998-06-04	23	PRIOR APPLICATION NUMBER: 60/090431
24	PRIOR APPLICATION NUMBER: 60/088167	24	PRIOR FILING DATE: 1998-06-24
25	PRIOR FILING DATE: 1998-06-05	25	PRIOR APPLICATION NUMBER: 60/090435
26	PRIOR APPLICATION NUMBER: 60/088202	26	PRIOR FILING DATE: 1998-06-24
27	PRIOR FILING DATE: 1998-06-05	27	PRIOR APPLICATION NUMBER: 60/090444
28	PRIOR APPLICATION NUMBER: 60/088212	28	PRIOR FILING DATE: 1998-06-24
29	PRIOR FILING DATE: 1998-06-05	29	PRIOR APPLICATION NUMBER: 60/090445
30	PRIOR APPLICATION NUMBER: 60/088217	30	PRIOR FILING DATE: 1998-06-24
31	PRIOR FILING DATE: 1998-06-05	31	PRIOR APPLICATION NUMBER: 60/090472
32	PRIOR APPLICATION NUMBER: 60/088655	32	PRIOR FILING DATE: 1998-06-24
33	PRIOR FILING DATE: 1998-06-09	33	PRIOR APPLICATION NUMBER: 60/090535
34	PRIOR APPLICATION NUMBER: 60/088734	34	PRIOR FILING DATE: 1998-06-24
35	PRIOR FILING DATE: 1998-06-10	35	PRIOR APPLICATION NUMBER: 60/090540
36	PRIOR APPLICATION NUMBER: 60/088738	36	PRIOR FILING DATE: 1998-06-24
37	PRIOR FILING DATE: 1998-06-10	37	PRIOR APPLICATION NUMBER: 60/090542
38	PRIOR APPLICATION NUMBER: 60/088742	38	PRIOR FILING DATE: 1998-06-24
39	PRIOR FILING DATE: 1998-06-10	39	PRIOR APPLICATION NUMBER: 60/090557
40	PRIOR APPLICATION NUMBER: 60/088810	40	PRIOR FILING DATE: 1998-06-24
41	PRIOR FILING DATE: 1998-06-10	41	PRIOR APPLICATION NUMBER: 60/090676
42	PRIOR APPLICATION NUMBER: 60/088824	42	PRIOR FILING DATE: 1998-06-25
43	PRIOR FILING DATE: 1998-06-10	43	PRIOR APPLICATION NUMBER: 60/090678
44	PRIOR APPLICATION NUMBER: 60/088826	44	PRIOR FILING DATE: 1998-06-25
45	PRIOR FILING DATE: 1998-06-10	45	PRIOR APPLICATION NUMBER: 60/090690
46	PRIOR APPLICATION NUMBER: 60/088858	46	PRIOR FILING DATE: 1998-06-25
47	PRIOR FILING DATE: 1998-06-11	47	PRIOR APPLICATION NUMBER: 60/090694
48	PRIOR APPLICATION NUMBER: 60/088861	48	PRIOR FILING DATE: 1998-06-25
49	PRIOR FILING DATE: 1998-06-11	49	PRIOR APPLICATION NUMBER: 60/090655
50	PRIOR APPLICATION NUMBER: 60/088876	50	PRIOR FILING DATE: 1998-06-25
51	PRIOR FILING DATE: 1998-06-11	51	PRIOR APPLICATION NUMBER: 60/090666
52	PRIOR APPLICATION NUMBER: 60/089105	52	PRIOR FILING DATE: 1998-06-25
53	PRIOR FILING DATE: 1998-06-12	53	PRIOR APPLICATION NUMBER: 60/090862
54	PRIOR APPLICATION NUMBER: 60/089440	54	PRIOR FILING DATE: 1998-06-26
55	PRIOR FILING DATE: 1998-06-16	55	PRIOR APPLICATION NUMBER: 60/090863
56	PRIOR APPLICATION NUMBER: 60/089512	56	PRIOR FILING DATE: 1998-06-26
57	PRIOR FILING DATE: 1998-06-16	57	PRIOR APPLICATION NUMBER: 60/091360
58	PRIOR APPLICATION NUMBER: 60/089514	58	PRIOR FILING DATE: 1998-07-01
59	PRIOR FILING DATE: 1998-06-16	59	PRIOR APPLICATION NUMBER: 60/091478
60	PRIOR APPLICATION NUMBER: 60/089532	60	PRIOR FILING DATE: 1998-07-02
61	PRIOR FILING DATE: 1998-06-17	61	PRIOR APPLICATION NUMBER: 60/091544
62	PRIOR APPLICATION NUMBER: 60/089538	62	PRIOR FILING DATE: 1998-07-01
63	PRIOR FILING DATE: 1998-06-17	63	PRIOR APPLICATION NUMBER: 60/091519
64	PRIOR APPLICATION NUMBER: 60/089598	64	PRIOR FILING DATE: 1998-07-02
65	PRIOR FILING DATE: 1998-06-17	65	PRIOR APPLICATION NUMBER: 60/091626
66	PRIOR APPLICATION NUMBER: 60/089599	66	PRIOR FILING DATE: 1998-07-02
67	PRIOR FILING DATE: 1998-06-17	67	PRIOR APPLICATION NUMBER: 60/091633
68	PRIOR APPLICATION NUMBER: 60/089600	68	PRIOR FILING DATE: 1998-07-02
69	PRIOR FILING DATE: 1998-06-17		


```
; PRIOR FILING DATE: 1998-07-09
Query Match      100.0%; Score 1772; DB 2; Length 335;
Best Local Similarity 100.0%; Pred.No. 4e-183;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAGSPCLTLLIYIMQITSSAASGPVKELVGSYGAVTTPPLSKKQVDSIWTFTTTL 60
DB      1 MAGSPCLTLLIYIMQITSSAASGPVKELVGSYGAVTTPPLSKKQVDSIWTFTTTL 60
QY      61 VTIQPEGGIIIVYQNNRRRVPDPDGGYSLKSKLKKDNGIYYVGYSSSQQPESTQRY 120
DB      61 VTIQPEGGIIIVYQNNRRRVPDPDGGYSLKSKLKKDNGIYYVGYSSSQQPESTQRY 120
QY      121 VAHYVHLSKPYVMGLQSNKNGTCVTNLTCCMEHEDEVIDIYTWKALGOANESHNGSIL 180
DB      121 VAHYVHLSKPYVMGLQSNKNGTCVTNLTCCMEHEDEVIDIYTWKALGOANESHNGSIL 180
QY      181 PISRWGESDMTFICVARNPVSRNFSPIIARKLCEGAADDPDSSWVLLCLLVPLLSL 240
DB      181 PISRWGESDMTFICVARNPVSRNFSPIIARKLCEGAADDPDSSWVLLCLLVPLLSL 240
QY      241 FVLGLFLWFLKRRQREYIEKKRVDICRETPNICHSSENTYDTIPIHTNRTILKEDA 300
DB      241 FVLGLFLWFLKRRQREYIEKKRVDICRETPNICHSSENTYDTIPIHTNRTILKEDA 300
QY      301 NTYVSTVEIPIKKMENPHSLITMPDPFRLPAYENVI 335
DB      301 NTYVSTVEIPIKKMENPHSLITMPDPFRLPAYENVI 335

RESULT 2
US-09-990-444-253
; Sequence 253, Application US/09990444
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kjaevin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
```

```
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/076910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
```

PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089601
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 4e-183;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTYIIMQLTGSAAGPVKELVGSVGAVTFPLKSKKKQVDSIVTWTFTPL 60
DB 1 MAGSPTCLTYIIMQLTGSAAGPVKELVGSVGAVTFPLKSKKKQVDSIVTWTFTPL 60
QY VTIOBEGTITVTORNRERYDPDGGYSLKSLKSKKNDGIIYVGIYSSSLQOPSTOBY 120
DB VTIOBEGTITVTORNRERYDPDGGYSLKSLKSKKNDGIIYVGIYSSSLQOPSTOBY 120
QY VLAHYEHLKSKPVTMGLQSNKNGTCVTNIJTCMEHGEEDVIYTMKALQOANESHNGSIL 180
DB VLAHYEHLKSKPVTMGLQSNKNGTCVTNIJTCMEHGEEDVIYTMKALQOANESHNGSIL 180
QY PISMRGSDMTFCVARNPVSRNFSPTLARKLCEGAADPDSSMTLCLLVPLLSL 240
DB PISMRGSDMTFCVARNPVSRNFSPTLARKLCEGAADPDSSMTLCLLVPLLSL 240
QY FYLGLFLWFLKREEROEYIEKKRVDICRETPNICPHSGENTEXYTIPIHRTTIKEDPA 300
DB FYLGLFLWFLKREEROEYIEKKRVDICRETPNICPHSGENTEXYTIPIHRTTIKEDPA 300
QY NTVYSTVEIPKKMENPHSLTMPDTPRLFAYENV 335
DB NTVYSTVEIPKKMENPHSLTMPDTPRLFAYENV 335

RESULT 3
US-09-997-333-253
Sequence 253, Application US/09997333
Patent No. 6953836
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary B.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC27
;; CURRENT APPLICATION NUMBER: US/09/997,333
;; CURRENT FILING DATE: 2001-11-15
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/067770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087609
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088021
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088028
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088030
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088655
;; PRIOR FILING DATE: 1998-06-09
;; PRIOR APPLICATION NUMBER: 60/088734
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088738
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088742
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088810
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089440
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089600
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694

```
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090695
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090696
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090862
/ PRIOR FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: 60/090863
/ PRIOR FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: 60/091360
/ PRIOR FILING DATE: 1998-07-01
/ PRIOR APPLICATION NUMBER: 60/091478
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091544
/ PRIOR FILING DATE: 1998-07-01
/ PRIOR APPLICATION NUMBER: 60/091519
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091626
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091633
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091978
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/091982
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09
```

```
Query Match      100.0%; Score 1772; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 4e-183;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1  MAGSPCTCLTIYIIMQLTSSAASGPVKELVSGAVTEPLSKYKQVDSIVTFTNTPL 60
DB      1  MAGSTCLTIYIIMQLTSSAASGPVKELVSGAVTEPLSKYKQVDSIVTFTNTPL 60

QY      61  VTIQEGGTTIVTQNRNRVDPDGGYSLKSKLKNDSGIYVYSSIQOPSTORY 120
DB      61  VTIQEGGTTIVTQNRNRVDPDGGYSLKSKLKNDSGIYVYSSIQOPSTORY 120

QY      121  VLAHVEHLSKPYVTGLQSNKNGTCVTNLTCCMEHGEERVITYWKALGOAANESHNGSL 180
DB      121  VLAHVEHLSKPYVTGLQSNKNGTCVTNLTCCMEHGEERVITYWKALGOAANESHNGSL 180

QY      181  PISMRGESDMTFICVARRPVSRNFSSPIIARLCEGADDDSSWVLLCLLVPLLSL 240
DB      181  PISMRGESDMTFICVARRPVSRNFSSPIIARLCEGADDDSSWVLLCLLVPLLSL 240

QY      241  FVLGLFLWFLKKEOEYIEKKRVDICRETPNICHSGEENTYDTIPTNRTILKEDPA 300
DB      241  FVLGLFLWFLKKEOEYIEKKRVDICRETPNICHSGEENTYDTIPTNRTILKEDPA 300

QY      301  NTVYSTVEIPKKNENPHSLITMPDTRFLAYENVI 335
DB      301  NTVYSTVEIPKKNENPHSLITMPDTRFLAYENVI 335
```

```
RESULT 4
US-09-992-598-253
Sequence 253, Application US/09992598
```

GENERAL INFORMATION:

```
/ Patent No. 6956108
/ APPLICANT: Abkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Geritsen, Mary B.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
```

```
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730P1C20
/ CURRENT APPLICATION NUMBER: US/09/992,598
/ PRIOR FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/049787
/ PRIOR FILING DATE: 1997-06-16
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/065186
/ PRIOR FILING DATE: 1997-11-12
/ PRIOR APPLICATION NUMBER: 60/065311
/ PRIOR FILING DATE: 1997-11-13
/ PRIOR APPLICATION NUMBER: 60/066770
/ PRIOR FILING DATE: 1997-11-24
/ PRIOR APPLICATION NUMBER: 60/075945
/ PRIOR FILING DATE: 1998-02-25
/ PRIOR APPLICATION NUMBER: 60/076910
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/083322
/ PRIOR FILING DATE: 1998-04-28
/ PRIOR APPLICATION NUMBER: 60/084600
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/087106
/ PRIOR FILING DATE: 1998-05-28
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/087609
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/087759
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/087827
/ PRIOR FILING DATE: 1998-06-03
/ PRIOR APPLICATION NUMBER: 60/088021
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088025
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088026
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088028
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088029
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088030
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088033
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088326
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088167
/ PRIOR FILING DATE: 1998-06-05
/ PRIOR APPLICATION NUMBER: 60/088202
/ PRIOR FILING DATE: 1998-06-05
/ PRIOR APPLICATION NUMBER: 60/088212
/ PRIOR FILING DATE: 1998-06-05
/ PRIOR APPLICATION NUMBER: 60/088217
/ PRIOR FILING DATE: 1998-06-05
/ PRIOR APPLICATION NUMBER: 60/088655
/ PRIOR FILING DATE: 1998-06-09
/ PRIOR APPLICATION NUMBER: 60/088734
```

;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088738
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088742
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088810
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089440
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089600
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24

;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090662
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 4e-183;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGSPCTCTLTLYILMOLTGSASGPVKEIVGSVGAVTFFPKSKVKOVDSIVMTFNTPL 60
Db 1 MAGSPCTCTLTLYILMOLTGSASGPVKEIVGSVGAVTFFPKSKVKOVDSIVMTFNTPL 60
Qy VTIOPEGATIIIVTONRRRERYDPDGGYSILSKLXKXNDGSIYYVGIYSSSLQOPSTOEX 120
Db VTIOPEGATIIIVTONRRRERYDPDGGYSILSKLXKXNDGSIYYVGIYSSSLQOPSTOEX 120
Qy 121 VLAHYEHLKRPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOANESHNSIL 180
Db 121 VLAHYEHLKRPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOANESHNSIL 180
Qy 121 VLAHYEHLKRPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOANESHNSIL 180
Db 121 VLAHYEHLKRPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOANESHNSIL 180
Qy 181 PISWRMESDMTFCVARNPVSRRFSSPIIARXLCBAADDPDSMTLCLLVPILLSL 240
Db 181 PISWRMESDMTFCVARNPVSRRFSSPIIARXLCBAADDPDSMTLCLLVPILLSL 240
Qy 241 FVLGLFWMFLKREGEYIEBKRRVDICRETPNICPSGENTEXTDTIPHTRTILKEDPA 300
Db 241 FVLGLFWMFLKREGEYIEBKRRVDICRETPNICPSGENTEXTDTIPHTRTILKEDPA 300
Qy 301 NTVYSTVIEIPKRMENPHSLTMDPTFRLFAVENYI 335
Db 301 NTVYSTVIEIPKRMENPHSLTMDPTFRLFAVENYI 335

RESULT 5
US-09-513-999C-4472
; Sequence 4472, Application US/09513999C

```
Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4472
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -22...-1
; OTHER INFORMATION: score 5.9
; OTHER INFORMATION: seq LYLIMQLTGSAA/SG
US-09-513-999C-4472
```

```
Query Match      28.1%; Score 498; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.9e-46;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MAGSPCTCTIYIIMQLTGSAAAGVKKLVSGVGNATFPLKSKYQVDSIVMTFTPL 60
Db 1 MAGSPCTCTIYIIMQLTGSAAAGVKKLVSGVGNATFPLKSKYQVDSIVMTFTPL 60
Qy 61 VTIOPEGGITVTONRNRERYDFPDGYSLSKLSK 97
Db 61 VTIOPEGGITVTONRNRERYDFPDGYSLSKLSK 97
```

```
RESULT 6
US-09-949-016-6428
; Sequence 6428, Application US/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6428
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6428
```

```
Query Match      20.5%; Score 362.5; DB 2; Length 328;
Best Local Similarity 31.5%; Pred. No. 2.1e-30;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;
```

```
Qy 14 LMOI-----TGSAGSPVVELV---GSVGAATFPLK-SKVRQVDSIVMTFTPLVTLQ 64
Db 6 LMIILICLOTWPEAAKXSEIRITVNGIGESVTFPNIDEPQVKIATISTSVAYVTP 65
Qy 65 PEGGT---IIVTONRNRERYDFPDGYSLSKLSKKNDSIYVGIYSSLSQOPSTQERY 121
Db 65 PEGGT---IIVTONRNRERYDFPDGYSLSKLSKKNDSIYVGIYSSLSQOPSTQERY 121
```

```
Db 66 GDSEIAPVTVTHNRYERJHALGPNYNLYISDLRMDAGDYKADINTQADPTTKRYN 125
Qy 122 LHYEHLSKRPVTMGLOSNGKGTCTVNTLTCMHEGEDVITYMKALCOANESNGSILP 181
Db 126 LQYRRRLKPKITQSLASVSTCNVLTCSVEKEKNVYNNPSLDE-----EGNVLQ 179
Qy 182 ISMRGSDMTFCVANNPVSRRNPSPILRKLCGAADPDS-----SKVLLCLLVP 235
Db 180 IFQPEQDELTYTTAONPVSN-SDSISARQLCADIAMGERTHTHTGLSLVAMFLLVL 238
Qy 236 LLSLFLVGLFLMFLKEREQERYIEKRVYDICTETPNICPHSGENTETPTTNRVTL 295
Db 239 ILSVFLFLRLF-----KRGDASAKKITYTYIWAHSNTQP--AESRIYDEILQSKVLPS 290
Qy 296 KEDPANTVYSTVEIPKQKQENPHSLITMPDTPRLFAERYNI 335
Db 291 KEPPNTVYSEVQFADKMGKASTQDSKP--PGTSSYEIVI 328

RESULT 7
US-09-149-476-483
; Sequence 483, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
```

1	EARLIER APPLICATION NUMBER: 60/047,492
2	EARLIER FILING DATE: 1997-05-23
3	EARLIER APPLICATION NUMBER: 60/047,598
4	EARLIER FILING DATE: 1997-05-23
5	EARLIER APPLICATION NUMBER: 60/047,613
6	EARLIER FILING DATE: 1997-05-23
7	EARLIER APPLICATION NUMBER: 60/047,582
8	EARLIER FILING DATE: 1997-05-23
9	EARLIER APPLICATION NUMBER: 60/047,596
10	EARLIER FILING DATE: 1997-05-23
11	EARLIER APPLICATION NUMBER: 60/047,612
12	EARLIER FILING DATE: 1997-05-23
13	EARLIER APPLICATION NUMBER: 60/047,632
14	EARLIER FILING DATE: 1997-05-23
15	EARLIER APPLICATION NUMBER: 60/047,601
16	EARLIER FILING DATE: 1997-05-23
17	EARLIER APPLICATION NUMBER: 60/043,580
18	EARLIER FILING DATE: 1997-04-11
19	EARLIER APPLICATION NUMBER: 60/043,568
20	EARLIER FILING DATE: 1997-04-11
21	EARLIER APPLICATION NUMBER: 60/043,314
22	EARLIER FILING DATE: 1997-04-11
23	EARLIER APPLICATION NUMBER: 60/043,569
24	EARLIER FILING DATE: 1997-04-11
25	EARLIER APPLICATION NUMBER: 60/043,311
26	EARLIER FILING DATE: 1997-04-11
27	EARLIER APPLICATION NUMBER: 60/043,671
28	EARLIER FILING DATE: 1997-04-11
29	EARLIER APPLICATION NUMBER: 60/043,674
30	EARLIER FILING DATE: 1997-04-11
31	EARLIER APPLICATION NUMBER: 60/043,669
32	EARLIER FILING DATE: 1997-04-11
33	EARLIER APPLICATION NUMBER: 60/043,312
34	EARLIER FILING DATE: 1997-04-11
35	EARLIER APPLICATION NUMBER: 60/043,313
36	EARLIER FILING DATE: 1997-04-11
37	EARLIER APPLICATION NUMBER: 60/043,672
38	EARLIER FILING DATE: 1997-04-11
39	EARLIER APPLICATION NUMBER: 60/043,315
40	EARLIER FILING DATE: 1997-04-11
41	EARLIER APPLICATION NUMBER: 60/048,974
42	EARLIER FILING DATE: 1997-06-06
43	EARLIER APPLICATION NUMBER: 60/056,886
44	EARLIER FILING DATE: 1997-08-22
45	EARLIER APPLICATION NUMBER: 60/056,877
46	EARLIER FILING DATE: 1997-08-22
47	EARLIER APPLICATION NUMBER: 60/056,889
48	EARLIER FILING DATE: 1997-08-22
49	EARLIER APPLICATION NUMBER: 60/056,893
50	EARLIER FILING DATE: 1997-08-22
51	EARLIER APPLICATION NUMBER: 60/056,630
52	EARLIER FILING DATE: 1997-08-22
53	EARLIER APPLICATION NUMBER: 60/056,878
54	EARLIER FILING DATE: 1997-08-22
55	EARLIER APPLICATION NUMBER: 60/056,662
56	EARLIER FILING DATE: 1997-08-22
57	EARLIER APPLICATION NUMBER: 60/056,872
58	EARLIER FILING DATE: 1997-08-22
59	EARLIER APPLICATION NUMBER: 60/056,882
60	EARLIER FILING DATE: 1997-08-22
61	EARLIER APPLICATION NUMBER: 60/056,637
62	EARLIER FILING DATE: 1997-08-22
63	EARLIER APPLICATION NUMBER: 60/056,903
64	EARLIER FILING DATE: 1997-08-22
65	EARLIER APPLICATION NUMBER: 60/056,888
66	EARLIER FILING DATE: 1997-08-22
67	EARLIER APPLICATION NUMBER: 60/056,879
68	EARLIER FILING DATE: 1997-08-22
69	EARLIER APPLICATION NUMBER: 60/056,880
70	EARLIER FILING DATE: 1997-08-22
71	EARLIER APPLICATION NUMBER: 60/056,894
72	EARLIER FILING DATE: 1997-08-22
73	EARLIER APPLICATION NUMBER: 60/056,911

EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056,636#
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056,874#
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056,910#
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056,864#
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056,631#
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056,845#
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/047,599#
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,599#
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,588#
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,588#
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,588#
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,588#
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,588#
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,588#
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,588#
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,588#
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,588#
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,588#
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/049,610#
EARLIER	FILING DATE:	1997-06-13


```

; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match          20.5%; Score 362.5; DB 2; Length 329;
Best Local Similarity 31.5%; Pred. No. 2.1e-30;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

QY 14 LMQL-----TGSAAAGPYKELV---GSVGAATVPLK-SKVQVDSIVWTFNTPLVLTIQ 64
DB 6 LMILLICQTPBEAKGKSEIFTVNGILGESVTFPVNIQEPKQVILIMTSKTSVAVYTP 65
QY 65 PEGGT---IIVTONRERVDPPDGGYSIKLSKKNDSGIYVGIYSSLSQOPESTQRYV 121
DB 66 GDSFAPVYVTVTHRYRERIHALGPYNYLVISDLRMEADAGYKADINTQADPYTTTKRYN 125
QY 122 LHVYHLSKPYTMGLQSNKNGTCVTNLTCCMEHEBDIYTWKALGOANESHNGSLTP 181
DB 126 LQIYRLGPKITQSLMASVNSTCVNLTLCVSEKEKKNVTYMSPLGE-----EGNVLIQ 179
QY 182 ISWRGSDMTFTICVARNPVSRNFSPIIARKLCGGAADDDPS-----SMVLCLILVLP 235
DB 180 IFQPEDELTITCTAQNPPVSN--SDSISARQLCADIAMGFRTHHTGLSLVAMFLLVL 238
QY 236 LLSLFLVGLFWLFLKRROEYIEKKRVDICRETPNICPHSGENTEDTTPHTNRITL 295
DB 239 ILSVFLRLP-----KRDQDASKTIYTYIMASRNTQF--AESRIYDEILQSKVLPS 290
QY 296 KEDPANTYSTEIPIKKNENPHSLTMPDTRLPAYENVI 335
DB 291 KEEPNTVYSEVQFADKKGKASTQDSKP--PGTSSYEIYI 328

RESULT 8
US-09-949-016-7327
; Sequence 7327, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7327
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7327

Query Match          20.5%; Score 362.5; DB 2; Length 332;
Best Local Similarity 31.5%; Pred. No. 2.1e-30;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

QY 14 LMQL-----TGSAAAGPYKELV---GSVGAATVPLK-SKVQVDSIVWTFNTPLVLTIQ 64
DB 10 LMILLICQTPBEAKGKSEIFTVNGILGESVTFPVNIQEPKQVILIMTSKTSVAVYTP 69
QY 65 PEGGT---IIVTONRERVDPPDGGYSIKLSKKNDSGIYVGIYSSLSQOPESTQRYV 121
DB 70 GDSFAPVYVTVTHRYRERIHALGPYNYLVISDLRMEADAGYKADINTQADPYTTTKRYN 129
QY 122 LHVYHLSKPYTMGLQSNKNGTCVTNLTCCMEHEBDIYTWKALGOANESHNGSLTP 181
DB 130 LQIYRLGPKITQSLMASVNSTCVNLTLCVSEKEKKNVTYMSPLGE-----EGNVLIQ 183

```

```

QY 182 ISWRGSDMTFTICVARNPVSRNFSPIIARKLCGGAADDDPS-----SMVLCLILVLP 235
DB 184 IFQPEDELTITCTAQNPPVSN--SDSISARQLCADIAMGFRTHHTGLSLVAMFLLVL 242
QY 236 LLSLFLVGLFWLFLKRROEYIEKKRVDICRETPNICPHSGENTEDTTPHTNRITL 295
DB 243 ILSVFLRLP-----KRDQDASKTIYTYIMASRNTQF--AESRIYDEILQSKVLPS 294

QY 296 KEDPANTYSTEIPIKKNENPHSLTMPDTRLPAYENVI 335
DB 295 KEEPNTVYSEVQFADKKGKASTQDSKP--PGTSSYEIYI 332

RESULT 9
US-08-348-792-10
; Sequence 10, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan B.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,792
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CHUNG, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-348-792-10

Query Match          10.5%; Score 186; DB 1; Length 343;
Best Local Similarity 24.3%; Pred. No. 3e-11;
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;

QY 8 LTLIYIQLTGSAAAG---PVKELVSGVGAATVPL-----KSKYKQVDSIVWTFN 56
DB 12 LILFLSLAFSLSYGTGGVWDCPV--ILQKLGQDTWLPITNEHQINKSVKSVRIIV-TWA 68
QY 57 TTPVLTIQPEGGTIIVTONRERVD-----PD-----GGY-----SLTSLKKNKD 99
DB 69 TSP-----GSKSNKTIYSFDLSKGSYPDHLDDGHHFQSKNLSTKILGNRRS 115
QY 100 SGIYVGIYSS-SLQOPESTQRYVLAHVYHLSKP--KVTMGLQSNKNGTCVTNLTCCMEHG 156
DB 116 EGVYIVASVENYSVQFPCKQ---LKLRYGVSPPEIKVINKRQENENGTCSLLACGVKKG 172
QY 157 EBDVIYTWK-----ALGOANESHNGSLTPISWRGSDMTFTICVARNPV-----SRNFSF 208

```


Db 173 DH-VTYSNDSDEAGTHLSRANRSH---LHHTTLSNQHDSTYNCTASNPVSSISSTFN-- 226
Qy 209 ILARKICGAADDPSSMWLLCLLVPLLSLFVLGLFLMFLKRRROEYIE---EKKRV 265
Db 227 -LSSQACKQSSSESSPMWQYTLVPLGVIIIFILVFETAIIMKKGKSNHCOPPEBKSL 285
Qy 266 DICRETENICPSGENTGYDTIPHTNRITLKEDPANTVY--STVEIPKGMENP-----HS 318
Db 286 TTYAQVQKSGPO--EKKLHD-----ALTDODPCTTIYVATBPAPESVQEPNPTTYA 336
Qy 319 LITMPDT 325
Db 337 SVTLPEB 343
RESULT 10
US-08-462-738-10
; Sequence 10, Application US/08462738
; Patent No. 5977303
; GENERAL INFORMATION:
; APPLICANT: Averea, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan B.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,738
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-738-10
Query Match 10.5%; Score 186; DB 1; Length 343;
Best Local Similarity 24.3%; Pred. No. 3e-11;
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;

Qy 100 SGITYVGYSS-SLQOPSTQEVLAHYEHLKSP--KYTMGLQSNKNGCVTNLTCCMEHG 156
Db 116 EGMVIVSYEENVSVOQFCQ---LKLVEQVSPPEIKVNTKQENENGTCISLLACTVKGK 172
Qy 157 EEDVYITWK-----ALGOANESHNSGILPISMRWGESDMTFICVAPRV---SNFESP 208
Db 173 DH-VTYSNDSDEAGTHLSRANRSH---LHHTTLSNQHDSTYNCTASNPVSSISSTFN-- 226
Qy 209 ILARKICGAADDPSSMWLLCLLVPLLSLFVLGLFLMFLKRRROEYIE---EKKRV 265
Db 227 -LSSQACKQSSSESSPMWQYTLVPLGVIIIFILVFETAIIMKKGKSNHCOPPEBKSL 285
Qy 266 DICRETENICPSGENTGYDTIPHTNRITLKEDPANTVY--STVEIPKGMENP-----HS 318
Db 286 TTYAQVQKSGPO--EKKLHD-----ALTDODPCTTIYVATBPAPESVQEPNPTTYA 336
Qy 319 LITMPDT 325
Db 337 SVTLPEB 343
RESULT 11
US-09-199-955-10
; Sequence 10, Application US/09199955
; Patent No. 6372899
; GENERAL INFORMATION:
; APPLICANT: Averea, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan B.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/199,955
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/461,473
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-199-955-10
Query Match 10.5%; Score 186; DB 2; Length 343;
Best Local Similarity 24.3%; Pred. No. 3e-11;
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;


```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-348-792-2

Query Match      10.3%; Score 182.5; DB 1; Length 335;
Best Local Similarity 22.5%; Pred. No. 6.9e-11;
Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;

QY 8 LTLIYILM-QLTGSAAAGP-----VKELVSGVGAATFPL-----KSKYKQVDSIYWT 54
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 7 LSLTFVLFLSLAFGASVGTGGRMNNCPKILRLQLSKVLPLTYERINKSNKSIHIVWTM 66
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 55 FNT-----TLVNTIQP-EGGTIIYTONRNRVDPDGGYSLKSLKNDSGIYYGI 107
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 67 AKSLNSVENKIVSLDPSBAG---PPRYLGRYKFYIENLTLGIRSRKDEBGMVLTMTL 122
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 108 YSS-SLQDPSTQEVYLAHYEHLKRPVTWGLQSNKNGTCVTNLTCMEHGEEDVIYTW-- 164
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 123 EKNSVQRFCLQ---LRLEYQVSTPEIKVLANKTQENGCTILIGCTVEKGDH-VAYSMSB 178
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 165 KALGQANESHNGSILPISRWGSDMTFCVARNPVSRNFS--SPILARKLCBGAADP 222
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 179 KAGTHPLNPANSHLSLTLPQHADNIYICTVSNPISNNSQTSP-----WPCRTDP 232
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 223 DSSM-----VLCLLIVPLLISLFLGLFLMWLKRQREBYE---EKRRVDIC 268
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 223 SETKMAVAYAGLGGVIMILIMVILQ-----LRRGKKNHQTVEKKSILTY 281
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 269 RETPNICPSGENTEDTIPHTNRTILKEDPANTVY--STVEIPKMKENPSL-----LT 321
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 282 AQVQKPGP---LQKKLDSFP-----AQDPTTIYVAATPVPESVQENSIITYASVT 331
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 322 MPDT 325
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 332 LPES 335

RESULT 14
US-08-462-738-2
; Sequence 2, Application US/08462738
; Patent No. 5977303
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,738
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
```

```

; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: Dk0436GB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-738-2

Query Match      10.3%; Score 182.5; DB 1; Length 335;
Best Local Similarity 22.5%; Pred. No. 6.9e-11;
Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;

QY 8 LTLIYILM-QLTGSAAAGP-----VKELVSGVGAATFPL-----KSKYKQVDSIYWT 54
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 7 LSLTFVLFLSLAFGASVGTGGRMNNCPKILRLQLSKVLPLTYERINKSNKSIHIVWTM 66
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 55 FNT-----TLVNTIQP-EGGTIIYTONRNRVDPDGGYSLKSLKNDSGIYYGI 107
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 67 AKSLNSVENKIVSLDPSBAG---PPRYLGRYKFYIENLTLGIRSRKDEBGMVLTMTL 122
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 108 YSS-SLQDPSTQEVYLAHYEHLKRPVTWGLQSNKNGTCVTNLTCMEHGEEDVIYTW-- 164
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 123 EKNSVQRFCLQ---LRLEYQVSTPEIKVLANKTQENGCTILIGCTVEKGDH-VAYSMSB 178
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 165 KALGQANESHNGSILPISRWGSDMTFCVARNPVSRNFS--SPILARKLCBGAADP 222
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 179 KAGTHPLNPANSHLSLTLPQHADNIYICTVSNPISNNSQTSP-----WPCRTDP 232
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 223 DSSM-----VLCLLIVPLLISLFLGLFLMWLKRQREBYE---EKRRVDIC 268
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 223 SETKMAVAYAGLGGVIMILIMVILQ-----LRRGKKNHQTVEKKSILTY 281
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 269 RETPNICPSGENTEDTIPHTNRTILKEDPANTVY--STVEIPKMKENPSL-----LT 321
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 282 AQVQKPGP---LQKKLDSFP-----AQDPTTIYVAATPVPESVQENSIITYASVT 331
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 322 MPDT 325
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 332 LPES 335

RESULT 15
US-09-199-955-2
; Sequence 2, Application US/09199955
; Patent No. 6372899
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/199,955
```


Thu Dec 29 17:40:31 2005

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 11:08:20 ; Search time 13 Seconds

(without alignments)
173.601 Million cell updates/sec

Perfect score: 1772

Sequence: 1 MAGSPTCTLIYIMQLTGS.....PHSLTMDPTRLPAYENV 335

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51470 seqs, 6736768 residues

51470

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1772	100.0	335	7	US-11-102-240-46	Sequence 46, Appl
2	1315.5	17.8	346	7	US-11-174-150-33	Sequence 33, Appl
3	251	14.2	220	7	US-11-174-150-32	Sequence 32, Appl
4	124.5	7.0	344	7	US-11-080-991-4	Sequence 4, Appl
5	124.5	7.0	344	7	US-11-186-284-20	Sequence 20, Appl
6	124.5	7.0	344	7	US-11-077-386-16	Sequence 16, Appl
7	119.5	6.7	365	7	US-11-102-978-9	Sequence 9, Appl
8	119.5	6.7	365	7	US-11-080-991-78	Sequence 78, Appl
9	117	6.6	324	7	US-11-077-386-15	Sequence 15, Appl
11	98.5	5.6	404	7	US-11-069-642-115	Sequence 115, Appl
12	93	5.2	419	6	US-10-821-234-1664	Sequence 1664, Ap
14	92.5	5.2	299	7	US-11-000-463-275	Sequence 275, Appl
15	92.5	5.2	299	7	US-11-000-463-747	Sequence 747, Appl
16	92.5	5.2	299	7	US-11-000-463-748	Sequence 748, Appl
17	92.5	5.2	299	7	US-11-173-037-7	Sequence 7, Appl
19	92	5.2	2828	7	US-11-080-991-54	Sequence 54, Appl
20	92	5.2	2828	7	US-11-186-284-49	Sequence 49, Appl
21	89.5	5.1	845	7	US-11-147-047-46	Sequence 46, Appl
22	87	4.9	583	7	US-11-080-991-64	Sequence 64, Appl
23	86	4.9	259	7	US-11-000-463-276	Sequence 276, Appl
24	85.5	4.8	2491	6	US-10-995-561-769	Sequence 769, Appl
25	84	4.7	668	7	US-11-111-239-13	Sequence 13, Appl
28	83.5	4.7	515	7	US-11-093-274-38	Sequence 38, Appl
29	82	4.6	567	7	US-11-016-503-10	Sequence 10, Appl
30	81.5	4.6	7968	7	US-11-186-731-5	Sequence 5, Appl
31	81	4.6	254	7	US-11-054-515-1843	Sequence 1843, Ap

32	81	4.6	829	7	US-11-090-739-122	Sequence 122, Appl
33	81	4.6	829	7	US-11-186-284-18	Sequence 18, Appl
34	80.5	4.5	313	6	US-10-723-207-3	Sequence 3, Appl
35	79.5	4.5	859	7	US-11-188-743-16	Sequence 16, Appl
36	79	4.5	490	7	US-11-063-343-31	Sequence 31, Appl
37	78.5	4.4	212	7	US-11-025-834A-16	Sequence 16, Appl
38	78.5	4.4	628	7	US-11-080-991-108	Sequence 108, Appl
39	78.5	4.4	727	6	US-10-995-561-864	Sequence 864, Appl
40	78.5	4.4	782	6	US-10-995-561-861	Sequence 861, Appl
41	78.5	4.4	847	6	US-10-995-561-863	Sequence 863, Appl
42	78.5	4.4	847	6	US-10-995-561-865	Sequence 865, Appl
43	77	4.3	1897	6	US-10-821-234-1635	Sequence 1635, Ap
44	77	4.3	1907	7	US-11-000-463-250	Sequence 250, Appl
45	76.5	4.3	1451	6	US-10-995-561-829	Sequence 829, Appl
46	76	4.3	462	7	US-11-016-503-8	Sequence 8, Appl
47	76	4.3	567	7	US-11-016-503-2	Sequence 2, Appl
48	76	4.3	1694	7	US-11-135-855-36	Sequence 36, Appl
49	76	4.3	1709	7	US-11-135-855-35	Sequence 35, Appl
50	75	4.2	527	7	US-11-113-424-81	Sequence 81, Appl
51	74.5	4.2	555	6	US-10-821-234-1015	Sequence 1015, Ap
52	74.5	4.2	4655	6	US-10-995-561-586	Sequence 586, Appl
53	74	4.2	1488	6	US-10-821-234-1333	Sequence 1333, Ap
54	74	4.2	343	7	US-11-080-091-4	Sequence 4, Appl
55	74	4.2	1649	6	US-10-995-561-974	Sequence 974, Appl
56	74	4.2	1709	6	US-10-995-561-973	Sequence 973, Appl
57	73.5	4.1	304	7	US-11-025-834A-21	Sequence 21, Appl
58	73.5	4.1	304	7	US-11-080-091-10	Sequence 10, Appl
59	73.5	4.1	334	7	US-11-113-424-80	Sequence 80, Appl
61	73	4.1	257	7	US-11-067-121-18	Sequence 18, Appl
62	73	4.1	406	7	US-11-000-463-377	Sequence 377, Appl
63	73	4.1	406	7	US-11-000-463-849	Sequence 849, Appl
64	73	4.1	864	7	US-11-194-246-343	Sequence 343, Appl
66	72.5	4.1	426	6	US-10-821-234-1585	Sequence 1585, Ap
67	72	4.1	452	7	US-11-016-503-6	Sequence 6, Appl
68	72	4.1	528	6	US-10-793-626-1930	Sequence 1930, Ap
69	72	4.1	557	7	US-11-016-503-4	Sequence 4, Appl
70	72	4.1	840	7	US-11-108-117-1102	Sequence 1102, Ap
71	72	4.1	4419	6	US-10-821-234-1155	Sequence 1155, Ap
72	71.5	4.0	298	7	US-11-080-091-9	Sequence 9, Appl
73	71.5	4.0	314	7	US-11-143-980-56	Sequence 56, Appl
74	71.5	4.0	391	6	US-10-995-561-670	Sequence 67, Appl
75	71.5	4.0	1032	6	US-10-392-234A-67	Sequence 67, Appl
76	71.5	4.0	3063	7	US-11-186-284-26	Sequence 26, Appl
77	71	4.0	362	7	US-11-186-284-26	Sequence 12, Appl
78	71	4.0	488	6	US-10-995-561-860	Sequence 860, Appl
79	71	4.0	1338	6	US-10-821-234-1622	Sequence 1622, Ap
80	71	4.0	1338	7	US-11-109-156-23	Sequence 23, Appl
81	71	4.0	2897	6	US-10-499-715-2	Sequence 2, Appl
82	71	4.0	3588	6	US-10-995-561-672	Sequence 672, Appl
83	71	4.0	4346	6	US-10-995-561-671	Sequence 671, Appl
84	71	4.0	4347	6	US-10-995-561-670	Sequence 670, Appl
85	70.5	4.0	246	7	US-11-132-839-8	Sequence 8, Appl
86	70.5	4.0	333	6	US-10-878-556A-48	Sequence 48, Appl
87	70.5	4.0	472	6	US-10-793-626-1352	Sequence 1352, Ap
88	70.5	4.0	644	6	US-10-821-234-1107	Sequence 1107, Ap
89	70.5	4.0	915	7	US-11-144-987-22	Sequence 22, Appl
90	70.5	4.0	1095	7	US-11-113-751-48	Sequence 48, Appl
91	70.5	4.0	1133	7	US-10-995-561-905	Sequence 905, Appl
92	70.5	4.0	1306	6	US-10-995-561-904	Sequence 904, Appl
93	70.5	4.0	1356	6	US-10-995-561-906	Sequence 906, Appl
94	70.5	4.0	1356	6	US-10-995-561-906	Sequence 906, Appl
95	70	4.0	508	7	US-11-093-274-41	Sequence 41, Appl
96	70	4.0	783	7	US-11-192-219-7	Sequence 7, Appl
97	70	4.0	1070	7	US-11-1062	Sequence 4, Appl
98	69.5	3.9	180	6	US-10-467-657-962	Sequence 962, Appl
99	69.5	3.9	298	7	US-11-025-834A-14	Sequence 14, Appl
100	69.5	3.9	1062	7	US-11-137-466-43	Sequence 43, Appl
101	69	3.9	329	6	US-10-793-626-414	Sequence 414, Appl
102	69	3.9	447	7	US-10-467-657-5834	Sequence 5834, Ap
103	69	3.9	484	7	US-11-147-725-2	Sequence 2, Appl
104	69	3.9	751	6	US-10-467-657-1418	Sequence 1418, Ap
105	69	3.9	1161	7	US-11-075-646-8	Sequence 8, Appl
106	69	3.9	1250	7	US-11-137-466-62	Sequence 62, Appl

107	68.5	3.9	972	6	US-10-821-234-1587	Sequence 1587, Ap	183	63.5	3.6	923	7	US-11-192-219-4	Sequence 4, Appli
108	68	3.8	155	7	US-11-194-246-319	Sequence 319, App	184	63.5	3.6	932	7	US-11-188-743-17	Sequence 17, Appl
109	68	3.8	340	6	US-10-467-962B-79	Sequence 79, Appl	185	63.5	3.6	932	7	US-11-188-743-18	Sequence 18, Appl
110	68	3.8	837	6	US-10-995-5561-698	Sequence 698, App	186	63.5	3.6	952	7	US-11-174-166-18	Sequence 18, Appl
111	68	3.8	963	7	US-11-174-166-20	Sequence 20, Appl	187	63.5	3.6	964	7	US-11-089-551A-30	Sequence 30, Appl
112	68	3.8	1174	6	US-10-995-5561-697	Sequence 697, App	188	63.5	3.6	1165	7	US-11-192-219-2	Sequence 2, Appli
113	67.5	3.8	4374	6	US-11-128-572-2	Sequence 2, Appli	189	63.5	3.6	2314	7	US-11-013-759-11	Sequence 11, Appl
114	67	3.8	367	6	US-10-793-626-1102	Sequence 1202, Ap	190	63	3.6	108	7	US-11-054-669-94	Sequence 94, Appl
115	67	3.8	590	7	US-11-131-212-73	Sequence 73, Appl	191	63	3.6	251	7	US-11-054-515-85	Sequence 85, App
116	67	3.8	617	6	US-10-995-5561-890	Sequence 890, App	192	63	3.6	251	7	US-11-054-515-1556	Sequence 1556, Ap
117	67	3.8	740	7	US-11-137-465-61	Sequence 61, Appl	193	63	3.6	251	7	US-11-054-515-1840	Sequence 1840, Ap
118	67	3.8	820	7	US-11-147-047-31	Sequence 31, Appl	194	63	3.6	252	6	US-10-401-386B-38	Sequence 38, Appl
119	67	3.8	1115	7	US-11-113-751-46	Sequence 46, Appl	195	63	3.6	340	6	US-10-999-866-32	Sequence 32, Appl
120	67	3.8	1170	6	US-10-831-997-2	Sequence 2, Appli	196	63	3.6	340	6	US-11-061-821-32	Sequence 32, Appl
121	67	3.8	1170	6	US-10-995-5561-594	Sequence 594, App	197	63	3.6	497	6	US-10-999-866-34	Sequence 34, Appl
122	67	3.8	1170	6	US-10-995-5561-595	Sequence 595, App	198	63	3.6	497	6	US-11-061-821-34	Sequence 34, Appl
123	67	3.8	1170	6	US-10-995-5561-596	Sequence 596, App	199	63	3.6	794	6	US-10-485-517-355	Sequence 355, App
124	67	3.8	1170	7	US-11-046-456-28	Sequence 28, Appl	200	63	3.6	977	7	US-11-093-274-39	Sequence 39, Appl
125	67	3.8	1170	7	US-11-046-644-28	Sequence 28, Appl	201	63	3.6	1126	6	US-10-485-517-748	Sequence 248, App
126	66.5	3.8	193	6	US-10-967-527A-28	Sequence 28, Appl	202	62.5	3.5	130	6	US-10-667-295-159	Sequence 159, App
127	66.5	3.8	199	6	US-10-967-527A-4	Sequence 4, Appli	203	62.5	3.5	176	6	US-10-793-626-1262	Sequence 3262, Ap
128	66.5	3.8	199	6	US-10-996-628-4	Sequence 4, Appli	204	62.5	3.5	346	6	US-10-793-626-2034	Sequence 2034, Ap
129	66.5	3.8	2353	7	US-11-097-728-6	Sequence 6, Appli	205	62.5	3.5	374	7	US-11-084-220-3	Sequence 3, Appli
132	66	3.7	738	6	US-10-995-5561-682	Sequence 692, App	206	62.5	3.5	519	7	US-11-080-991-106	Sequence 106, App
133	66	3.7	738	6	US-10-995-5561-693	Sequence 693, App	207	62.5	3.5	610	6	US-10-793-626-482	Sequence 482, App
134	66	3.7	766	6	US-10-821-234-1691	Sequence 1691, Ap	208	62.5	3.5	648	6	US-10-793-626-568	Sequence 568, App
135	66	3.7	769	6	US-10-485-517-401	Sequence 401, App	209	62.5	3.5	898	7	US-11-166-720-3	Sequence 3, Appli
136	66	3.7	1101	6	US-10-878-556A-107	Sequence 107, App	210	62.5	3.5	909	7	US-11-076-187-4	Sequence 4, Appli
137	66	3.7	1263	6	US-10-485-517-127	Sequence 127, App	211	62.5	3.5	914	7	US-11-108-172-1066	Sequence 1066, Ap
138	65.5	3.7	262	6	US-10-793-626-516	Sequence 516, App	212	62.5	3.5	914	7	US-11-148-108-41	Sequence 41, Appl
139	65.5	3.7	298	7	US-11-138-949-9	Sequence 9, Appli	213	62.5	3.5	958	7	US-11-108-172-1087	Sequence 1087, Ap
140	65.5	3.7	509	6	US-10-793-626-2880	Sequence 2880, Ap	214	62.5	3.5	974	7	US-11-115-086-7	Sequence 7, Appli
141	65.5	3.7	1614	7	US-11-108-528-82	Sequence 82, Appl	215	62	3.5	248	7	US-11-054-515-1254	Sequence 1254, Ap
142	65.5	3.7	1981	6	US-10-374-954-23	Sequence 23, Appl	216	62	3.5	250	7	US-11-054-669-110	Sequence 110, App
143	65.5	3.7	1998	6	US-10-374-954-21	Sequence 21, Appl	217	62	3.5	253	6	US-10-995-5561-555	Sequence 555, App
144	65.5	3.7	2009	6	US-10-401-386B-2	Sequence 2, Appli	218	62	3.5	258	7	US-11-054-515-1239	Sequence 1239, Ap
145	65	3.7	255	6	US-10-401-386B-34	Sequence 34, Appl	219	62	3.5	258	7	US-11-054-515-1245	Sequence 1245, Ap
146	65	3.7	388	7	US-11-082-389-220	Sequence 220, App	220	62	3.5	332	6	US-10-467-657-128	Sequence 128, App
147	65	3.7	487	6	US-10-467-657-2272	Sequence 2272, Ap	221	62	3.5	332	6	US-10-467-657-3310	Sequence 3310, App
149	65	3.7	607	7	US-11-176-863-2	Sequence 2, Appli	222	62	3.5	340	7	US-11-092-353-1	Sequence 1, Appli
150	65	3.7	898	6	US-10-624-932-2	Sequence 2, Appli	223	62	3.5	371	7	US-11-129-143-69	Sequence 69, Appl
151	65	3.7	1058	7	US-11-069-642-105	Sequence 105, App	224	62	3.5	412	6	US-10-467-657-2714	Sequence 2714, Ap
152	64.5	3.6	246	7	US-11-054-515-1634	Sequence 1834, Ap	225	62	3.5	457	7	US-11-194-246-326	Sequence 326, App
153	64.5	3.6	249	7	US-11-054-515-615	Sequence 615, App	226	62	3.5	463	7	US-11-000-463-872	Sequence 872, App
154	64.5	3.6	252	7	US-11-054-515-1376	Sequence 1376, Ap	227	62	3.5	472	6	US-10-650-326B-12	Sequence 12, Appl
155	64.5	3.6	260	7	US-11-054-515-1036	Sequence 1036, Ap	228	62	3.5	472	7	US-11-092-353-3	Sequence 3, Appli
156	64.5	3.6	273	7	US-11-196-475-13	Sequence 13, Appl	229	62	3.5	511	7	US-11-012-762-48	Sequence 48, Appl
157	64.5	3.6	351	7	US-11-000-463-346	Sequence 346, App	230	62	3.5	748	6	US-10-821-234-1479	Sequence 1479, Ap
158	64.5	3.6	643	6	US-10-510-386-8	Sequence 8, Appli	231	62	3.5	970	6	US-10-770-726-86	Sequence 86, Appl
159	64.5	3.6	647	7	US-11-080-991-32	Sequence 32, Appl	232	62	3.5	1346	7	US-11-060-005-2	Sequence 2, Appli
160	64.5	3.6	671	7	US-11-029-003-6	Sequence 6, Appli	233	61.5	3.5	89	6	US-10-467-657-2954	Sequence 2954, Ap
161	64.5	3.6	917	7	US-11-144-987-24	Sequence 24, Appl	234	61.5	3.5	204	7	US-11-128-440-7	Sequence 7, Appli
162	64.5	3.6	917	7	US-11-144-987-26	Sequence 26, Appl	235	61.5	3.5	236	7	US-11-000-463-394	Sequence 394, App
163	64.5	3.6	948	6	US-10-485-517-131	Sequence 131, App	236	61.5	3.5	359	7	US-11-080-091-1	Sequence 1, Appli
164	64	3.6	243	7	US-11-054-515-1533	Sequence 1533, Ap	237	61.5	3.5	359	7	US-11-116-939-15	Sequence 15, Appl
165	64	3.6	279	7	US-11-074-176-100	Sequence 100, App	238	61.5	3.5	378	7	US-11-080-091-3	Sequence 3, Appli
166	64	3.6	297	7	US-11-138-949-6	Sequence 6, Appli	239	61.5	3.5	438	6	US-11-080-091-11	Sequence 11, Appl
167	64	3.6	418	7	US-11-074-176-328	Sequence 328, App	240	61.5	3.5	708	6	US-10-967-527A-16	Sequence 16, Appl
168	64	3.6	567	7	US-11-000-463-400	Sequence 400, App	241	61.5	3.5	708	6	US-10-636-320-2	Sequence 2, Appli
169	64	3.6	1058	6	US-10-821-234-1473	Sequence 1473, Ap	242	61.5	3.5	742	6	US-10-658-986-2	Sequence 2, Appli
170	64	3.6	1058	6	US-10-878-556A-63	Sequence 63, Appl	243	61.5	3.5	748	6	US-10-821-234-888	Sequence 888, App
171	64	3.6	5179	7	US-11-108-172-1068	Sequence 1068, Ap	244	61.5	3.5	977	6	US-10-658-986-4	Sequence 4, Appl
172	63.5	3.6	139	7	US-11-125-837-20	Sequence 20, Appl	245	61.5	3.5	988	6	US-10-995-5561-696	Sequence 696, App
173	63.5	3.6	187	6	US-10-667-295-137	Sequence 137, App	246	61.5	3.5	1458	6	US-11-096-274-2	Sequence 2, Appli
174	63.5	3.6	251	6	US-10-467-657-2306	Sequence 2306, Ap	248	61.5	3.5	1474	6	US-10-995-561-873	Sequence 873, App
175	63.5	3.6	253	6	US-10-793-626-2218	Sequence 2218, Ap	249	61.5	3.5	1615	7	US-11-108-528-80	Sequence 80, Appl
176	63.5	3.6	423	6	US-10-793-626-3160	Sequence 3160, Ap	250	61.5	3.5	1798	7	US-11-080-991-96	Sequence 96, Appl
177	63.5	3.6	478	7	US-11-139-499-8	Sequence 8, Appli	251	61.5	3.5	1818	6	US-10-995-5561-913	Sequence 913, App
178	63.5	3.6	535	6	US-10-793-626-1024	Sequence 1024, Ap	252	61.5	3.5	1818	6	US-10-995-5561-913	Sequence 913, App
179	63.5	3.6	732	6	US-10-518-599-22	Sequence 22, Appl	253	61.5	3.5	1960	7	US-11-077-386-29	Sequence 29, Appl
180	63.5	3.6	750	7	US-11-073-347-1	Sequence 1, Appli	254	61.5	3.5	2061	7	US-11-077-386-27	Sequence 27, Appl
181	63.5	3.6	809	6	US-10-467-657-1106	Sequence 1106, Ap	255	61.5	3.5	2296	6	US-10-995-5561-653	Sequence 653, App
182	63.5	3.6	896	7	US-11-192-219-3	Sequence 3, Appli	256	61.5	3.5	2296	6	US-10-995-5561-653	Sequence 653, App

257	61.5	3.5	2355	6	US-10-995-561-623	Sequence 623, App	330	60	3.4	612	6	US-10-821-234-1101	Sequence 1101, Ap
258	61.5	3.5	2355	6	US-10-995-561-627	Sequence 627, App	331	60	3.4	824	6	US-10-821-234-1108	Sequence 1108, Ap
259	61.5	3.5	2384	6	US-10-821-234-1545	Sequence 1545, Ap	332	60	3.4	1259	6	US-10-995-561-625	Sequence 625, App
260	61.5	3.5	2386	6	US-10-995-561-626	Sequence 626, App	333	60	3.4	1286	6	US-10-995-561-628	Sequence 630, App
261	61	3.4	131	6	US-10-469-561-24	Sequence 24, App	334	60	3.4	1315	6	US-10-995-561-630	Sequence 631, App
262	61	3.4	215	6	US-10-374-954-9	Sequence 9, Appl	335	60	3.4	1341	6	US-10-995-561-621	Sequence 621, App
263	61	3.4	267	7	US-11-186-284-215	Sequence 215, Appl	336	60	3.4	1348	6	US-10-995-561-624	Sequence 624, App
264	61	3.4	288	6	US-10-821-234-1062	Sequence 1062, App	337	59.5	3.4	112	7	US-11-054-186-1	Sequence 1, Appl
265	61	3.4	300	7	US-11-055-822-536	Sequence 536, App	338	59.5	3.4	244	7	US-11-054-515-1069	Sequence 2069, Ap
266	61	3.4	300	7	US-11-055-822-630	Sequence 630, App	339	59.5	3.4	245	7	US-11-054-515-1950	Sequence 1950, Ap
267	61	3.4	304	6	US-10-793-626-1652	Sequence 1652, Ap	340	59.5	3.4	246	7	US-11-128-440-18	Sequence 18, Appl
268	61	3.4	370	7	US-11-129-143-68	Sequence 68, Appl	341	59.5	3.4	248	7	US-11-054-515-921	Sequence 921, App
269	61	3.4	380	7	US-11-090-439-54	Sequence 54, Appl	342	59.5	3.4	248	7	US-11-128-440-19	Sequence 19, App
270	61	3.4	469	6	US-10-510-386-14	Sequence 14, Appl	343	59.5	3.4	249	7	US-11-054-515-126	Sequence 326, App
271	61	3.4	476	7	US-11-139-499-4	Sequence 4, Appl	344	59.5	3.4	250	7	US-11-128-440-20	Sequence 20, Appl
272	61	3.4	510	6	US-10-793-626-2860	Sequence 2860, Ap	345	59.5	3.4	257	7	US-11-054-515-1327	Sequence 1327, Ap
273	61	3.4	649	7	US-11-102-240-132	Sequence 132, App	346	59.5	3.4	259	7	US-11-056-825-7	Sequence 7, Appl
274	61	3.4	711	7	US-11-087-100-18	Sequence 18, Appl	347	59.5	3.4	263	6	US-10-467-657-5102	Sequence 5102, Ap
275	61	3.4	711	7	US-11-087-084-18	Sequence 18, Appl	348	59.5	3.4	273	6	US-10-353-783-55	Sequence 55, App
276	61	3.4	711	7	US-11-087-084-18	Sequence 18, Appl	349	59.5	3.4	293	6	US-10-793-626-2542	Sequence 2542, Ap
277	61	3.4	1142	7	US-11-044-051-73	Sequence 73, Appl	350	59.5	3.4	311	7	US-11-000-463-629	Sequence 629, App
278	61	3.4	1238	7	US-11-078-735-21	Sequence 21, Appl	351	59.5	3.4	353	7	US-11-022-289-9	Sequence 9, Appl
279	61	3.4	2910	7	US-11-087-100-2	Sequence 2, Appl	352	59.5	3.4	354	6	US-10-999-866-31	Sequence 31, Appl
280	61	3.4	2910	7	US-11-087-084-2	Sequence 2, Appl	353	59.5	3.4	354	7	US-11-064-821-31	Sequence 31, Appl
281	61	3.4	2910	7	US-11-087-085-2	Sequence 2, Appl	354	59.5	3.4	359	6	US-10-510-386-190	Sequence 190, App
282	60.5	3.4	62	6	US-10-467-657-5768	Sequence 5768, Ap	355	59.5	3.4	455	6	US-10-847-867-29	Sequence 29, Appl
283	60.5	3.4	108	6	US-10-925-366A-292	Sequence 292, App	356	59.5	3.4	594	6	US-10-997-247-2	Sequence 2, Appl
284	60.5	3.4	139	6	US-10-467-657-2748	Sequence 2748, Ap	357	59.5	3.4	595	6	US-10-995-561-995	Sequence 995, App
285	60.5	3.4	206	7	US-11-128-440-5	Sequence 5, Appl	358	59.5	3.4	662	7	US-11-090-439-9	Sequence 9, Appl
286	60.5	3.4	231	7	US-11-128-440-16	Sequence 16, Appl	359	59.5	3.4	707	7	US-11-069-662-113	Sequence 113, App
287	60.5	3.4	231	7	US-11-128-440-17	Sequence 17, Appl	360	59.5	3.4	737	6	US-10-878-556A-99	Sequence 99, Appl
288	60.5	3.4	276	7	US-11-091-100-16	Sequence 16, Appl	361	59.5	3.4	794	7	US-11-102-476-34	Sequence 34, Appl
289	60.5	3.4	292	6	US-10-821-234-966	Sequence 966, App	362	59.5	3.4	1049	7	US-11-137-465-42	Sequence 42, Appl
290	60.5	3.4	335	7	US-11-182-946-7	Sequence 7, Appl	363	59.5	3.4	1061	7	US-11-000-463-347	Sequence 347, App
291	60.5	3.4	360	6	US-10-467-657-5722	Sequence 5722, Ap	364	59.5	3.4	1091	7	US-11-000-463-348	Sequence 348, App
292	60.5	3.4	429	7	US-11-093-674-37	Sequence 37, Appl	365	59.5	3.4	1141	6	US-10-995-561-1009	Sequence 1009, Ap
293	60.5	3.4	444	7	US-11-172-320-6	Sequence 6, Appl	366	59.5	3.4	1141	6	US-10-995-561-1010	Sequence 1010, Ap
294	60.5	3.4	444	7	US-11-173-969-6	Sequence 6, Appl	367	59.5	3.4	1149	6	US-11-110-082-30	Sequence 30, Appl
295	60.5	3.4	466	6	US-10-467-657-2360	Sequence 2360, Ap	368	59.5	3.4	1405	6	US-10-995-561-1529	Sequence 529, App
296	60.5	3.4	669	7	US-11-076-187-3	Sequence 3, Appl	369	59.5	3.4	1424	7	US-11-102-476-4	Sequence 4, Appl
297	60.5	3.4	747	7	US-11-182-599-2	Sequence 2, Appl	370	59.5	3.4	2214	7	US-11-080-991-94	Sequence 94, Appl
298	60.5	3.4	821	7	US-11-087-227-90	Sequence 90, Appl	371	59	3.3	120	7	US-11-125-837-36	Sequence 36, Appl
299	60.5	3.4	832	7	US-11-108-172-1081	Sequence 1081, Ap	372	59	3.3	193	7	US-11-085-775-4	Sequence 4, Appl
300	60.5	3.4	853	6	US-10-420-192-6	Sequence 6, Appl	373	59	3.3	242	7	US-11-054-515-1830	Sequence 1830, Ap
301	60.5	3.4	858	6	US-10-613-744-6	Sequence 6, Appl	374	59	3.3	245	7	US-11-054-515-165	Sequence 1516, Ap
302	60.5	3.4	1029	6	US-10-821-234-908	Sequence 908, App	375	59	3.3	249	7	US-11-054-515-665	Sequence 665, App
303	60.5	3.4	1187	6	US-10-821-234-955	Sequence 955, App	376	59	3.3	251	7	US-11-054-515-269	Sequence 269, App
304	60.5	3.4	1730	7	US-11-192-967-4	Sequence 4, Appl	377	59	3.3	251	7	US-11-054-515-304	Sequence 304, App
305	60.5	3.4	1730	7	US-11-193-715-4	Sequence 4, Appl	378	59	3.3	256	7	US-11-054-515-1027	Sequence 1027, Ap
306	60	3.4	104	7	US-11-000-463-939	Sequence 939, App	379	59	3.3	258	7	US-11-054-515-865	Sequence 865, App
307	60	3.4	106	7	US-10-463-467	Sequence 467, App	380	59	3.3	258	7	US-11-054-515-1029	Sequence 1029, Ap
308	60	3.4	136	6	US-10-821-234-913	Sequence 913, App	381	59	3.3	259	7	US-11-054-515-1277	Sequence 1277, Ap
309	60	3.4	226	6	US-10-467-657-2428	Sequence 2428, Ap	382	59	3.3	259	7	US-11-054-515-1481	Sequence 1481, Ap
310	60	3.4	228	6	US-10-793-626-3190	Sequence 3190, Ap	383	59	3.3	277	6	US-10-924-074-24	Sequence 24, Appl
311	60	3.4	236	6	US-10-927-641-72	Sequence 72, Appl	384	59	3.3	279	6	US-11-182-946-10	Sequence 10, Appl
312	60	3.4	248	7	US-11-054-515-1037	Sequence 1037, Ap	385	59	3.3	279	6	US-10-467-657-2232	Sequence 2232, Ap
313	60	3.4	249	7	US-11-054-515-739	Sequence 739, App	386	59	3.3	281	7	US-11-055-822-260	Sequence 260, App
314	60	3.4	251	7	US-11-054-515-1229	Sequence 1229, Ap	387	59	3.3	425	6	US-10-995-561-616	Sequence 616, App
315	60	3.4	253	7	US-11-054-515-909	Sequence 909, App	388	59	3.3	455	7	US-11-182-946-3	Sequence 3, Appl
316	60	3.4	253	7	US-11-054-515-1167	Sequence 1167, Ap	389	59	3.3	476	7	US-11-008-727-22	Sequence 22, Appl
317	60	3.4	253	7	US-11-054-515-1235	Sequence 1235, Ap	390	59	3.3	493	6	US-10-995-561-611	Sequence 611, App
318	60	3.4	253	7	US-11-054-515-1375	Sequence 1375, Ap	391	59	3.3	532	6	US-10-857-780-18	Sequence 18, Appl
319	60	3.4	254	7	US-11-054-515-844	Sequence 844, App	392	59	3.3	532	6	US-10-995-561-997	Sequence 897, App
320	60	3.4	257	7	US-11-054-515-1710	Sequence 1710, Ap	393	59	3.3	532	7	US-11-104-812-2	Sequence 2, Appl
321	60	3.4	271	6	US-10-793-626-1156	Sequence 1156, Ap	394	59	3.3	532	7	US-11-105-279-2	Sequence 2, Appl
322	60	3.4	285	6	US-10-821-234-1304	Sequence 1304, Ap	395	59	3.3	592	7	US-11-135-855-34	Sequence 24, Appl
323	60	3.4	286	6	US-10-793-626-2192	Sequence 2192, Ap	396	59	3.3	832	6	US-10-512-109-39	Sequence 29, Appl
324	60	3.4	336	6	US-11-113-424-83	Sequence 83, Appl	397	59	3.3	1158	7	US-11-075-646-6	Sequence 6, Appl
325	60	3.4	380	7	US-11-090-439-52	Sequence 52, Appl	399	59	3.3	1179	7	US-11-097-125-1	Sequence 1, Appl
326	60	3.4	421	6	US-10-793-626-144	Sequence 144, App	400	59	3.3	1196	6	US-10-995-561-921	Sequence 921, App
327	60	3.4	463	7	US-11-102-240-86	Sequence 86, Appl	401	59	3.3	1436	6	US-10-995-561-631	Sequence 531, App
328	60	3.4	502	6	US-10-793-626-3136	Sequence 3136, Ap	402	59	3.3	1532	6	US-10-821-234-914	Sequence 914, App
329	60	3.4	610	6	US-10-606-302-1	Sequence 1, Appl	403	59	3.3	1857	7	US-11-057-058-60	Sequence 60, Appl

404	59	3.3	1857	7	US-11-057-058-61	Sequence 61, Appl	479	57.5	3.2	244	6	US-10-793-626-2780	Sequence 2780, Ap
405	58.5	3.3	135	7	US-11-012-353-81	Sequence 81, Appl	480	57.5	3.2	249	7	US-11-054-515-340	Sequence 340, App
406	58.5	3.3	135	7	US-11-012-353-85	Sequence 85, Appl	481	57.5	3.2	249	7	US-11-054-515-957	Sequence 957, App
407	58.5	3.3	166	6	US-10-793-626-1978	Sequence 1978, Ap	482	57.5	3.2	253	7	US-11-054-515-1964	Sequence 1964, Ap
408	58.5	3.3	175	6	US-10-967-527A-7	Sequence 7, Appl	483	57.5	3.2	256	7	US-11-054-515-1026	Sequence 1026, Ap
409	58.5	3.3	179	6	US-10-793-626-1092	Sequence 1092, Ap	484	57.5	3.2	256	7	US-11-054-515-1600	Sequence 1600, Ap
410	58.5	3.3	255	7	US-11-054-515-1532	Sequence 1532, Ap	485	57.5	3.2	308	6	US-10-467-657-1192	Sequence 1192, Ap
411	58.5	3.3	245	7	US-11-054-515-1642	Sequence 1642, Ap	486	57.5	3.2	344	7	US-11-108-172-1085	Sequence 1085, Ap
412	58.5	3.3	276	7	US-11-029-003-18	Sequence 18, Appl	487	57.5	3.2	379	7	US-11-129-143-66	Sequence 66, Appl
413	58.5	3.3	289	6	US-10-987-663-2	Sequence 2, Appl	488	57.5	3.2	380	6	US-10-485-517-89	Sequence 289, App
414	58.5	3.3	290	7	US-11-113-424-78	Sequence 78, Appl	489	57.5	3.2	384	7	US-11-000-463-805	Sequence 804, App
415	58.5	3.3	305	7	US-11-080-031-2	Sequence 21, Appl	490	57.5	3.2	384	7	US-11-000-463-806	Sequence 806, App
416	58.5	3.3	311	7	US-11-000-463-817	Sequence 817, App	491	57.5	3.2	384	7	US-11-000-463-807	Sequence 807, App
417	58.5	3.3	326	6	US-10-485-517-306	Sequence 306, Appl	492	57.5	3.2	423	7	US-11-000-463-375	Sequence 375, App
418	58.5	3.3	349	6	US-10-515-419-2	Sequence 2, Appl	493	57.5	3.2	451	7	US-11-120-338-25	Sequence 25, Appl
419	58.5	3.3	352	6	US-10-515-419-3	Sequence 3, Appl	494	57.5	3.2	452	7	US-11-120-338-17	Sequence 17, Appl
420	58.5	3.3	359	6	US-10-995-561-712	Sequence 712, App	495	57.5	3.2	476	7	US-11-139-499-12	Sequence 12, Appl
421	58.5	3.3	359	6	US-10-995-561-716	Sequence 716, App	496	57.5	3.2	476	6	US-10-984-376-1	Sequence 1, Appl
422	58.5	3.3	388	6	US-10-995-561-713	Sequence 713, App	497	57.5	3.2	488	6	US-10-984-376-4	Sequence 4, Appl
423	58.5	3.3	391	7	US-11-056-727-119	Sequence 119, App	498	57.5	3.2	567	6	US-10-793-626-184	Sequence 3184, Ap
424	58.5	3.3	391	7	US-11-056-727-121	Sequence 121, App	501	57.5	3.2	736	7	US-11-053-100-45	Sequence 45, Appl
425	58.5	3.3	391	7	US-11-058-727-123	Sequence 123, App	503	57.5	3.2	897	6	US-10-821-234-1523	Sequence 1523, Ap
426	58.5	3.3	391	7	US-11-108-389-119	Sequence 119, App	504	57.5	3.2	934	7	US-11-108-664-19	Sequence 19, Appl
427	58.5	3.3	391	7	US-11-108-389-121	Sequence 121, App	505	57.5	3.2	1094	6	US-10-821-234-1097	Sequence 1097, Ap
428	58.5	3.3	391	7	US-11-108-389-123	Sequence 123, App	506	57.5	3.2	1122	7	US-11-191-374-3	Sequence 3, Appl
429	58.5	3.3	394	6	US-10-995-561-714	Sequence 714, App	507	57.5	3.2	1122	7	US-11-191-375-3	Sequence 3, Appl
430	58.5	3.3	394	6	US-10-995-561-715	Sequence 715, App	508	57.5	3.2	1167	6	US-11-053-100-46	Sequence 46, Appl
431	58.5	3.3	455	6	US-10-847-867-1	Sequence 1, Appl	509	57.5	3.2	1186	7	US-11-053-100-10	Sequence 10, Appl
432	58.5	3.3	479	7	US-11-194-246-310	Sequence 310, App	510	57.5	3.2	2376	7	US-11-096-051-2	Sequence 2, Appl
433	58.5	3.3	480	6	US-10-847-867-3	Sequence 3, Appl	511	57.5	3.2	2715	7	US-11-096-051-2	Sequence 2, Appl
434	58.5	3.3	500	7	US-11-102-240-84	Sequence 84, Appl	512	57.5	3.2	2715	7	US-11-113-424-51	Sequence 51, Appl
435	58.5	3.3	636	6	US-10-485-517-170	Sequence 170, App	513	57.5	3.2	2715	7	US-11-113-424-51	Sequence 51, Appl
437	58.5	3.3	629	7	US-11-078-735-19	Sequence 19, Appl	514	57.5	3.2	2721	7	US-11-096-051-8	Sequence 8, Appl
438	58.5	3.3	729	7	US-11-099-691-3	Sequence 3, Appl	515	57.5	3.2	2725	7	US-11-096-051-8	Sequence 8, Appl
439	58.5	3.3	995	7	US-11-113-424-62	Sequence 62, Appl	516	57.5	3.2	4868	7	US-11-044-111-24	Sequence 24, Appl
440	58.5	3.3	1148	7	US-11-110-082-29	Sequence 29, Appl	517	57	3.2	77	7	US-11-113-424-189	Sequence 189, App
441	58.5	3.3	5405	7	US-11-108-172-1116	Sequence 116, Ap	518	57	3.2	116	6	US-10-793-626-1680	Sequence 1680, App
442	58	3.3	177	6	US-10-999-866-61	Sequence 61, Appl	519	57	3.2	241	7	US-11-054-515-1888	Sequence 1888, Ap
443	58	3.3	199	6	US-10-967-527A-25	Sequence 25, Appl	520	57	3.2	244	7	US-11-054-515-1491	Sequence 1491, Ap
444	58	3.3	205	6	US-10-995-561-1028	Sequence 1028, Ap	521	57	3.2	244	7	US-11-054-515-1582	Sequence 1582, Ap
445	58	3.3	205	6	US-10-995-561-1029	Sequence 1029, Ap	522	57	3.2	250	7	US-11-054-515-1540	Sequence 1540, Ap
446	58	3.3	233	6	US-10-858-730-234	Sequence 234, App	523	57	3.2	251	7	US-11-054-515-165	Sequence 165, App
447	58	3.3	233	6	US-11-055-822-54	Sequence 54, Appl	524	57	3.2	254	7	US-11-054-515-1469	Sequence 1469, App
448	58	3.3	251	7	US-11-054-515-196	Sequence 196, App	525	57	3.2	256	7	US-11-054-515-1258	Sequence 1258, Ap
449	58	3.3	253	7	US-11-054-515-1125	Sequence 1125, Ap	526	57	3.2	257	7	US-11-054-515-1028	Sequence 1028, Ap
450	58	3.3	257	7	US-11-054-515-1240	Sequence 1240, Ap	527	57	3.2	257	7	US-11-054-515-1283	Sequence 1283, Ap
451	58	3.3	257	7	US-11-054-515-1252	Sequence 1252, Ap	528	57	3.2	258	7	US-11-054-515-1265	Sequence 1265, Ap
452	58	3.3	258	7	US-11-054-515-1243	Sequence 1243, Ap	529	57	3.2	258	7	US-11-054-515-1266	Sequence 1266, Ap
453	58	3.3	258	7	US-11-054-515-1255	Sequence 1255, Ap	530	57	3.2	258	7	US-11-054-515-1274	Sequence 1274, Ap
454	58	3.3	258	7	US-11-054-515-1276	Sequence 1276, Ap	531	57	3.2	258	7	US-11-054-515-1365	Sequence 1365, Ap
455	58	3.3	259	7	US-11-054-515-1034	Sequence 1034, Ap	532	57	3.2	259	7	US-11-054-515-1032	Sequence 1032, Ap
456	58	3.3	259	7	US-11-054-515-1350	Sequence 1043, Ap	533	57	3.2	259	7	US-11-054-515-1041	Sequence 1041, Ap
457	58	3.3	259	7	US-11-054-515-147	Sequence 1247, Ap	534	57	3.2	286	7	US-11-179-977-9	Sequence 9, Appl
458	58	3.3	259	7	US-11-054-515-1247	Sequence 1247, Ap	535	57	3.2	324	6	US-10-793-626-640	Sequence 640, App
459	58	3.3	259	7	US-11-054-515-1263	Sequence 1263, App	536	57	3.2	367	6	US-10-793-626-2876	Sequence 2876, App
460	58	3.3	259	7	US-11-054-515-1270	Sequence 1270, Ap	537	57	3.2	447	7	US-11-196-476-162	Sequence 162, App
461	58	3.3	260	7	US-11-054-515-1275	Sequence 1275, Ap	538	57	3.2	451	6	US-10-923-337-9	Sequence 9, Appl
462	58	3.3	260	7	US-11-054-515-1350	Sequence 1282, Ap	539	57	3.2	451	6	US-10-923-337-9	Sequence 9, Appl
463	58	3.3	261	7	US-11-054-515-1503	Sequence 1503, Ap	540	57	3.2	456	6	US-10-1467-657-624	Sequence 624, App
464	58	3.3	263	7	US-11-116-939-10	Sequence 10, Appl	541	57	3.2	589	7	US-11-174-150-28	Sequence 28, Appl
465	58	3.3	293	7	US-11-116-939-12	Sequence 12, Appl	542	57	3.2	589	7	US-11-074-176-238	Sequence 238, App
466	58	3.3	324	6	US-10-858-730-92	Sequence 92, Appl	543	57	3.2	545	57	US-10-821-234-1358	Sequence 1358, Ap
467	58	3.3	412	7	US-11-116-939-19	Sequence 19, Appl	544	57	3.2	545	57	US-11-113-424-82	Sequence 82, Appl
468	58	3.3	451	6	US-10-793-626-210	Sequence 210, App	545	57	3.2	545	57	US-10-467-657-1408	Sequence 1408, Ap
469	58	3.3	824	7	US-11-116-939-11	Sequence 11, Appl	546	57	3.2	589	6	US-10-467-657-624	Sequence 624, App
470	58	3.3	860	7	US-11-022-562-217	Sequence 217, App	547	57	3.2	718	7	US-11-174-150-28	Sequence 28, Appl
471	58	3.3	1060	7	US-11-090-739-120	Sequence 120, App	548	57	3.2	723	7	US-11-074-176-18	Sequence 18, Appl
472	58	3.3	1271	6	US-10-770-726-46	Sequence 46, Appl	549	57	3.2	801	7	US-11-174-150-29	Sequence 29, Appl
473	58	3.3	2644	6	US-10-770-726-45	Sequence 45, Appl	550	57	3.2	876	7	US-11-077-550-128	Sequence 128, App
474	58	3.3	135	7	US-11-012-353-77	Sequence 77, Appl	551	57	3.2	877	7	US-11-077-550-126	Sequence 126, App
475	57.5	3.2	135	6	US-10-467-657-4246	Sequence 4246, Ap	552	57	3.2	877	7	US-11-077-550-130	Sequence 130, App
476	57.5	3.2	145	6	US-10-793-626-826	Sequence 826, App	553	57	3.2	881	7	US-11-077-550-124	Sequence 124, App
477	57.5	3.2	182	6	US-11-170-653-60	Sequence 60, Appl	554	57	3.2	902	7	US-11-077-550-132	Sequence 132, App
478	57.5	3.2	217	7			555	57	3.2				

556	57	3.2	912	7	US-11-077-550-116	Sequence 116, App	633	56	3.2	291	6	US-10-821-234-1025	Sequence 1025, App
557	57	3.2	914	7	US-11-077-550-120	Sequence 120, App	634	56	3.2	331	6	US-10-821-234-1650	Sequence 1650, App
558	57	3.2	944	7	US-11-077-550-122	Sequence 122, App	635	56	3.2	351	6	US-11-095-624-5	Sequence 5, App11
559	57	3.2	950	7	US-11-077-550-118	Sequence 118, App	636	56	3.2	357	6	US-10-793-626-1360	Sequence 1360, App
560	57	3.2	1073	6	US-10-467-657-5230	Sequence 5230, App	637	56	3.2	447	6	US-10-884-730-379	Sequence 379, App
561	57	3.2	1225	7	US-11-102-476-2	Sequence 2, App11	638	56	3.2	459	6	US-10-793-626-2462	Sequence 2462, App
562	57	3.2	1254	6	US-10-528-031-47	Sequence 47, App1	639	56	3.2	473	6	US-10-793-626-20	Sequence 60, App1
563	57	3.2	2314	7	US-11-097-728-2	Sequence 2, App11	640	56	3.2	495	6	US-10-613-744-5	Sequence 5, App11
564	57	3.2	3056	7	US-11-109-156-20	Sequence 20, App1	641	56	3.2	548	7	US-11-022-289-3	Sequence 3, App11
565	57	3.2	100	7	US-11-054-669-75	Sequence 75, App1	642	56	3.2	652	6	US-10-821-234-1016	Sequence 1016, App
566	56.5	3.2	100	7	US-11-084-554-107	Sequence 107, App	643	56	3.2	654	7	US-11-046-668-4	Sequence 4, App1
567	56.5	3.2	100	7	US-11-084-554-118	Sequence 118, App	644	56	3.2	683	7	US-11-046-668-2	Sequence 2, App11
568	56.5	3.2	112	7	US-11-012-353-58	Sequence 58, App1	646	56	3.2	685	7	US-11-089-551A-2	Sequence 2, App11
569	56.5	3.2	158	6	US-10-467-657-260	Sequence 260, App	647	56	3.2	734	7	US-11-093-274-40	Sequence 19, App
570	56.5	3.2	158	6	US-10-467-657-3592	Sequence 3592, App	648	56	3.2	805	6	US-10-485-517-198	Sequence 161, App
571	56.5	3.2	158	6	US-10-467-657-6438	Sequence 6438, App	649	56	3.2	814	6	US-10-878-556A-161	Sequence 161, App
572	56.5	3.2	160	6	US-10-467-657-5090	Sequence 5090, App	650	56	3.2	857	6	US-10-613-744-11	Sequence 11, App1
573	56.5	3.2	168	6	US-11-108-172-198	Sequence 198, App	651	56	3.2	859	7	US-11-000-463-423	Sequence 423, App
574	56.5	3.2	216	6	US-10-467-657-482	Sequence 482, App	652	56	3.2	859	7	US-11-000-463-895	Sequence 895, App
575	56.5	3.2	236	7	US-11-144-248-51	Sequence 51, App1	653	56	3.2	1151	7	US-11-113-751-36	Sequence 36, App1
576	56.5	3.2	236	7	US-11-054-515-1884	Sequence 1884, App	654	56	3.2	1159	7	US-11-194-246-439	Sequence 439, App
577	56.5	3.2	242	7	US-11-054-515-2084	Sequence 2084, App	655	56	3.2	1218	7	US-11-078-735-20	Sequence 20, App1
578	56.5	3.2	248	7	US-11-054-515-1988	Sequence 1988, App	656	56	3.2	2764	6	US-10-995-561-691	Sequence 691, App
579	56.5	3.2	250	7	US-11-054-515-1804	Sequence 1804, App	657	56	3.2	2813	6	US-10-995-561-688	Sequence 688, App
580	56.5	3.2	250	7	US-11-056-825-2	Sequence 2, App11	658	56	3.2	2919	6	US-10-821-234-1133	Sequence 1133, App
581	56.5	3.2	273	6	US-10-353-783-54	Sequence 54, App1	659	55.5	3.1	100	7	US-11-054-669-81	Sequence 81, App1
582	56.5	3.2	279	6	US-10-793-626-870	Sequence 870, App	660	55.5	3.1	100	7	US-11-084-554-112	Sequence 112, App1
583	56.5	3.2	305	7	US-11-080-091-13	Sequence 13, App1	661	55.5	3.1	112	7	US-11-012-353-60	Sequence 60, App1
586	56.5	3.2	334	7	US-11-140-417-8	Sequence 8, App11	662	55.5	3.1	125	6	US-10-789-470-6	Sequence 6, App11
587	56.5	3.2	335	6	US-10-995-561-704	Sequence 704, App	663	55.5	3.1	216	7	US-11-128-440-13	Sequence 13, App1
588	56.5	3.2	335	7	US-11-141-947-2	Sequence 2, App11	664	55.5	3.1	244	7	US-11-054-515-1568	Sequence 1568, App
589	56.5	3.2	344	7	US-11-083-800-10	Sequence 10, App1	665	55.5	3.1	248	7	US-11-054-515-2094	Sequence 2094, App
590	56.5	3.2	348	6	US-10-467-657-6602	Sequence 6602, App	666	55.5	3.1	250	7	US-11-054-515-1439	Sequence 1439, App
591	56.5	3.2	348	6	US-10-467-657-7662	Sequence 7662, App	667	55.5	3.1	250	7	US-11-054-515-1581	Sequence 1581, App
594	56.5	3.2	451	7	US-11-120-338-22	Sequence 22, App	668	55.5	3.1	252	7	US-11-054-515-1646	Sequence 1646, App
595	56.5	3.2	452	7	US-11-120-338-14	Sequence 14, App1	669	55.5	3.1	273	6	US-10-353-783-42	Sequence 42, App1
596	56.5	3.2	458	7	US-11-016-503-16	Sequence 16, App1	670	55.5	3.1	275	6	US-10-995-561-735	Sequence 735, App
597	56.5	3.2	458	7	US-11-089-803-6	Sequence 6, App11	671	55.5	3.1	287	6	US-10-995-561-730	Sequence 730, App
598	56.5	3.2	467	6	US-10-467-657-2612	Sequence 2612, App	672	55.5	3.1	295	6	US-10-987-663-30	Sequence 30, App1
599	56.5	3.2	471	6	US-10-858-730-125	Sequence 125, App	673	55.5	3.1	305	7	US-11-000-463-391	Sequence 391, App
600	56.5	3.2	485	6	US-10-508-263-22	Sequence 22, App1	674	55.5	3.1	305	7	US-11-000-463-863	Sequence 863, App
601	56.5	3.2	496	7	US-11-110-082-31	Sequence 31, App1	675	55.5	3.1	325	6	US-10-793-626-598	Sequence 598, App
602	56.5	3.2	509	7	US-11-008-727-16	Sequence 16, App1	676	55.5	3.1	330	6	US-10-793-626-1330	Sequence 1330, App
603	56.5	3.2	524	6	US-10-467-657-8122	Sequence 8122, App	677	55.5	3.1	330	7	US-11-022-289-1	Sequence 1, App1
604	56.5	3.2	581	7	US-11-045-802-30	Sequence 30, App1	678	55.5	3.1	330	7	US-11-022-289-11	Sequence 11, App1
605	56.5	3.2	687	7	US-11-117-169-6	Sequence 6, App11	679	55.5	3.1	330	7	US-11-075-351-1	Sequence 1, App1
606	56.5	3.2	727	7	US-11-117-169-8	Sequence 8, App11	680	55.5	3.1	330	7	US-11-165-141-15	Sequence 15, App1
607	56.5	3.2	745	6	US-10-995-561-659	Sequence 659, App	681	55.5	3.1	335	7	US-11-024-251-35	Sequence 35, App1
608	56.5	3.2	745	7	US-11-109-156-14	Sequence 14, App1	682	55.5	3.1	339	6	US-10-999-866-35	Sequence 35, App1
609	56.5	3.2	879	7	US-11-022-562-340	Sequence 340, App	683	55.5	3.1	339	7	US-11-061-821-35	Sequence 35, App1
610	56.5	3.2	932	7	US-11-071-581-1	Sequence 1, App11	684	55.5	3.1	365	6	US-10-875-716-9	Sequence 9, App11
611	56.5	3.2	1116	7	US-11-113-751-34	Sequence 34, App1	685	55.5	3.1	367	7	US-11-117-169-12	Sequence 12, App1
612	56.5	3.2	1138	7	US-11-012-762-28	Sequence 28, App1	686	55.5	3.1	370	7	US-11-055-822-180	Sequence 180, App
613	56.5	3.2	1403	7	US-11-091-928-1	Sequence 1, App11	687	55.5	3.1	370	7	US-11-055-822-190	Sequence 190, App
614	56.5	3.2	1476	6	US-10-647-956A-4	Sequence 4, App1	688	55.5	3.1	377	6	US-10-858-730-286	Sequence 286, App
615	56.5	3.2	1476	6	US-11-144-248-20	Sequence 20, App1	689	55.5	3.1	377	7	US-11-055-822-178	Sequence 178, App
616	56	3.2	216	7	US-11-186-284-217	Sequence 217, App	690	55.5	3.1	377	7	US-11-055-822-188	Sequence 188, App
617	56	3.2	217	7	US-11-188-281-18	Sequence 18, App1	691	55.5	3.1	379	6	US-10-858-730-212	Sequence 212, App
618	56	3.2	230	7	US-11-188-281-4	Sequence 4, App11	692	55.5	3.1	402	7	US-11-024-251-31	Sequence 31, App1
619	56	3.2	232	6	US-10-467-657-3352	Sequence 3352, App	693	55.5	3.1	421	6	US-10-763-712A-2	Sequence 2, App11
620	56	3.2	237	7	US-11-083-055-2	Sequence 2, App11	694	55.5	3.1	421	6	US-10-763-712A-103	Sequence 103, App
621	56	3.2	244	7	US-11-054-515-1498	Sequence 1498, App	695	55.5	3.1	438	7	US-11-074-176-152	Sequence 15, App1
622	56	3.2	248	7	US-11-054-515-1267	Sequence 1267, App	696	55.5	3.1	442	7	US-11-120-338-15	Sequence 15, App1
623	56	3.2	249	7	US-11-054-515-604	Sequence 604, App	697	55.5	3.1	454	7	US-11-136-475-160	Sequence 160, App
624	56	3.2	249	7	US-11-054-515-628	Sequence 628, App	698	55.5	3.1	474	7	US-11-000-463-384	Sequence 384, App
625	56	3.2	249	7	US-11-054-515-783	Sequence 783, App	699	55.5	3.1	477	7	US-11-000-463-395	Sequence 395, App
626	56	3.2	250	7	US-11-054-515-1022	Sequence 1022, App	701	55.5	3.1	531	6	US-10-485-517-776	Sequence 276, App
627	56	3.2	251	7	US-11-054-515-187	Sequence 187, App	702	55.5	3.1	551	7	US-11-022-289-7	Sequence 7, App11
628	56	3.2	265	6	US-10-793-626-2422	Sequence 2422, App	703	55.5	3.1	551	7	US-11-022-289-8	Sequence 8, App11
629	56	3.2	266	7	US-11-054-515-3229	Sequence 3229, App	704	55.5	3.1	557	7	US-11-022-289-2	Sequence 2, App11
630	56	3.2	271	7	US-11-089-551A-17	Sequence 17, App1	705	55.5	3.1	557	7	US-11-022-289-5	Sequence 5, App11
631	56	3.2	286	6	US-10-793-626-1020	Sequence 1020, App	706	55.5	3.1	557	7	US-11-022-289-5	Sequence 5, App11
632	56	3.2	286	7	US-11-194-246-320	Sequence 320, App	707	55.5	3.1	557	7	US-11-022-289-6	Sequence 6, App11

708	55.5	3.1	564	7	US-11-022-289-10	Sequence 10, Appl	782	55	3.1	400	6	US-10-793-626-1056	Sequence 1056, Ap
709	55.5	3.1	579	7	US-11-174-186-41	Sequence 41, Appl	783	55	3.1	407	6	US-10-793-626-886	Sequence 886, Ap
710	55.5	3.1	656	6	US-10-995-561-871	Sequence 871, App	784	55	3.1	430	7	US-11-016-503-17	Sequence 17, Appl
711	55.5	3.1	664	6	US-10-485-517-308	Sequence 308, App	785	55	3.1	430	7	US-11-194-246-138	Sequence 438, Ap
712	55.5	3.1	679	6	US-10-995-561-872	Sequence 872, App	786	55	3.1	445	6	US-10-793-626-1294	Sequence 1294, Ap
713	55.5	3.1	708	7	US-11-174-150-25	Sequence 25, Appl	787	55	3.1	458	7	US-11-016-503-12	Sequence 12, Appl
714	55.5	3.1	715	7	US-11-089-551A-47	Sequence 47, Appl	788	55	3.1	458	7	US-11-089-803-2	Sequence 2, Appl
716	55.5	3.1	736	7	US-11-174-150-26	Sequence 26, Appl	789	55	3.1	470	7	US-11-008-727-20	Sequence 20, Appl
717	55.5	3.1	963	6	US-10-995-561-973	Sequence 923, App	790	55	3.1	546	7	US-11-143-980-38	Sequence 38, Appl
718	55.5	3.1	1066	7	US-11-055-822-370	Sequence 370, App	791	55	3.1	550	7	US-11-184-380-14	Sequence 14, Appl
719	55.5	3.1	1066	7	US-11-055-822-1002	Sequence 1002, Ap	792	55	3.1	581	6	US-10-793-626-28	Sequence 28, Appl
720	55.5	3.1	1092	6	US-10-821-234-999	Sequence 999, App	793	55	3.1	581	6	US-10-793-626-1080	Sequence 1080, Ap
721	55.5	3.1	1113	7	US-11-055-822-368	Sequence 368, App	794	55	3.1	592	6	US-10-995-561-994	Sequence 994, App
722	55.5	3.1	1113	7	US-11-055-822-1000	Sequence 1000, Ap	795	55	3.1	615	6	US-10-995-561-940	Sequence 940, App
723	55.5	3.1	1141	6	US-10-601-368-24	Sequence 24, Appl	796	55	3.1	659	6	US-10-995-561-573	Sequence 573, App
724	55.5	3.1	1158	6	US-10-858-730-70	Sequence 70, Appl	797	55	3.1	662	6	US-10-995-561-943	Sequence 943, App
725	55.5	3.1	1166	6	US-10-601-368-22	Sequence 22, Appl	798	55	3.1	701	6	US-10-995-561-575	Sequence 575, App
726	55.5	3.1	1188	6	US-10-601-368-21	Sequence 21, Appl	799	55	3.1	702	6	US-10-995-561-942	Sequence 942, App
727	55.5	3.1	1410	6	US-10-878-536A-136	Sequence 136, App	801	55	3.1	716	6	US-11-147-047-52	Sequence 52, Appl
728	55.5	3.1	1538	6	US-10-995-561-772	Sequence 772, App	802	55	3.1	751	6	US-10-995-561-578	Sequence 578, App
729	55.5	3.1	1586	6	US-10-821-234-901	Sequence 901, App	803	55	3.1	752	6	US-10-793-626-1036	Sequence 1036, Ap
730	55.5	3.1	1889	7	US-11-102-476-46	Sequence 46, Appl	804	55	3.1	752	6	US-10-995-561-941	Sequence 941, App
731	55.5	3.1	1970	6	US-10-821-234-1641	Sequence 1641, Ap	805	55	3.1	808	6	US-10-995-561-574	Sequence 574, App
732	55.5	3.1	3002	6	US-10-821-234-916	Sequence 916, App	806	55	3.1	808	7	US-11-105-268-53	Sequence 53, Appl
733	55.5	3.1	5335	6	US-10-995-561-777	Sequence 777, App	807	55	3.1	808	7	US-11-110-082-38	Sequence 38, Appl
734	55.5	3.1	5406	6	US-10-995-561-774	Sequence 774, App	808	55	3.1	834	6	US-10-645-441-9	Sequence 9, Appl
735	55.5	3.1	5415	6	US-10-995-561-779	Sequence 779, App	809	55	3.1	848	6	US-10-763-712A-48	Sequence 48, Appl
736	55.5	3.1	5464	6	US-10-995-561-775	Sequence 775, App	810	55	3.1	881	7	US-11-191-374-12	Sequence 12, Appl
737	55.5	3.1	5935	6	US-10-995-561-776	Sequence 776, App	811	55	3.1	881	7	US-11-191-375-12	Sequence 12, Appl
738	55	3.1	97	7	US-11-144-248-44	Sequence 44, Appl	812	55	3.1	897	7	US-11-137-465-35	Sequence 35, Appl
739	55	3.1	97	7	US-11-054-669-51	Sequence 51, Appl	813	55	3.1	993	7	US-11-137-465-36	Sequence 36, Appl
740	55	3.1	97	7	US-11-084-554-53	Sequence 53, Appl	814	55	3.1	1005	7	US-11-113-424-63	Sequence 63, Appl
741	55	3.1	117	7	US-11-012-353-162	Sequence 57, Appl	815	55	3.1	1137	6	US-10-499-715-4	Sequence 4, Appl
742	55	3.1	125	7	US-11-096-074-57	Sequence 57, Appl	816	55	3.1	1162	6	US-10-451-375-3	Sequence 3, Appl
743	55	3.1	168	6	US-10-793-626-2068	Sequence 2068, Ap	817	55	3.1	1663	6	US-10-982-545-6	Sequence 6, Appl
744	55	3.1	195	6	US-10-995-561-553	Sequence 563, App	818	55	3.1	2323	6	US-10-793-626-760	Sequence 760, App
745	55	3.1	217	6	US-10-793-626-502	Sequence 502, App	819	55	3.1	3375	7	US-11-044-111-23	Sequence 23, Appl
746	55	3.1	233	6	US-10-467-657-12	Sequence 12, Appl	820	55	3.1	108	6	US-10-925-366A-173	Sequence 173, App
747	55	3.1	233	6	US-10-467-657-5530	Sequence 5530, Ap	821	55	3.1	171	6	US-10-793-626-510	Sequence 510, App
748	55	3.1	236	7	US-11-008-727-4	Sequence 4, Appl	822	55	3.1	171	6	US-10-793-626-1546	Sequence 1546, Ap
749	55	3.1	237	6	US-10-884-730-356	Sequence 356, App	823	55	3.1	204	7	US-11-109-156-26	Sequence 26, Appl
750	55	3.1	240	6	US-10-793-626-1972	Sequence 1972, App	825	55	3.1	248	7	US-11-054-515-2000	Sequence 2000, Ap
751	55	3.1	241	7	US-11-054-515-1887	Sequence 1887, App	826	55	3.1	249	7	US-11-054-515-327	Sequence 327, App
752	55	3.1	241	7	US-11-054-515-1901	Sequence 1901, Ap	827	55	3.1	249	7	US-11-054-515-425	Sequence 425, App
753	55	3.1	242	7	US-11-054-515-1844	Sequence 1844, Ap	828	55	3.1	249	7	US-11-054-515-495	Sequence 495, App
754	55	3.1	243	7	US-11-054-515-1515	Sequence 1515, Ap	829	55	3.1	249	7	US-11-054-515-586	Sequence 586, App
755	55	3.1	243	7	US-11-054-515-1863	Sequence 1863, Ap	830	55	3.1	249	7	US-11-054-515-586	Sequence 586, App
756	55	3.1	244	7	US-11-054-515-1124	Sequence 1124, Ap	831	55	3.1	249	7	US-11-054-515-766	Sequence 766, App
757	55	3.1	244	7	US-11-054-515-1569	Sequence 1569, App	832	55	3.1	249	7	US-11-054-515-766	Sequence 766, App
758	55	3.1	244	7	US-11-054-515-1845	Sequence 1845, Ap	833	55	3.1	250	6	US-10-793-626-310	Sequence 310, App
759	55	3.1	245	7	US-11-054-515-1521	Sequence 1521, Ap	834	55	3.1	250	6	US-10-793-626-2174	Sequence 2174, Ap
760	55	3.1	245	7	US-11-054-515-1523	Sequence 1523, Ap	835	55	3.1	251	6	US-11-054-515-1833	Sequence 1833, Ap
761	55	3.1	245	7	US-11-054-515-1528	Sequence 1528, Ap	836	55	3.1	251	7	US-11-054-515-1833	Sequence 1833, Ap
762	55	3.1	245	7	US-11-054-515-1447	Sequence 1547, App	837	55	3.1	252	7	US-11-054-515-1475	Sequence 1475, Ap
763	55	3.1	245	7	US-11-054-515-1530	Sequence 1530, App	838	55	3.1	252	7	US-11-054-515-1505	Sequence 1505, App
764	55	3.1	245	7	US-11-054-515-1839	Sequence 1839, App	839	55	3.1	254	7	US-11-054-515-1699	Sequence 1699, App
765	55	3.1	245	7	US-11-054-515-1860	Sequence 1860, App	840	55	3.1	263	7	US-11-054-515-2081	Sequence 2081, Ap
766	55	3.1	247	7	US-11-054-515-1112	Sequence 1112, App	841	55	3.1	273	7	US-11-113-424-74	Sequence 74, Appl
767	55	3.1	247	7	US-11-054-515-1492	Sequence 1492, App	842	55	3.1	282	7	US-11-102-240-60	Sequence 60, Appl
768	55	3.1	247	7	US-11-054-515-1711	Sequence 1711, App	843	55	3.1	304	6	US-10-467-657-1000	Sequence 1000, App
769	55	3.1	250	7	US-11-054-515-1529	Sequence 1529, App	844	55	3.1	306	6	US-10-995-561-894	Sequence 894, App
770	55	3.1	250	7	US-11-135-855-41	Sequence 41, Appl	845	55	3.1	350	6	US-10-467-657-524	Sequence 524, App
771	55	3.1	251	7	US-11-054-515-315	Sequence 315, Appl	846	55	3.1	350	6	US-10-467-657-512	Sequence 512, App
772	55	3.1	251	7	US-11-054-515-1050	Sequence 1050, App	847	55	3.1	352	7	US-11-068-686-20	Sequence 20, Appl
773	55	3.1	251	7	US-11-054-515-1538	Sequence 1538, App	848	55	3.1	365	6	US-10-624-932-24	Sequence 24, Appl
774	55	3.1	252	7	US-11-054-515-1538	Sequence 1538, App	849	55	3.1	380	6	US-10-624-932-20	Sequence 20, Appl
775	55	3.1	252	7	US-11-054-515-1529	Sequence 1517, App	850	55	3.1	380	7	US-11-108-528-28	Sequence 28, Appl
776	55	3.1	253	6	US-10-509-691-2	Sequence 2, Appl	851	55	3.1	381	7	US-11-108-528-30	Sequence 30, Appl
777	55	3.1	254	7	US-11-054-515-1522	Sequence 1522, App	852	55	3.1	381	7	US-11-055-822-414	Sequence 414, App
778	55	3.1	254	7	US-11-054-515-1038	Sequence 1038, App	853	55	3.1	381	7	US-11-055-822-706	Sequence 706, App
779	55	3.1	308	6	US-10-467-657-3858	Sequence 3858, App	855	55	3.1	448	6	US-10-510-386-24	Sequence 24, Appl
780	55	3.1	330	7	US-11-184-380-12	Sequence 12, Appl	856	55	3.1	452	6	US-10-624-932-28	Sequence 28, Appl
781	55	3.1	334	6	US-10-793-626-230	Sequence 230, App	857	55	3.1	455	6	US-10-847-867-28	Sequence 28, Appl

858	54.5	3.1	455	6	US-10-847-867-30	Sequence 30, Appl	932	54	3.0	535	6	US-10-995-561-510	Sequence 610, App
859	54.5	3.1	455	6	US-10-847-867-31	Sequence 31, Appl	933	54	3.0	538	6	US-10-793-626-3134	Sequence 3134, Ap
860	54.5	3.1	455	6	US-10-847-867-33	Sequence 33, Appl	934	54	3.0	617	7	US-11-172-145-8	Sequence 8, Appl
861	54.5	3.1	455	6	US-10-847-867-34	Sequence 34, Appl	935	54	3.0	687	6	US-10-467-657-1300	Sequence 1300, Ap
862	54.5	3.1	455	7	US-11-016-503-14	Sequence 14, Appl	936	54	3.0	733	6	US-10-821-234-1147	Sequence 1147, Ap
863	54.5	3.1	455	7	US-11-089-803-4	Sequence 4, Appl	937	54	3.0	791	6	US-10-467-657-5014	Sequence 5014, Ap
864	54.5	3.1	497	6	US-10-984-376-3	Sequence 3, Appl	938	54	3.0	827	6	US-10-821-224-1685	Sequence 1685, Ap
865	54.5	3.1	547	6	US-10-770-726-87	Sequence 87, Appl	939	54	3.0	829	6	US-10-512-109-27	Sequence 27, Appl
866	54.5	3.1	585	7	US-11-074-176-190	Sequence 190, App	940	54	3.0	896	7	US-11-080-991-98	Sequence 27, Appl
867	54.5	3.1	597	6	US-10-884-730-381	Sequence 381, App	941	54	3.0	953	7	US-11-057-058-56	Sequence 56, Appl
868	54.5	3.1	700	6	US-10-995-561-922	Sequence 922, App	942	54	3.0	1041	6	US-10-995-561-780	Sequence 780, App
869	54.5	3.1	700	6	US-10-995-561-924	Sequence 924, App	943	54	3.0	1041	6	US-10-995-561-782	Sequence 782, App
870	54.5	3.1	700	6	US-11-196-475-74	Sequence 74, Appl	944	54	3.0	1122	6	US-10-821-234-1657	Sequence 1657, Ap
871	54.5	3.1	746	6	US-10-793-626-652	Sequence 652, App	946	54	3.0	1531	7	US-11-087-227-24	Sequence 24, Appl
872	54.5	3.1	781	6	US-11-194-246-344	Sequence 344, App	947	54	3.0	1531	7	US-11-168-284-211	Sequence 211, App
873	54.5	3.1	793	6	US-10-995-561-925	Sequence 925, App	948	54	3.0	1596	7	US-11-060-005-4	Sequence 4, Appl
874	54.5	3.1	816	7	US-11-090-439-48	Sequence 48, Appl	949	54	3.0	4128	6	US-10-770-726-77	Sequence 77, Appl
875	54.5	3.1	862	7	US-11-128-420-11	Sequence 11, Appl	950	54	3.0	7968	7	US-11-143-960-49	Sequence 49, Appl
876	54.5	3.1	865	6	US-10-467-962B-33	Sequence 33, Appl	951	53.5	3.0	99	7	US-11-084-554-206	Sequence 206, App
877	54.5	3.1	984	7	US-11-113-424-60	Sequence 60, Appl	952	53.5	3.0	108	6	US-10-925-366A-149	Sequence 149, App
879	54.5	3.1	1042	7	US-11-067-811-1	Sequence 1, Appl	953	53.5	3.0	120	7	US-11-102-201-1	Sequence 1, Appl
880	54.5	3.1	1096	6	US-10-995-561-710	Sequence 710, App	954	53.5	3.0	217	7	US-11-128-440-11	Sequence 11, Appl
881	54.5	3.1	1311	6	US-10-509-422-5	Sequence 4, Appl	955	53.5	3.0	218	7	US-11-188-281-6	Sequence 6, Appl
882	54.5	3.1	2256	7	US-11-144-368-4	Sequence 5, Appl	956	53.5	3.0	218	7	US-11-188-281-17	Sequence 17, Appl
883	54	3.0	91	7	US-11-075-351-58	Sequence 58, Appl	957	53.5	3.0	221	6	US-10-793-626-2216	Sequence 2216, Ap
884	54	3.0	97	7	US-11-054-669-52	Sequence 52, Appl	958	53.5	3.0	234	6	US-10-821-234-1515	Sequence 3, Appl
885	54	3.0	109	7	US-11-053-076-20	Sequence 20, Appl	959	53.5	3.0	234	7	US-11-188-281-3	Sequence 3, Appl
886	54	3.0	119	6	US-10-467-657-5240	Sequence 5240, Ap	960	53.5	3.0	247	7	US-11-054-515-2072	Sequence 2072, Ap
887	54	3.0	128	7	US-11-096-074-24	Sequence 24, Appl	961	53.5	3.0	248	7	US-11-054-515-1456	Sequence 1456, Ap
888	54	3.0	129	6	US-10-967-527A-11	Sequence 11, Appl	962	53.5	3.0	248	7	US-11-054-515-1890	Sequence 1890, Ap
889	54	3.0	136	6	US-10-839-799-29	Sequence 29, Appl	963	53.5	3.0	249	7	US-11-054-515-121	Sequence 121, App
890	54	3.0	159	7	US-11-132-285-7	Sequence 7, Appl	964	53.5	3.0	249	7	US-11-054-515-146	Sequence 146, App
891	54	3.0	199	6	US-10-793-626-142	Sequence 1342, Ap	965	53.5	3.0	249	7	US-11-054-515-410	Sequence 410, App
892	54	3.0	226	7	US-11-132-285-5	Sequence 5, Appl	966	53.5	3.0	249	7	US-11-054-515-420	Sequence 420, App
893	54	3.0	232	6	US-10-510-386-116	Sequence 116, App	967	53.5	3.0	249	7	US-11-054-515-466	Sequence 466, App
894	54	3.0	236	7	US-11-139-499-10	Sequence 10, Appl	968	53.5	3.0	249	7	US-11-054-515-492	Sequence 492, App
895	54	3.0	241	6	US-10-467-657-1400	Sequence 1400, Ap	969	53.5	3.0	249	7	US-11-054-515-542	Sequence 542, App
896	54	3.0	244	7	US-11-054-515-1513	Sequence 1513, Ap	970	53.5	3.0	249	7	US-11-054-515-703	Sequence 703, App
897	54	3.0	244	7	US-11-054-515-1524	Sequence 1524, Ap	971	53.5	3.0	249	7	US-11-054-515-753	Sequence 753, App
898	54	3.0	248	7	US-11-054-515-1524	Sequence 1705, Ap	972	53.5	3.0	251	7	US-11-054-515-1023	Sequence 1023, Ap
899	54	3.0	249	7	US-11-054-515-1705	Sequence 462, App	973	53.5	3.0	251	7	US-11-054-515-1162	Sequence 1162, Ap
900	54	3.0	249	7	US-11-054-515-462	Sequence 519, App	974	53.5	3.0	252	6	US-10-512-184-28	Sequence 28, Appl
901	54	3.0	249	7	US-11-054-515-519	Sequence 570, App	975	53.5	3.0	254	7	US-11-054-515-977	Sequence 977, App
902	54	3.0	249	7	US-11-054-515-700	Sequence 700, App	976	53.5	3.0	255	7	US-11-054-515-1153	Sequence 1153, Ap
903	54	3.0	249	7	US-11-054-515-708	Sequence 708, App	977	53.5	3.0	258	7	US-11-054-515-2090	Sequence 2090, Ap
904	54	3.0	249	7	US-11-113-424-30	Sequence 30, Appl	978	53.5	3.0	266	7	US-11-082-544-10	Sequence 10, Appl
905	54	3.0	251	6	US-10-793-626-3050	Sequence 3050, Ap	979	53.5	3.0	281	6	US-10-821-234-1288	Sequence 1288, Ap
906	54	3.0	251	7	US-11-054-515-123	Sequence 123, App	980	53.5	3.0	283	7	US-11-008-331-6	Sequence 6, Appl
907	54	3.0	251	7	US-11-054-515-252	Sequence 252, App	981	53.5	3.0	290	7	US-11-113-424-77	Sequence 77, Appl
908	54	3.0	252	7	US-11-054-515-1164	Sequence 1164, Ap	982	53.5	3.0	310	7	US-11-000-463-357	Sequence 357, App
909	54	3.0	253	7	US-11-054-515-1987	Sequence 1987, Ap	983	53.5	3.0	322	6	US-10-793-626-1912	Sequence 1912, Ap
910	54	3.0	256	7	US-11-054-515-1253	Sequence 1253, Ap	984	53.5	3.0	322	6	US-11-109-156-33	Sequence 33, Appl
911	54	3.0	256	7	US-11-054-515-1693	Sequence 1693, Ap	985	53.5	3.0	332	6	US-10-793-626-2562	Sequence 2562, App
912	54	3.0	265	6	US-10-467-657-5000	Sequence 5000, Ap	986	53.5	3.0	338	6	US-10-878-556A-19	Sequence 19, Appl
913	54	3.0	269	6	US-10-467-657-7302	Sequence 7302, Ap	987	53.5	3.0	391	7	US-11-105-172-4	Sequence 4, Appl
914	54	3.0	296	6	US-10-510-386-58	Sequence 58, Appl	988	53.5	3.0	398	6	US-10-821-234-1583	Sequence 1583, Ap
915	54	3.0	303	6	US-10-467-962B-16	Sequence 16, Appl	989	53.5	3.0	402	7	US-11-174-150-47	Sequence 47, Appl
916	54	3.0	303	6	US-10-467-962B-45	Sequence 45, Appl	990	53.5	3.0	413	7	US-11-060-029-4	Sequence 4, Appl
917	54	3.0	353	7	US-11-067-884-6	Sequence 6, Appl	991	53.5	3.0	436	7	US-11-080-991-102	Sequence 102, App
918	54	3.0	354	6	US-10-821-234-1618	Sequence 1618, Ap	992	53.5	3.0	441	6	US-10-510-386-162	Sequence 162, App
919	54	3.0	376	6	US-10-485-517-218	Sequence 218, App	993	53.5	3.0	455	6	US-10-847-867-32	Sequence 32, Appl
920	54	3.0	384	6	US-10-999-866-33	Sequence 33, Appl	994	53.5	3.0	467	6	US-10-510-386-56	Sequence 56, Appl
921	54	3.0	384	6	US-11-061-882-33	Sequence 33, Appl	995	53.5	3.0	490	7	US-11-069-642-23	Sequence 23, Appl
922	54	3.0	397	7	US-11-192-219-47	Sequence 47, Appl	996	53.5	3.0	564	6	US-10-485-517-98	Sequence 298, App
923	54	3.0	431	7	US-11-092-140-6	Sequence 6, Appl	997	53.5	3.0	579	6	US-10-528-673-2	Sequence 2, Appl
924	54	3.0	443	6	US-10-467-657-5762	Sequence 5762, Ap	998	53.5	3.0	693	6	US-11-126-475-72	Sequence 72, Appl
925	54	3.0	479	7	US-11-024-251-33	Sequence 33, Appl	999	53.5	3.0	915	7	US-11-144-987-16	Sequence 16, Appl
926	54	3.0	491	6	US-10-793-626-2808	Sequence 2808, Ap	1000	53.5	3.0	917	7	US-11-144-987-18	Sequence 18, Appl
927	54	3.0	493	7	US-11-067-121-10	Sequence 10, Appl	1001	53.5	3.0	917	7	US-11-144-987-20	Sequence 20, Appl
928	54	3.0	520	6	US-10-508-263-26	Sequence 26, Appl	1002	53.5	3.0	985	7	US-11-113-424-61	Sequence 61, Appl
929	54	3.0	520	6	US-10-878-556A-38	Sequence 38, Appl	1003	53.5	3.0	1070	7	US-11-000-463-721	Sequence 721, App
930	54	3.0	522	6	US-10-793-626-456	Sequence 456, App	1004	53.5	3.0	1137	7	US-11-012-762-70	Sequence 70, Appl
931	54	3.0	522	6	US-10-793-626-2042	Sequence 2042, Ap	1005	53.5	3.0	1167	6	US-10-601-368-18	Sequence 18, Appl

1006	53.5	3.0	1194	7	US-11-000-463-249	Sequence 249, App	1079	53	3.0	433	7	US-11-074-176-162	Sequence 162, App
1007	53.5	3.0	1206	6	US-10-467-657-72	Sequence 72, Appl	1080	53	3.0	450	7	US-11-025-712-12	Sequence 12, Appl
1008	53.5	3.0	1206	6	US-10-467-657-72	Sequence 3892, Ap	1081	53	3.0	461	7	US-11-082-389-176	Sequence 176, App
1009	53.5	3.0	1210	7	US-11-108-172-692	Sequence 692, App	1082	53	3.0	474	6	US-10-467-657-5978	Sequence 5978, Ap
1010	53.5	3.0	1230	7	US-10-995-561-870	Sequence 870, App	1083	53	3.0	474	6	US-10-467-657-7518	Sequence 7518, Ap
1011	53.5	3.0	1365	6	US-10-995-561-867	Sequence 867, App	1084	53	3.0	475	6	US-10-510-386-98	Sequence 98, Appl
1012	53.5	3.0	1366	6	US-10-995-561-868	Sequence 866, App	1085	53	3.0	491	7	US-11-098-662-14	Sequence 14, Appl
1013	53.5	3.0	1411	6	US-10-995-561-869	Sequence 866, App	1086	53	3.0	491	7	US-11-165-141-2	Sequence 2, Appl1
1014	53.5	3.0	1437	7	US-11-074-176-96	Sequence 96, App	1088	53	3.0	540	6	US-10-770-726-80	Sequence 80, Appl1
1015	53.5	3.0	1548	7	US-11-108-172-1095	Sequence 1095, Ap	1089	53	3.0	567	6	US-10-420-192-8	Sequence 8, Appl1
1016	53.5	3.0	1992	7	US-11-013-759-3	Sequence 3, Appl1	1090	53	3.0	591	6	US-10-510-386-22	Sequence 22, Appl
1017	53.5	3.0	1992	7	US-11-013-759-13	Sequence 13, Appl1	1092	53	3.0	609	6	US-10-821-234-1611	Sequence 1611, Ap
1018	53.5	3.0	2047	7	US-11-013-759-4	Sequence 4, Appl1	1094	53	3.0	653	7	US-11-135-855-25	Sequence 25, Appl
1019	53.5	3.0	2047	7	US-11-013-759-7	Sequence 7, Appl1	1095	53	3.0	688	7	US-11-113-424-48	Sequence 48, Appl1
1020	53.5	3.0	2107	6	US-10-995-561-827	Sequence 827, App	1096	53	3.0	688	7	US-11-113-424-48	Sequence 49, Appl1
1021	53.5	3.0	2480	6	US-10-995-561-825	Sequence 825, App	1097	53	3.0	694	7	US-11-074-176-150	Sequence 150, App
1022	53.5	3.0	2647	6	US-10-821-234-1303	Sequence 1303, Ap	1098	53	3.0	697	7	US-11-074-176-150	Sequence 150, App
1023	53.5	3.0	3116	6	US-10-995-561-826	Sequence 826, App	1099	53	3.0	700	7	US-11-196-475-66	Sequence 66, Appl
1024	53.5	3.0	3433	6	US-10-714-781A-67	Sequence 67, Appl1	1100	53	3.0	751	7	US-11-012-762-26	Sequence 26, Appl
1025	53.5	3.0	97	7	US-11-144-248-36	Sequence 36, Appl1	1101	53	3.0	786	6	US-10-467-962B-103	Sequence 103, App
1026	53	3.0	97	7	US-11-054-669-42	Sequence 42, Appl1	1102	53	3.0	841	6	US-10-770-726-88	Sequence 88, Appl
1027	53	3.0	97	7	US-11-084-554-54	Sequence 54, Appl1	1103	53	3.0	1189	7	US-11-074-176-134	Sequence 134, App
1028	53	3.0	99	7	US-11-084-554-208	Sequence 208, App	1104	53	3.0	1375	6	US-10-995-561-809	Sequence 809, App
1029	53	3.0	107	6	US-10-793-626-1586	Sequence 1586, Ap	1105	53	3.0	2432	6	US-10-821-234-899	Sequence 899, App
1030	53	3.0	108	6	US-10-473-037-50	Sequence 50, Appl	1106	52.5	3.0	113	6	US-10-932-334-61	Sequence 61, Appl
1031	53	3.0	108	6	US-10-999-866-6	Sequence 6, Appl1	1107	52.5	3.0	117	7	US-11-012-353-53	Sequence 53, Appl1
1032	53	3.0	108	7	US-11-061-821-6	Sequence 6, Appl1	1108	52.5	3.0	132	6	US-10-789-273-5	Sequence 5, Appl1
1033	53	3.0	118	6	US-10-932-334-75	Sequence 75, Appl1	1109	52.5	3.0	132	6	US-10-789-273-11	Sequence 11, Appl1
1034	53	3.0	120	6	US-11-173-071-2	Sequence 2, Appl1	1110	52.5	3.0	143	6	US-10-467-657-8684	Sequence 8684, Ap
1035	53	3.0	128	6	US-10-473-037-2	Sequence 2, Appl1	1111	52.5	3.0	168	7	US-11-020-772-35	Sequence 35, Appl
1036	53	3.0	184	6	US-10-742-634-9	Sequence 9, Appl1	1112	52.5	3.0	213	7	US-11-174-186-42	Sequence 42, Appl
1037	53	3.0	184	6	US-10-967-527A-8	Sequence 8, Appl1	1113	52.5	3.0	225	6	US-11-209-208-1	Sequence 1, Appl1
1038	53	3.0	199	6	US-10-467-657-2368	Sequence 2368, Ap	1114	52.5	3.0	225	6	US-10-209-208-40	Sequence 40, Appl1
1039	53	3.0	246	7	US-11-054-515-1264	Sequence 1264, Ap	1115	52.5	3.0	225	6	US-10-209-208-20	Sequence 20, Appl1
1040	53	3.0	248	7	US-11-054-515-895	Sequence 895, App	1116	52.5	3.0	226	7	US-11-170-653-63	Sequence 63, Appl
1041	53	3.0	248	7	US-11-054-515-970	Sequence 970, App	1117	52.5	3.0	233	7	US-11-170-653-28	Sequence 28, Appl
1042	53	3.0	249	7	US-11-054-515-310	Sequence 310, App	1118	52.5	3.0	236	7	US-11-022-289-12	Sequence 12, Appl
1043	53	3.0	249	7	US-11-054-515-485	Sequence 485, App	1119	52.5	3.0	236	6	US-10-995-561-725	Sequence 725, App
1044	53	3.0	249	7	US-11-054-515-588	Sequence 588, App	1120	52.5	3.0	249	7	US-11-054-515-637	Sequence 637, App
1045	53	3.0	249	7	US-11-054-515-612	Sequence 612, App	1121	52.5	3.0	244	7	US-11-054-515-1991	Sequence 1991, Ap
1046	53	3.0	249	7	US-11-054-515-620	Sequence 620, App	1122	52.5	3.0	248	7	US-11-054-515-1248	Sequence 1248, Ap
1047	53	3.0	249	7	US-11-054-515-740	Sequence 740, App	1123	52.5	3.0	249	7	US-11-054-515-406	Sequence 406, App
1048	53	3.0	250	7	US-11-054-515-1142	Sequence 1142, Ap	1124	52.5	3.0	249	7	US-11-054-515-412	Sequence 412, App
1049	53	3.0	250	7	US-11-054-515-1851	Sequence 1851, Ap	1125	52.5	3.0	249	7	US-11-054-515-418	Sequence 418, App
1050	53	3.0	251	7	US-11-054-515-118	Sequence 118, App	1126	52.5	3.0	249	7	US-11-054-515-433	Sequence 433, App
1051	53	3.0	251	7	US-11-054-515-209	Sequence 209, App	1127	52.5	3.0	249	7	US-11-054-515-438	Sequence 438, App
1052	53	3.0	251	7	US-11-054-515-270	Sequence 270, App	1128	52.5	3.0	249	7	US-11-054-515-506	Sequence 506, App
1053	53	3.0	251	7	US-11-054-515-288	Sequence 288, App	1129	52.5	3.0	249	7	US-11-054-515-540	Sequence 540, App
1054	53	3.0	251	7	US-11-054-515-1542	Sequence 1542, App	1130	52.5	3.0	249	7	US-11-054-515-599	Sequence 599, App
1055	53	3.0	252	6	US-10-485-517-156	Sequence 156, App	1131	52.5	3.0	249	7	US-11-054-515-637	Sequence 637, App
1056	53	3.0	252	6	US-10-467-657-276	Sequence 276, App	1132	52.5	3.0	249	7	US-11-054-515-747	Sequence 747, App
1057	53	3.0	252	6	US-10-467-657-4008	Sequence 4008, App	1133	52.5	3.0	249	7	US-11-054-515-829	Sequence 829, App
1058	53	3.0	252	7	US-11-054-515-1201	Sequence 1201, App	1134	52.5	3.0	249	7	US-11-054-515-833	Sequence 833, App
1059	53	3.0	252	7	US-11-054-515-1994	Sequence 1994, App	1135	52.5	3.0	250	7	US-11-054-515-1977	Sequence 1977, App
1060	53	3.0	253	7	US-11-054-515-1000	Sequence 1000, App	1136	52.5	3.0	250	7	US-11-054-515-691	Sequence 691, App
1061	53	3.0	253	7	US-11-054-515-1042	Sequence 1042, App	1137	52.5	3.0	251	7	US-11-054-515-991	Sequence 991, App
1062	53	3.0	258	7	US-11-054-515-1260	Sequence 1260, App	1138	52.5	3.0	252	7	US-11-054-515-1506	Sequence 1506, App
1063	53	3.0	259	7	US-11-054-515-864	Sequence 864, App	1139	52.5	3.0	253	6	US-10-995-561-721	Sequence 721, App
1064	53	3.0	259	7	US-11-054-515-1025	Sequence 1025, App	1140	52.5	3.0	253	6	US-10-995-561-129	Sequence 729, App
1065	53	3.0	259	7	US-11-054-515-1262	Sequence 1262, App	1141	52.5	3.0	253	6	US-11-054-515-1530	Sequence 1530, App
1066	53	3.0	260	7	US-11-054-515-1244	Sequence 1244, App	1142	52.5	3.0	256	7	US-11-054-515-1015	Sequence 1015, App
1067	53	3.0	283	7	US-11-087-072-2	Sequence 2, Appl1	1143	52.5	3.0	257	7	US-11-054-515-1596	Sequence 1596, App
1068	53	3.0	288	6	US-10-467-657-1870	Sequence 1870, App	1144	52.5	3.0	265	6	US-10-995-561-724	Sequence 724, App
1069	53	3.0	307	7	US-11-053-185-20	Sequence 20, Appl	1145	52.5	3.0	265	6	US-10-995-561-733	Sequence 733, App
1070	53	3.0	330	7	US-11-085-812-2	Sequence 2, Appl1	1146	52.5	3.0	273	7	US-11-113-424-75	Sequence 75, Appl
1071	53	3.0	332	6	US-10-467-657-3868	Sequence 3868, App	1147	52.5	3.0	273	6	US-10-878-556A-120	Sequence 120, App
1072	53	3.0	332	6	US-10-467-657-7154	Sequence 7154, App	1148	52.5	3.0	286	7	US-11-089-551A-17	Sequence 17, Appl
1073	53	3.0	347	7	US-11-186-284-226	Sequence 226, App	1150	52.5	3.0	310	7	US-11-025-834A-15	Sequence 15, Appl
1074	53	3.0	360	7	US-11-082-389-90	Sequence 90, Appl	1151	52.5	3.0	312	7	US-11-055-822-16	Sequence 16, Appl
1075	53	3.0	360	7	US-11-082-389-92	Sequence 92, Appl	1152	52.5	3.0	325	7	US-11-074-176-368	Sequence 368, App
1076	53	3.0	428	6	US-10-793-626-484	Sequence 484, App	1153	52.5	3.0	358	7	US-11-095-624-6	Sequence 6, Appl1
1077	53	3.0	428	7	US-11-074-176-344	Sequence 344, App	1154	52.5	3.0	362	6	US-10-821-234-1148	Sequence 1148, App
1078	53	3.0	432	7	US-11-056-354-4	Sequence 4, Appl1	1155	52.5	3.0	374	7	US-11-000-463-453	Sequence 453, App

1156	52.5	3.0	381	6	US-10-510-386-168	Sequence 168, App	1230	52	2.9	250	7	US-11-054-515-1017	Sequence 1017, Ap
1157	52.5	3.0	382	6	US-10-392-234A-55	Sequence 65, Appl	1231	52	2.9	250	7	US-11-054-515-1563	Sequence 1563, Ap
1158	52.5	3.0	413	6	US-10-821-234-989	Sequence 989, App	1232	52	2.9	250	7	US-11-054-515-1564	Sequence 1564, Ap
1159	52.5	3.0	416	7	US-11-061-869-18	Sequence 18, Appl	1233	52	2.9	250	7	US-11-054-515-1574	Sequence 1574, Ap
1160	52.5	3.0	422	7	US-11-055-822-626	Sequence 626, App	1234	52	2.9	252	7	US-11-054-515-1874	Sequence 1874, Ap
1161	52.5	3.0	429	6	US-10-793-628-3174	Sequence 3174, App	1235	52	2.9	252	7	US-11-054-515-1954	Sequence 1954, Ap
1162	52.5	3.0	442	6	US-10-821-234-1594	Sequence 1594, Ap	1236	52	2.9	253	7	US-11-054-515-1349	Sequence 1349, Ap
1163	52.5	3.0	443	7	US-11-054-385-4	Sequence 4, Appl1	1237	52	2.9	253	7	US-11-054-515-1848	Sequence 1848, Ap
1164	52.5	3.0	447	6	US-10-967-527A-14	Sequence 14, Appl	1238	52	2.9	254	7	US-11-054-515-173	Sequence 873, App
1165	52.5	3.0	466	7	US-11-102-240-104	Sequence 104, App	1239	52	2.9	254	7	US-11-054-515-888	Sequence 888, App
1166	52.5	3.0	494	6	US-10-467-657-4376	Sequence 4376, Ap	1240	52	2.9	254	7	US-11-054-515-1087	Sequence 1087, App
1167	52.5	3.0	499	6	US-10-508-263-94	Sequence 94, Appl	1241	52	2.9	254	7	US-11-067-323-784	Sequence 1186, Ap
1168	52.5	3.0	503	7	US-11-113-424-72	Sequence 72, Appl	1242	52	2.9	254	7	US-11-067-323-784	Sequence 784, App
1169	52.5	3.0	524	6	US-10-507-106-4	Sequence 4, Appl1	1243	52	2.9	258	7	US-11-054-515-1716	Sequence 1716, Ap
1170	52.5	3.0	541	7	US-11-000-463-238	Sequence 238, App	1244	52	2.9	258	7	US-11-054-515-1083	Sequence 2083, Ap
1172	52.5	3.0	570	7	US-11-113-424-69	Sequence 69, Appl	1245	52	2.9	267	6	US-10-623-155-352	Sequence 355, App
1173	52.5	3.0	570	7	US-11-113-424-71	Sequence 71, Appl	1246	52	2.9	278	6	US-10-957-569-49	Sequence 45, Appl
1174	52.5	3.0	620	7	US-11-113-424-70	Sequence 70, Appl	1247	52	2.9	284	6	US-10-467-657-536	Sequence 536, App
1175	52.5	3.0	638	6	US-10-995-561-1025	Sequence 1025, Ap	1248	52	2.9	295	7	US-11-143-980-31	Sequence 31, Appl
1176	52.5	3.0	693	7	US-11-167-856-2	Sequence 2, Appl	1249	52	2.9	301	6	US-10-793-626-206	Sequence 206, App
1177	52.5	3.0	720	7	US-11-113-424-28	Sequence 28, Appl	1250	52	2.9	319	6	US-10-493-210A-1	Sequence 1, Appl1
1178	52.5	3.0	743	6	US-10-467-657-4082	Sequence 4082, Ap	1251	52	2.9	319	6	US-10-793-626-792	Sequence 792, App
1179	52.5	3.0	747	7	US-11-113-424-26	Sequence 26, Appl	1252	52	2.9	319	6	US-10-793-626-2008	Sequence 2008, Ap
1180	52.5	3.0	826	7	US-11-055-822-214	Sequence 214, App	1253	52	2.9	333	6	US-10-846-172A-6	Sequence 6, Appl1
1181	52.5	3.0	826	7	US-11-055-822-712	Sequence 712, App	1254	52	2.9	348	6	US-10-821-234-1614	Sequence 1614, Ap
1182	52.5	3.0	833	7	US-11-055-822-212	Sequence 212, App	1255	52	2.9	348	6	US-10-857-780-24	Sequence 24, Appl
1183	52.5	3.0	833	7	US-11-055-822-710	Sequence 710, App	1256	52	2.9	359	6	US-10-467-657-1676	Sequence 1676, Ap
1184	52.5	3.0	912	7	US-11-042-988-12	Sequence 12, Appl	1257	52	2.9	377	7	US-11-152-892-8	Sequence 8, Appl1
1185	52.5	3.0	922	7	US-11-115-086-9	Sequence 9, Appl1	1258	52	2.9	390	7	US-11-184-380-2	Sequence 2, Appl1
1186	52.5	3.0	1121	7	US-11-113-751-13	Sequence 13, Appl	1259	52	2.9	397	6	US-10-467-657-7944	Sequence 3944, Ap
1187	52.5	3.0	1127	6	US-10-858-730-13	Sequence 13, Appl	1260	52	2.9	399	7	US-11-147-047-35	Sequence 35, Appl
1188	52.5	3.0	1144	6	US-10-467-657-89	Sequence 89, Appl	1261	52	2.9	403	7	US-11-109-156-99	Sequence 99, Appl
1189	52.5	3.0	1159	6	US-11-113-751-27	Sequence 27, Appl	1262	52	2.9	408	7	US-11-055-822-910	Sequence 910, App
1190	52.5	3.0	1160	6	US-10-995-561-1019	Sequence 1019, Ap	1263	52	2.9	416	6	US-10-821-234-1375	Sequence 1375, Ap
1191	52.5	3.0	1221	6	US-10-858-730-222	Sequence 222, App	1264	52	2.9	421	7	US-11-055-822-366	Sequence 366, App
1192	52.5	3.0	1302	6	US-10-995-561-1024	Sequence 1024, Ap	1265	52	2.9	432	7	US-11-056-354-2	Sequence 2, Appl1
1193	52.5	3.0	1306	6	US-10-995-561-1027	Sequence 1027, Ap	1266	52	2.9	436	6	US-10-467-657-77	Sequence 77, Appl
1194	52.5	3.0	1438	6	US-10-511-559-73	Sequence 73, Appl	1267	52	2.9	443	7	US-11-196-475-165	Sequence 166, App
1195	52.5	3.0	1467	6	US-10-507-956-1	Sequence 1, Appl1	1268	52	2.9	447	6	US-10-467-657-4836	Sequence 4836, Ap
1196	52.5	3.0	1613	7	US-11-108-528-84	Sequence 84, Appl	1269	52	2.9	465	7	US-11-037-829A-14	Sequence 904, App
1197	52.5	3.0	1614	6	US-10-821-234-903	Sequence 903, App	1270	52	2.9	467	6	US-10-821-234-904	Sequence 68, Appl
1198	52.5	3.0	2096	6	US-10-995-561-606	Sequence 606, App	1271	52	2.9	468	7	US-11-055-822-68	Sequence 2956, Ap
1199	52.5	3.0	2351	6	US-10-995-561-608	Sequence 608, App	1272	52	2.9	479	6	US-10-793-626-3956	Sequence 6158, Ap
1200	52.5	3.0	2630	7	US-11-186-731-2	Sequence 2, Appl1	1273	52	2.9	489	6	US-10-467-657-6158	Sequence 12, Appl
1201	52.5	3.0	4384	6	US-10-821-234-1120	Sequence 1120, Ap	1274	52	2.9	561	7	US-11-029-465-12	Sequence 10, Appl
1202	52	2.9	97	7	US-11-054-669-53	Sequence 53, Appl	1275	52	2.9	562	6	US-10-507-928-10	Sequence 10, Appl
1203	52	2.9	107	7	US-11-105-268-18	Sequence 18, Appl	1276	52	2.9	567	7	US-10-507-928-12	Sequence 12, Appl
1204	52	2.9	115	6	US-10-467-657-480	Sequence 490, App	1277	52	2.9	562	7	US-11-029-465-10	Sequence 30, Appl
1205	52	2.9	120	6	US-10-932-334-71	Sequence 71, Appl	1278	52	2.9	567	7	US-11-167-856-30	Sequence 214, App
1206	52	2.9	120	6	US-10-932-334-72	Sequence 72, Appl	1279	52	2.9	574	6	US-10-518-341-1	Sequence 11, Appl1
1207	52	2.9	154	6	US-10-721-763-25	Sequence 25, Appl	1280	52	2.9	574	7	US-11-022-562-214	Sequence 214, App
1208	52	2.9	169	6	US-10-467-657-784	Sequence 784, App	1281	52	2.9	584	7	US-11-045-802-91	Sequence 91, Appl
1209	52	2.9	200	7	US-11-055-822-1022	Sequence 1022, Ap	1282	52	2.9	588	6	US-10-821-234-1137	Sequence 1137, Ap
1210	52	2.9	204	7	US-11-128-440-3	Sequence 3, Appl1	1283	52	2.9	588	7	US-11-196-475-122	Sequence 122, App
1211	52	2.9	220	6	US-10-965-972-3	Sequence 3, Appl1	1284	52	2.9	610	7	US-11-184-380-3	Sequence 3, Appl1
1212	52	2.9	231	6	US-10-467-657-4662	Sequence 4662, Ap	1285	52	2.9	621	6	US-10-632-150-28	Sequence 28, Appl
1213	52	2.9	232	7	US-11-000-463-343	Sequence 343, App	1286	52	2.9	621	7	US-11-073-457-88	Sequence 28, Appl
1214	52	2.9	246	7	US-11-054-515-1241	Sequence 1241, Ap	1287	52	2.9	621	7	US-11-073-457-88	Sequence 28, Appl
1215	52	2.9	247	7	US-11-113-424-76	Sequence 76, Appl	1288	52	2.9	655	7	US-11-045-802-29	Sequence 29, Appl
1216	52	2.9	248	7	US-11-054-515-1816	Sequence 1816, Ap	1289	52	2.9	687	6	US-10-485-517-574	Sequence 274, App
1217	52	2.9	248	7	US-11-054-515-1955	Sequence 1955, Ap	1290	52	2.9	693	7	US-11-196-475-68	Sequence 68, Appl
1218	52	2.9	248	7	US-11-054-515-2091	Sequence 2091, Ap	1291	52	2.9	721	7	US-11-060-920-5	Sequence 5, Appl1
1219	52	2.9	249	7	US-11-054-515-402	Sequence 402, App	1292	52	2.9	721	7	US-11-060-920-5	Sequence 5, Appl1
1220	52	2.9	249	7	US-11-054-515-536	Sequence 536, App	1293	52	2.9	725	6	US-10-995-561-938	Sequence 938, App
1221	52	2.9	249	7	US-11-054-515-689	Sequence 689, App	1294	52	2.9	732	6	US-10-467-657-1888	Sequence 988, Ap
1222	52	2.9	249	7	US-11-054-515-707	Sequence 707, App	1295	52	2.9	757	7	US-11-110-082-35	Sequence 35, Appl
1223	52	2.9	249	7	US-11-054-515-722	Sequence 722, App	1296	52	2.9	761	7	US-11-110-082-34	Sequence 34, Appl
1224	52	2.9	249	7	US-11-054-515-789	Sequence 789, App	1297	52	2.9	792	7	US-11-088-686-29	Sequence 29, Appl
1225	52	2.9	249	7	US-11-054-515-1570	Sequence 1570, Ap	1298	52	2.9	824	6	US-10-957-569-31	Sequence 31, Appl
1226	52	2.9	249	7	US-11-054-515-1618	Sequence 1618, Ap	1299	52	2.9	858	6	US-10-645-441-25	Sequence 25, Appl
1227	52	2.9	249	7	US-11-054-515-1838	Sequence 1838, Ap	1300	52	2.9	866	7	US-11-147-047-32	Sequence 32, Appl
1228	52	2.9	250	7	US-11-054-515-942	Sequence 942, App	1301	52	2.9	902	7	US-11-144-987-12	Sequence 12, Appl
1229	52	2.9	250	7	US-11-054-515-964	Sequence 964, App	1302	52	2.9	902	7	US-11-144-987-14	Sequence 14, Appl
1230	52	2.9	250	7	US-11-054-515-1017	Sequence 1017, Ap	1303	52	2.9	902	7	US-11-144-987-14	Sequence 14, Appl

1304	52	2.9	980	7	US-11-064-246-10	Sequence 10, Appl	1378	51.5	2.9	376	7	US-11-055-892-422	Sequence 422, Appl
1305	52	2.9	1018	7	US-11-067-121-17	Sequence 17, Appl	1379	51.5	2.9	380	6	US-10-624-932-22	Sequence 22, Appl
1307	52	2.9	1140	6	US-10-858-730-208	Sequence 108, App	1380	51.5	2.9	389	7	US-11-129-143-82	Sequence 82, Appl
1308	52	2.9	1151	6	US-10-793-626-2448	Sequence 2448, Ap	1381	51.5	2.9	395	7	US-11-053-185-8	Sequence 8, Appl1
1309	52	2.9	1167	6	US-10-601-368-4	Sequence 4, Appl1	1382	51.5	2.9	404	6	US-10-793-626-1204	Sequence 1204, Ap
1310	52	2.9	1167	6	US-10-942-072-13	Sequence 13, Appl	1383	51.5	2.9	419	6	US-10-821-234-1556	Sequence 1556, Ap
1311	52	2.9	1167	6	US-11-097-125-2	Sequence 2, Appl1	1385	51.5	2.9	445	7	US-11-074-176-185	Sequence 185, App
1312	52	2.9	1168	6	US-10-942-072-11	Sequence 11, Appl	1387	51.5	2.9	468	7	US-11-102-240-150	Sequence 150, App
1313	52	2.9	1188	6	US-10-601-368-3	Sequence 3, Appl1	1388	51.5	2.9	474	7	US-11-037-829A-13	Sequence 13, Appl
1314	52	2.9	1188	7	US-11-000-463-338	Sequence 338, App	1389	51.5	2.9	483	7	US-11-113-424-34	Sequence 24, Appl
1315	52	2.9	1188	7	US-11-000-463-810	Sequence 810, Appl	1390	51.5	2.9	492	6	US-10-467-657-1804	Sequence 1804, Ap
1316	52	2.9	1360	7	US-11-188-743-22	Sequence 22, Appl	1391	51.5	2.9	497	6	US-10-763-712A-2	Sequence 24, Appl
1317	52	2.9	1387	7	US-11-077-386-26	Sequence 26, Appl	1392	51.5	2.9	497	6	US-10-763-712A-91	Sequence 91, Appl
1318	52	2.9	1406	6	US-10-995-561-530	Sequence 530, App	1393	51.5	2.9	518	7	US-11-055-822-120	Sequence 420, App
1319	52	2.9	1481	7	US-11-077-386-30	Sequence 30, Appl	1394	51.5	2.9	524	7	US-11-113-424-64	Sequence 64, Appl
1320	52	2.9	1637	6	US-10-821-234-1204	Sequence 1204, Ap	1395	51.5	2.9	547	6	US-10-995-561-785	Sequence 785, App
1321	52	2.9	1827	7	US-11-057-058-62	Sequence 62, Appl	1396	51.5	2.9	547	6	US-10-995-561-787	Sequence 787, App
1322	52	2.9	2657	6	US-10-821-234-1262	Sequence 1252, Ap	1397	51.5	2.9	553	7	US-11-090-439-18	Sequence 18, Appl
1323	52	2.9	3803	6	US-10-995-561-773	Sequence 773, App	1398	51.5	2.9	583	6	US-10-793-626-1358	Sequence 1358, Ap
1324	52	2.9	3960	6	US-10-995-561-771	Sequence 771, App	1399	51.5	2.9	591	7	US-11-082-389-386	Sequence 386, App
1325	51.5	2.9	98	7	US-11-144-248-34	Sequence 34, Appl	1400	51.5	2.9	614	7	US-11-126-841A-2	Sequence 13, Appl1
1326	51.5	2.9	98	7	US-11-054-669-34	Sequence 34, Appl	1401	51.5	2.9	614	7	US-11-126-841A-13	Sequence 13, Appl1
1327	51.5	2.9	99	7	US-11-054-669-37	Sequence 37, Appl	1402	51.5	2.9	646	6	US-10-995-561-695	Sequence 695, App
1328	51.5	2.9	100	6	US-10-789-273-7	Sequence 7, Appl1	1403	51.5	2.9	651	6	US-10-821-234-1666	Sequence 1666, App
1329	51.5	2.9	100	6	US-11-012-353-59	Sequence 59, Appl	1404	51.5	2.9	759	6	US-10-467-657-4186	Sequence 4186, Ap
1330	51.5	2.9	100	7	US-11-054-669-78	Sequence 78, Appl	1405	51.5	2.9	870	7	US-10-933-025-3	Sequence 3, Appl1
1331	51.5	2.9	100	7	US-11-054-669-79	Sequence 79, Appl	1406	51.5	2.9	871	6	US-10-933-025-3	Sequence 3, Appl1
1332	51.5	2.9	100	7	US-11-054-669-80	Sequence 80, Appl	1407	51.5	2.9	979	6	US-10-636-320-6	Sequence 6, Appl1
1333	51.5	2.9	100	7	US-11-084-554-109	Sequence 109, App	1408	51.5	2.9	1178	6	US-10-995-561-851	Sequence 851, App
1334	51.5	2.9	100	7	US-11-084-554-110	Sequence 110, App	1409	51.5	2.9	1381	6	US-10-467-657-178	Sequence 178, App
1335	51.5	2.9	100	7	US-11-084-554-115	Sequence 115, App	1410	51.5	2.9	1400	6	US-10-821-234-1045	Sequence 1045, Ap
1336	51.5	2.9	101	7	US-11-084-554-117	Sequence 117, App	1411	51.5	2.9	1463	6	US-10-971-982-3	Sequence 3, Appl1
1337	51.5	2.9	108	6	US-10-925-366A-158	Sequence 158, App	1412	51.5	2.9	1613	7	US-11-108-528-86	Sequence 86, Appl
1338	51.5	2.9	128	7	US-11-155-775-54	Sequence 54, Appl	1413	51.5	2.9	2053	7	US-11-013-759-9	Sequence 9, Appl1
1339	51.5	2.9	132	6	US-10-793-626-404	Sequence 404, App	1414	51.5	2.9	2504	7	US-10-647-956A-8	Sequence 8, Appl1
1340	51.5	2.9	142	6	US-10-763-712A-117	Sequence 117, App	1415	51.5	2.9	2725	6	US-11-113-424-32	Sequence 52, Appl
1341	51.5	2.9	212	6	US-10-793-626-1496	Sequence 1496, Ap	1416	51.5	2.9	98	7	US-11-012-353-74	Sequence 44, Appl
1342	51.5	2.9	223	7	US-11-112-882-88	Sequence 88, Appl	1417	51.5	2.9	98	7	US-11-054-669-94	Sequence 74, Appl
1343	51.5	2.9	231	7	US-11-170-653-25	Sequence 25, Appl	1418	51.5	2.9	99	7	US-11-054-669-91	Sequence 41, Appl
1344	51.5	2.9	234	7	US-11-128-440-21	Sequence 21, Appl	1419	51.5	2.9	99	7	US-11-054-669-43	Sequence 43, Appl
1345	51.5	2.9	247	7	US-11-054-515-1892	Sequence 1892, Ap	1420	51.5	2.9	99	7	US-11-084-554-521	Sequence 52, Appl
1346	51.5	2.9	248	7	US-11-054-515-1860	Sequence 1860, App	1421	51.5	2.9	99	7	US-11-084-554-55	Sequence 55, Appl
1347	51.5	2.9	249	7	US-11-054-515-408	Sequence 408, App	1422	51.5	2.9	106	7	US-11-144-248-8	Sequence 26, Appl
1348	51.5	2.9	249	7	US-11-054-515-474	Sequence 474, App	1423	51.5	2.9	106	7	US-11-024-251-29	Sequence 29, Appl
1349	51.5	2.9	249	7	US-11-054-515-617	Sequence 617, App	1424	51.5	2.9	106	7	US-11-165-141-17	Sequence 17, Appl
1350	51.5	2.9	249	7	US-11-054-515-746	Sequence 746, App	1425	51.5	2.9	107	6	US-10-839-799-131	Sequence 131, App
1351	51.5	2.9	249	7	US-11-054-515-831	Sequence 831, App	1426	51.5	2.9	107	6	US-10-999-866-40	Sequence 40, Appl
1352	51.5	2.9	250	7	US-11-054-515-963	Sequence 963, App	1427	51.5	2.9	107	6	US-11-025-712-5	Sequence 5, Appl1
1353	51.5	2.9	250	7	US-11-054-515-1590	Sequence 1590, App	1428	51.5	2.9	107	7	US-11-025-712-5	Sequence 5, Appl1
1354	51.5	2.9	250	7	US-11-054-515-2073	Sequence 2073, Ap	1429	51.5	2.9	107	7	US-11-061-821-60	Sequence 61, Appl
1355	51.5	2.9	250	7	US-11-054-515-2095	Sequence 2095, Ap	1430	51.5	2.9	107	7	US-11-024-240-114	Sequence 114, App
1356	51.5	2.9	251	7	US-11-054-515-910	Sequence 910, App	1431	51.5	2.9	109	7	US-11-024-251-37	Sequence 37, Appl
1357	51.5	2.9	251	7	US-11-054-515-1459	Sequence 1459, App	1432	51.5	2.9	110	7	US-11-193-512-33	Sequence 33, Appl
1358	51.5	2.9	253	7	US-11-054-515-1664	Sequence 1364, App	1433	51.5	2.9	110	7	US-10-502-145-19	Sequence 19, Appl
1359	51.5	2.9	254	7	US-11-054-515-1266	Sequence 1266, App	1434	51.5	2.9	112	6	US-11-054-669-112	Sequence 112, App
1360	51.5	2.9	254	7	US-11-054-515-1302	Sequence 1302, App	1435	51.5	2.9	116	6	US-10-839-799-87	Sequence 87, Appl
1361	51.5	2.9	255	7	US-11-054-515-1849	Sequence 1849, App	1436	51.5	2.9	126	6	US-11-096-074-422	Sequence 22, Appl
1362	51.5	2.9	256	7	US-11-054-515-1607	Sequence 1607, App	1437	51.5	2.9	126	6	US-11-096-074-422	Sequence 22, Appl
1363	51.5	2.9	259	7	US-11-075-185-24	Sequence 24, Appl	1438	51.5	2.9	130	7	US-11-090-331-4	Sequence 4, Appl1
1364	51.5	2.9	268	6	US-10-995-561-718	Sequence 718, App	1439	51.5	2.9	132	6	US-10-468-561-52	Sequence 2, Appl1
1365	51.5	2.9	271	7	US-11-091-100-17	Sequence 17, Appl	1440	51.5	2.9	138	6	US-11-090-331-8	Sequence 8, Appl1
1370	51.5	2.9	298	7	US-10-485-517-155	Sequence 155, App	1441	51.5	2.9	146	6	US-10-721-763-17	Sequence 17, Appl
1371	51.5	2.9	330	6	US-10-846-172A-7	Sequence 2, Appl1	1442	51.5	2.9	159	6	US-10-689-742-130	Sequence 130, App
1372	51.5	2.9	338	7	US-11-152-892-6	Sequence 6, Appl1	1443	51.5	2.9	177	7	US-10-793-626-1502	Sequence 1502, App
1373	51.5	2.9	343	7	US-11-055-822-132	Sequence 132, App	1444	51.5	2.9	178	6	US-11-102-240-156	Sequence 156, App
1374	51.5	2.9	346	6	US-10-793-626-2514	Sequence 2514, App	1448	51.5	2.9	213	7	US-11-120-338-13	Sequence 13, Appl1
1375	51.5	2.9	355	6	US-10-995-561-720	Sequence 720, App	1450	51.5	2.9	213	7	US-11-173-969-4	Sequence 4, Appl1
1376	51.5	2.9	367	6	US-10-821-234-1058	Sequence 1058, App	1451	51.5	2.9	213	7	US-11-173-969-8	Sequence 8, Appl1
1377	51.5	2.9	374	6	US-10-793-626-3096	Sequence 3096, App	1452	51.5	2.9	214	7	US-11-025-712-11	Sequence 11, Appl1

1453	51	2.9	214	7	US-11-094-625-9	Sequence 9, Appli
1454	51	2.9	214	7	US-11-173-564-1	Sequence 1, Appli
1455	51	2.9	218	6	US-10-923-327-6	Sequence 6, Appli
1456	51	2.9	218	6	US-10-923-327-8	Sequence 8, Appli
1457	51	2.9	218	6	US-10-923-327-10	Sequence 10, Appli
1458	51	2.9	218	6	US-10-923-327-12	Sequence 12, Appli
1459	51	2.9	218	6	US-10-923-327-17	Sequence 17, Appli
1460	51	2.9	218	6	US-11-084-554-11	Sequence 11, Appli
1461	51	2.9	236	6	US-10-995-561-903	Sequence 903, App
1462	51	2.9	236	7	US-11-144-248-47	Sequence 47, Appl
1463	51	2.9	236	7	US-11-144-248-48	Sequence 48, Appl
1464	51	2.9	236	7	US-11-144-248-52	Sequence 52, Appl
1465	51	2.9	237	6	US-10-793-626-162	Sequence 162, App
1466	51	2.9	237	7	US-11-054-669-109	Sequence 109, App
1467	51	2.9	239	7	US-11-139-499-6	Sequence 6, Appli
1468	51	2.9	243	7	US-11-054-515-1943	Sequence 1943, Ap
1469	51	2.9	245	7	US-11-054-515-1895	Sequence 1896, Ap
1470	51	2.9	246	7	US-11-054-515-2075	Sequence 2075, Ap
1471	51	2.9	247	7	US-11-054-515-1651	Sequence 1651, Ap
1472	51	2.9	248	7	US-11-054-515-1440	Sequence 1440, Ap
1473	51	2.9	249	7	US-11-054-515-396	Sequence 396, App
1474	51	2.9	249	7	US-11-054-515-413	Sequence 413, App
1475	51	2.9	249	7	US-11-054-515-426	Sequence 426, App
1476	51	2.9	249	7	US-11-054-515-455	Sequence 455, App
1477	51	2.9	249	7	US-11-054-515-503	Sequence 503, App
1478	51	2.9	249	7	US-11-054-515-507	Sequence 507, App
1479	51	2.9	249	7	US-11-054-515-686	Sequence 686, App
1480	51	2.9	249	7	US-11-054-515-693	Sequence 693, App
1481	51	2.9	249	7	US-11-054-515-763	Sequence 763, App
1482	51	2.9	249	7	US-11-054-515-824	Sequence 824, App
1483	51	2.9	249	7	US-11-054-515-1572	Sequence 1572, Ap
1484	51	2.9	249	7	US-11-054-515-1573	Sequence 1573, Ap
1485	51	2.9	249	7	US-11-054-515-1956	Sequence 1956, Ap
1486	51	2.9	250	7	US-11-054-515-1228	Sequence 1228, Ap
1487	51	2.9	250	7	US-11-054-515-1548	Sequence 1548, Ap
1488	51	2.9	250	7	US-11-054-515-1565	Sequence 1565, Ap
1489	51	2.9	250	7	US-11-054-515-1566	Sequence 1566, Ap
1490	51	2.9	250	7	US-11-054-515-1715	Sequence 1715, Ap
1491	51	2.9	251	7	US-11-054-515-112	Sequence 112, App
1492	51	2.9	251	7	US-11-054-515-131	Sequence 131, App
1493	51	2.9	251	7	US-11-054-515-174	Sequence 174, App
1494	51	2.9	251	7	US-11-054-515-284	Sequence 284, App
1495	51	2.9	251	7	US-11-054-515-990	Sequence 990, App
1496	51	2.9	251	7	US-11-054-515-1148	Sequence 1148, Ap
1497	51	2.9	251	7	US-11-054-515-1397	Sequence 1397, Ap
1498	51	2.9	251	7	US-11-186-284-220	Sequence 220, App
1499	51	2.9	252	7	US-11-054-515-1048	Sequence 1048, Ap
1500	51	2.9	252	7	US-11-054-515-1208	Sequence 1208, Ap

Search completed: December 16, 2005, 11:21:27
Job time : 20 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
OM protein - protein search, using sw model ; Search time 191 Seconds
Run on: December 16, 2005, 11:20:57 (without alignments)
770.638 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 335
Sequence: 1 MAGSPCTLTITLYIMQLTGS.....PMSLMPDTPRLFAVENVI 335
SCORING SCHEME: Gapop 60.0 , Gapext 60.0
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Database : A_Geneseq_21:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV6701	standard;	protein;	335	AA.	
DE	Membrane-bound protein					PRO1138.
PN	WO963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 3;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 2						
ID	AAV70431	standard;	protein;	335	AA.	
DE	Human cell surface immunomodulator-1 (CSIMM-1).					
PN	WO20011150-A1.					
PD	02-MAR-2000.					
PA	(INCY-) INCYTE PHARM INC.					
Query Match		100.0%;	Score 335;	DB 3;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 3						
ID	AAV44609	standard;	protein;	335	AA.	
DE	Human myocardium protein-7.					
PN	WO9967387-A2.					
PD	29-DEC-1999.					
PA	(MILL-) MILLENNIUM PHARM INC.					
Query Match		100.0%;	Score 335;	DB 3;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 4						
ID	AAU29119	standard;	protein;	335	AA.	
DE	Human PRO polypeptide sequence #96.					
PN	WO20016848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 4;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 5						
ID	AAAB87548	standard;	protein;	335	AA.	
DE	Human PRO1138					
PN	WO20016318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 4;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 6						
ID	AAAB7321	standard;	protein;	335	AA.	
DE	APBX-1.					
PN	WO200146260-A2.					
PD	28-JUN-2001.					

PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 100.0%; | Score 335; | DB 4; | Length 335; | || Best Local Similarity | 100.0%; | Pred. No. 2.9e-314; | | | |
RESULT 7						
ID	AAAB5224	standard;	protein;	335	AA.	
DE	Human PRO1138 (UNQ576) protein sequence SEQ ID NO:253.					
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 4;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 8						
ID	ABG95873	standard;	protein;	335	AA.	
DE	Human secreted/transmembrane protein PRO1138.					
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 5;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 9						
ID	ABUS8495	standard;	protein;	335	AA.	
DE	Human PRO polypeptide #96.					
PN	US2003027272-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 6;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 10						
ID	ABU88043	standard;	protein;	335	AA.	
DE	Novel human secreted and transmembrane protein PRO1138.					
PN	US2003032127-A1.					
PD	13-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 6;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 11						
ID	ABU84358	standard;	protein;	335	AA.	
DE	Human secreted/transmembrane protein (PRO) #96.					
PN	US2003032112-A1.					
PD	13-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 6;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 12						
ID	ABR66232	standard;	protein;	335	AA.	
DE	Human secreted polypeptide PRO1138, SEQ ID NO:192.					
PN	US2003027278-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 6;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 13						
ID	ABR65622	standard;	protein;	335	AA.	
DE	Human secreted polypeptide PRO1138, SEQ ID NO:192.					
PN	US2003036159-A1.					
PD	20-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 6;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 14						
ID	ABU95952	standard;	protein;	335	AA.	
DE	Human secreted/transmembrane protein (PRO) #96.					
PN	US2003040070-A1.					
PD	27-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 6;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 15						
ID	ABU58039	standard;	protein;	335	AA.	
DE	Human PRO polypeptide #71.					
PN	US2003027163-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 335;	DB 6;	Length 335;	
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;			
RESULT 16						
ID	ABU59117	standard;	protein;	335	AA.	
DE	Novel human secreted or transmembrane protein PRO1138.					
PN	US2002134252-A1.					
PD	19-SEP-2002.					

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 17
ID ABU82629 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 18
ID ABU82801 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 19
ID ABU8922 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 20
ID ABR66171 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 21
ID ABU60548 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, #100.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 22
ID ABU96224 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 23
ID ABU92655 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 24
ID ABO08732 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 25
ID ABO02784 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 26
ID ABR74938 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;

Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 27
ID ABR94700 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 28
ID ABU13930 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 29
ID ABU85673 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 30
ID ABU98633 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 31
ID ABU98048 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 32
ID ABU91754 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 33
ID ABU89447 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 34
ID ABU86288 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 35
ID ABU67501 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 36
ID ABU80529 standard; protein; 335 AA.
DE Human PRO protein #96.
PN US2003036137-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 37
ID ABO72515 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003005531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 38
ID ABO90898 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 39
ID ABO33957 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO138.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 40
ID ABO99447 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 41
ID ABR98837 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 42
ID ABO16360 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 43
ID ABR92260 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 44
ID ABO16901 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 45
ID ABR76322 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 46
ID ABO71974 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO138.
PN US2003018163-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 47
ID ABO85058 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 48
ID ABO00197 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 49
ID ABO11529 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 50
ID ABO02174 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 51
ID ABO88748 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 52
ID ABO83443 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 53
ID ABO06244 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 54
ID ABR59280 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 55
ID ABO09342 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 56
ID ABO19206 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036118-A1.
PD 20-FEB-2003.

```
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 57
ID ABO11224 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 58
ID ABR66842 standard; protein; 335 AA.
DE Human secreted/polypeptide PRO1138, SEQ ID NO:192.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 59
ID ABO16055 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 60
ID ABO13761 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 61
ID ABU71528 standard; protein; 335 AA.
DE Human secreted/polypeptide PRO1138.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 62
ID ABU65664 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, SEQ ID 192.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 63
ID ABO07512 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 64
ID ABO03699 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 65
ID ABR67147 standard; protein; 335 AA.
DE Human secreted/polypeptide PRO1138, SEQ ID NO:192.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 66
ID ABO15750 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 67
ID ABU56031 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, PRO1138.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 68
ID ABU72309 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 69
ID ABU65359 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 70
ID ABU95304 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 71
ID ABU71207 standard; protein; 335 AA.
DE Human PRO1138 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 72
ID ABO07817 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 73
ID ABR70058 standard; protein; 335 AA.
DE Human secreted/polypeptide PRO1138, SEQ ID NO:192.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 74
ID ABR63991 standard; protein; 335 AA.
DE Human secreted/polypeptide PRO1138, SEQ ID NO:192.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 75
ID ABO01532 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003008353-A1.
PD 09-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 76
ID ABU81334 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003017542-A1.
PD 23-JAN-2003.
```

```
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 77
ID ABR60131 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 78
ID ABU90982 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 79
ID ABR67866 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 80
ID ABR65254 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 81
ID ABR68476 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 82
ID ABR71888 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 83
ID ABU59264 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, #100.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 84
ID ABU85368 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 85
ID ABU89058 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 86
ID ABU83138 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 87
ID ABU94994 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 88
ID ABU90542 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 89
ID ABU84053 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 90
ID ABU93704 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 91
ID ABO25961 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2002127576-A1.
PD 12-FEB-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 92
ID ABR64949 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 93
ID ABO27303 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO138.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 94
ID ABR68781 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 95
ID ABO06597 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 96
ID ABR99142 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 335; DB 6; Length 335;
```

```
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 97
ID ABU57026 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 98
ID ABU85978 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 99
ID ABU82265 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 100
ID ABU87276 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 101
ID ABU83748 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 102
ID ABO08122 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 103
ID ABU92498 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003045684-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 104
ID ABU81833 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 105
ID ABU65997 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 106
ID ABU81168 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 107
ID ABR59626 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 108
ID ABU94014 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 109
ID ABU99867 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 110
ID ABR66537 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 111
ID ABR90955 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 112
ID ABO53283 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO138.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 113
ID ABU58970 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, #100.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 114
ID ABU94382 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 115
ID ABU79264 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 116
ID ABU86593 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
```



```
RESULT 117
ID ABU86898 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 118
ID ABU94687 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 119
ID ABO04614 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 120
ID ABR70363 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 121
ID ABU92348 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 122
ID ABU98528 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 123
ID ABR65927 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 124
ID ABR64644 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 125
ID ABU59413 standard; protein; 335 AA.
DE Novel human secreted or transmembrane protein PRO1054.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 126
ID ABU79569 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 127
ID ABU92360 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 128
ID ABU95919 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 129
ID ABU91139 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 130
ID ABU90232 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 131
ID ABO09647 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 132
ID ABR58417 standard; protein; 335 AA.
DE Human NOV27a.
PN WO2003029423-A2.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 133
ID ABO10919 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 134
ID ABR70973 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 135
ID ABU98285 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002183493-A1.
PD 05-DEC-2002.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 136
ID ABU87581 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 137
ID ABU91449 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
```

PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 138
ID ABU89290 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US200303634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 139
ID ABU84663 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 140
ID ABR69753 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 141
ID ABU80130 standard; protein; 335 AA.
DE Human PRO protein #96.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 142
ID ABU82497 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 143
ID ABU92179 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 144
ID ABU93399 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 145
ID ABO09952 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 146
ID ABO09037 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 147
ID ABU96461 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003027993-A1.

PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 148
ID ABU10685 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 149
ID ABU10605 standard; protein; 335 AA.
DE Human secreted/transmembrane protein #96.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 150
ID ABU81637 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 151
ID ABU72131 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 152
ID ABU95614 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 153
ID ABU96823 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 154
ID ABR70668 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 155
ID ABO05019 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 156
ID ABO08427 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;

RESULT 157
ID AB088576 standard; protein; 335 AA.
DE Human secreted and transmembrane polypeptide PRO1138.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 158
ID ABO34090 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2003017981-A1.
PD 23-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 159
ID ABO05634 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 160
ID ABR74023 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 161
ID ABR95615 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 162
ID ABR80912 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 163
ID ABR81217 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 164
ID AM000913 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 165
ID ABR88515 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 166
ID AMV77336 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054479-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 167
ID ABO28820 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 168
ID ABO31565 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 169
ID ABM07982 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 170
ID ABO40462 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 171
ID ABO35887 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 172
ID ABO44026 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 173
ID ADA77944 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 174
ID AM24821 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 175
ID ABO03089 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;

```
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 176
ID ABR90345 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 177
ID ABM1259 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 178
ID ABR95005 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 179
ID ABR95310 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 180
ID ADB17103 standard; protein; 335 AA.
DE Human transmembrane PRO polypeptide (Seqid 46).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 181
ID ABO21548 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 182
ID ABR97812 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 183
ID ABR87600 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 184
ID ABM77641 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 185
ID ABM27871 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064447-A1.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 186
ID ABM06152 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 187
ID ABM03658 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 188
ID ABM35109 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 189
ID ABM26346 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 190
ID ABO48128 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 191
ID ABR92870 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 192
ID ABO24631 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 193
ID ADA37764 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 194
ID ABM1642 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064447-A1.
```

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 195
ID AEM02743 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 196
ID AEM16039 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 197
ID ABO27600 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 198
ID AEM29091 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 199
ID AEM07067 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 200
ID AEM21161 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 201
ID AEM09507 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 202
ID ABO41377 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 203
ID ABO36192 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068703-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 204
ID ABO43721 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 205
ID AEM76421 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 206
ID AEM76117 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 207
ID AEM25736 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 208
ID AEM26041 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 209
ID ADA21450 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO1138.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 210
ID ABO03394 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 211
ID ABO02479 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 212
ID ABO44261 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO 1138.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 213
ID ABR90650 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036130-A1.

PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 214
ID ABR73718 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 215
ID ABO16970 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 216
ID ABR94395 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 217
ID ABR75902 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 218
ID ABR71278 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 219
ID ABR93175 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 220
ID ABR93480 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 221
ID ADA10237 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, PRO1138.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 222
ID ABR87905 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 223

ID ABO27905 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 224
ID ABO30040 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 225
ID ABO33249 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 226
ID ABO44937 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 227
ID ABO0897 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 228
ID ABO36497 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 229
ID ABO35582 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 230
ID ABO39547 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 231
ID ABO10422 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 232
ID ABO11947 standard; protein; 335 AA.

DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 233
ID ABO52093 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 234
ID ABO52398 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 235
ID ADI19908 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 236
ID ABO23716 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 237
ID ADI17291 standard; protein; 335 AA.
DE Human transmembrane PRO polypeptide (SeqId 46).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 238
ID ADI17781 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 239
ID ABR97202 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 240
ID ABR86990 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 241
ID ABM1032 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 242
ID ABM28176 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 243
ID ABO32175 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 244
ID ABM15302 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 245
ID ABM06457 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 246
ID ABM04268 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 247
ID ABM23281 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 248
ID ABM07677 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 249
ID ABO40767 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 250
ID ABM35414 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 251
ID ABM3177 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 252
ID ABO52703 standard; protein; 335 AA.
DE Human pro polypeptide #96.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 253
ID ABO50263 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 254
ID ABU9257 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 255
ID ABO04309 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 256
ID ABO05939 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 257
ID ABM18479 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 258
ID ADA2789 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 259
ID ABR97507 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 260
ID ABR80607 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049740-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 261
ID ABM01218 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 262
ID ABR8820 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 263
ID ABM13472 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 264
ID ABM20856 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 265
ID ABO41987 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 266
ID ABO42597 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 267
ID ABM10117 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 268
ID ABO38632 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 269
ID ABM32872 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 270				
ID ABR62686 standard; protein; 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US200308723-A1.				
PD 08-MAY-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 271				
ID ABR74897 standard; protein; 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US200309635-A1.				
PD 22-MAY-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 272				
ID ADY79736 standard; protein; 335 AA.				
DE Human secreted/transmembrane protein (PRO) #96.				
PN US2003073173-A1.				
PD 17-APR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 273				
ID ABR56287 standard; protein; 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003054458-A1.				
PD 20-MAR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 274				
ID ABR02438 standard; protein; 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003059886-A1.				
PD 27-MAR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 275				
ID ABR66380 standard; protein; 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003049758-A1.				
PD 13-MAR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 276				
ID ABR66685 standard; protein; 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003049772-A1.				
PD 13-MAR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 277				
ID ABR16649 standard; protein; 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003064448-A1.				
PD 03-APR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 278				
ID ABR29701 standard; protein; 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003064456-A1.				
PD 03-APR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 279				
ID ABO29125 standard; protein; 335 AA.				
DE Human secreted/transmembrane protein (PRO) #96.				
PN US2003068693-A1.				
PD 10-APR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 280				
ID ABR23906 standard; protein; 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003068735-A1.				
PD 10-APR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 281				
ID ABR23296 standard; protein; 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003068753-A1.				
PD 10-APR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 282				
ID ABR22076 standard; protein; 335 AA.				
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.				
PN US2003068742-A1.				
PD 10-APR-2003.				
Query Match	100.0%;	Score 335;	DB 6;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 2.9e-314;		
RESULT 283				
ID ABO37717 standard; protein; 335 AA.				
DE Human secreted/transmembrane protein (PRO) #96.				
PN US2003068756-A1.				
PD 10-APR-2003.				
Query Match	100.0%;	Score 335;		

Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 289
ID ABR96592 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054460-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 290
ID ABO20328 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 291
ID ABO21243 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 292
ID ABO22158 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 293
ID ADA20080 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 294
ID ABO34189 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO 1138.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 295
ID ABR96592 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 296
ID ADA94469 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003055832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 297
ID ABR85770 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 298
ID ABR99752 standard; protein; 335 AA.

DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 299
ID ABR00608 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 300
ID ABR00303 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 301
ID ABO29735 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 302
ID ABR23601 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 303
ID ABR23996 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 304
ID ABO38327 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 305
ID ABO45627 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 306
ID ABR20551 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 307
ID ADA81463 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003092121-A1.
PD 15-MAY-2003.

```
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 308
ID ABO16665 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 309
ID ABO18291 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 310
ID ABO22718 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 311
ID ABO23023 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 312
ID ABR92565 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 313
ID ABR81522 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 314
ID AM77946 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 315
ID ABR89735 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 316
ID AM26651 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 317
ID AM13777 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 318
ID ABO28515 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 319
ID ABO30345 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 320
ID AM07372 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 321
ID AM03963 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 322
ID ABO37107 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 323
ID ABO41682 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 324
ID ABO35277 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 325
ID AM25126 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 326
ID ABO47518 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049742-A1.
PD 13-MAR-2003.
```

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 327
ID ABO47823 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 328
ID ABO48433 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 329
ID ABO51483 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 330
ID ABO51788 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 331
ID ABO50568 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 332
ID ABR79692 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 333
ID ABM16954 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 334
ID ABO17986 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 335
ID ABO20938 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 336

ID ABR96897 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 337
ID ADA38694 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 338
ID ABM12252 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 339
ID ABM16344 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 340
ID ABM24211 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 341
ID ABM14692 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 342
ID ABM04573 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 343
ID ABM06762 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 344
ID ABM09202 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 345
ID ABO39242 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068775-A1.
PD 10-APR-2003.

```
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 346
ID ABR75507 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 347
ID ABR25431 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 348
ID ABR19941 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 349
ID ABO46847 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 350
ID ABO47152 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 351
ID ADA83261 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 352
ID ABR71583 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 353
ID ABR72193 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 354
ID ABR98532 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 355
ID ABO06902 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 356
ID ABR84855 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 357
ID ABR73413 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 358
ID ABR76507 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 359
ID ABR73108 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 360
ID ABR18174 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 361
ID ABO20633 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 362
ID ABO25376 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 363
ID ABO25681 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 364
ID ABR94090 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
```

RESULT 365
ID ADA92815 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 366
ID ABR79997 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 367
ID ABM11337 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 368
ID ABO32944 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 369
ID ABO30650 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 370
ID ABO30955 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 371
ID ABM27261 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 372
ID ABM30006 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 373
ID ABM05542 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 374
ID ABM15607 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 375
ID ABM08592 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 376
ID ABO42292 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 377
ID ABO38022 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 378
ID ABO45932 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 379
ID ABM66735 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 380
ID ADB20304 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 381
ID ABM19636 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 382
ID ABO49348 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 335; DB 6; Length 335;
Pred. No. 2.9e-314;
RESULT 383
ID ABO49653 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049775-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 384
ID AOA78556 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 385
ID ABR88210 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 386
ID ADA00377 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO 138.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 387
ID ABM26956 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 388
ID ABM03353 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 389
ID ABO39852 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 390
ID ABO49958 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 391
ID ABO50873 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 392
ID ABO05329 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;

Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 393
ID ABR74633 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 394
ID ABR77112 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 395
ID ABM17869 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 396
ID ABR95920 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 397
ID ABO21853 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 398
ID ABO20023 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 399
ID ABO24326 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 400
ID ABR86075 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 401
ID ABM10727 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 402
ID ABM76726 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054465-A1.
PD 20-MAR-2003.

```
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 403
ID ABR89430 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 404
ID ABR12557 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 405
ID ABR05847 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 406
ID ABO34972 standard; protein; 335 AA.
DE Human pro polypeptide #96.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 407
ID ABR03048 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 408
ID ABR19026 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 409
ID ABR19331 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 410
ID ABO46542 standard; protein; 335 AA.
DE Human pro polypeptide #96.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 411
ID ABO49043 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 412
ID ABR69086 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 413
ID ABR89125 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 414
ID ABR72498 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 415
ID ABR74328 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 416
ID ABO18596 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 417
ID ABR80302 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 418
ID ABR01523 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 419
ID ABR02133 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 420
ID ABR87295 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 421
ID ABR12862 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073186-A1.
```

```
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 422
ID AEM30616 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 423
ID AEM24516 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 424
ID ABO29430 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 425
ID ABO31260 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 426
ID AEM14387 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 427
ID AEM09612 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 428
ID ABO38937 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 429
ID AEM34702 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 430
ID ABO51178 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 431
ID ABO04004 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 432
ID ABO10474 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 433
ID ABO53176 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 434
ID ABR77717 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 435
ID ABR78927 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 436
ID ABO24021 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 437
ID ABR93785 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 438
ID AEM01828 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003058883-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 439
ID AEM78251 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 440
ID ABR90040 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073177-A1.
```

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 441
ID ADA22376 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO1138.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 442
ID AEM27566 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN 03-APR-2003.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 443
ID AEM13167 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 444
ID ABO31870 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 445
ID AEM14082 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 446
ID AEM08287 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 447
ID ABO40157 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 448
ID AEM74592 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 449
ID AEM33787 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;

RESULT 450
ID AEM20246 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 451
ID ABO48738 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 452
ID ABO22546 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 453
ID ABR72803 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 454
ID ABO15445 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 455
ID ABR85160 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 456
ID ABO15140 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 457
ID ABO17275 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 458
ID AEM17564 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 459
ID ABO6542 standard; protein; 335 AA.
DE Human secreted/transmembrane PRO polypeptide #71.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;

RESULT 460
ID ADA39235 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003068782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 461
ID ABR85465 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003048746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 462
ID AAM77031 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 463
ID ABO28210 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 464
ID ABO28210 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 465
ID AAM22991 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 466
ID AAM21771 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 467
ID AAM21466 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 468
ID AAM14997 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 469
ID ABO41072 standard; protein; 335 AA.

DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 470
ID ABO36802 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 471
ID ABO37412 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 472
ID AAM75202 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 473
ID AAM33482 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 474
ID ABO46237 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 475
ID ADA82627 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 476
ID ADB85619 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003048735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 477
ID ADB96261 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 478
ID AAM31836 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068680-A1.

```
PD 10-APR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 479
ID ABM31226 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 480
ID ADB85935 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 481
ID ABM32141 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 482
ID ABM32446 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 483
ID ADB68298 standard; protein; 335 AA.
DE Human PRO1138 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 484
ID ADB68105 standard; protein; 335 AA.
DE Human PRO1138 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 485
ID ABM31531 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 486
ID ABM30921 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 487
ID ADB90922 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 488
ID ADC57733 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003027154-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 489
ID ADC55097 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 490
ID ADC11964 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003048681-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 491
ID ADC07002 standard; protein; 335 AA.
DE Human PRO1138 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 492
ID ADC56386 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 493
ID ADC117181 standard; protein; 335 AA.
DE Mammalian PRO polypeptide (SeqID 46).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 494
ID ADC07441 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 495
ID ADC11431 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 496
ID ADC14879 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 497
ID ADC52374 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003138882-A1.
PD 24-JUL-2003.
```

```

PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 498
ID ADCL4553 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 499
ID ADD08085 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 500
ID ADC81910 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 501
ID ADD07552 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 502
ID ADC82443 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 503
ID ADD05665 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 504
ID ADD08623 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 505
ID ADD06872 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 506
ID ADC89503 standard; protein; 335 AA.
DE Human natural killer cell surface receptor CSI.
PN US2003113332-A1.
PD 19-JUN-2003.
PA (UYNT-) UNIV NORTH TEXAS HEALTH SCI CENT.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 507
ID ADC83119 standard; protein; 335 AA.
DE Human PRO polypeptide #71.

```

```

PN US2003059763-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 508
ID ADD67525 standard; protein; 335 AA.
DE Human Ly1728P protein SEQ ID NO:2.
PN NO2003062401-A2.
PD 31-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 509
ID ADD55226 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 510
ID ADD36050 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 511
ID ADD56184 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 512
ID ADD54622 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 513
ID ADE26776 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 514
ID ADE26243 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 515
ID ADP67180 standard; protein; 335 AA.
DE Human PRO1138 amino acid sequence SEQ ID NO:253.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 516
ID ADG01051 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 517

```


ID ADG08604 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 518
ID ADG02660 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 519
ID ADG01367 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 520
ID ADP95542 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 521
ID ADP95225 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 522
ID ADG13357 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 523
ID ADH24078 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 524
ID ADH34104 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 525
ID ADH29937 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 526
ID ADH32908 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.

PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 527
ID ADH09017 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 528
ID ADG85312 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 529
ID ADH24588 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 530
ID ADH37444 standard; protein; 335 AA.
DE Human secreted and transmembrane protein PRO138 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 531
ID ADH02033 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 532
ID ADH37614 standard; protein; 335 AA.
DE Human secreted and transmembrane protein PRO138 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 533
ID ADG85652 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 534
ID ADH24248 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 535
ID ADH38542 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181643-A1.

PD	25-SEP-2003.	PD	ADH37784 standard; protein; 335 AA.
PA	(GETH) GENENTECH INC.	PD	ADH37961 standard; protein; 335 AA.
Query Match	100.0%; Score 335; DB 7; Length 335;	PD	ADH37961 standard; protein; 335 AA.
Best Local Similarity	100.0%; Pred. No. 2.9e-314;	PN	US2003181647-A1.
RESULT 536		PD	25-SEP-2003.
ID	ADG83563 standard; protein; 335 AA.	PA	(GETH) GENENTECH INC.
DE	Human PRO polypeptide #23.	Query Match	100.0%; Score 335; DB 7; Length 335;
PN	US2003180794-A1.	Best Local Similarity	100.0%; Pred. No. 2.9e-314;
PD	25-SEP-2003.	RESULT 537	
PA	(GETH) GENENTECH INC.	ID	ADH29471 standard; protein; 335 AA.
Query Match	100.0%; Score 335; DB 7; Length 335;	DE	Novel human secreted and transmembrane protein PRO1138.
Best Local Similarity	100.0%; Pred. No. 2.9e-314;	PN	US2003180860-A1.
RESULT 538		PD	25-SEP-2003.
ID	ADH27587 standard; protein; 335 AA.	PA	(GETH) GENENTECH INC.
Best Local Similarity	100.0%; Pred. No. 2.9e-314;	Query Match	100.0%; Score 335; DB 7; Length 335;
RESULT 539		Best Local Similarity	100.0%; Pred. No. 2.9e-314;
ID	ADH37784 standard; protein; 335 AA.	RESULT 539	
DE	Human secreted and transmembrane protein PRO1138 CDNA.	ID	ADH37784 standard; protein; 335 AA.
PN	US2003181647-A1.	DE	Human secreted and transmembrane protein PRO1138 CDNA.
PD	25-SEP-2003.	PN	US2003181647-A1.
PA	(GETH) GENENTECH INC.	PD	25-SEP-2003.
Query Match	100.0%; Score 335; DB 7; Length 335;	PA	(GETH) GENENTECH INC.
Best Local Similarity	100.0%; Pred. No. 2.9e-314;	Query Match	100.0%; Score 335; DB 7; Length 335;
RESULT 540		Best Local Similarity	100.0%; Pred. No. 2.9e-314;
ID	ADH37961 standard; protein; 335 AA.	RESULT 540	
DE	Human secreted and transmembrane protein PRO138 CDNA.	ID	ADH37961 standard; protein; 335 AA.
PN	US2003181649-A1.	DE	Human secreted and transmembrane protein PRO138 CDNA.
PD	25-SEP-2003.	PN	US2003181649-A1.
PA	(GETH) GENENTECH INC.	PD	25-SEP-2003.
Query Match	100.0%; Score 335; DB 7; Length 335;	PA	(GETH) GENENTECH INC.
Best Local Similarity	100.0%; Pred. No. 2.9e-314;	Query Match	100.0%; Score 335; DB 7; Length 335;
RESULT 541		Best Local Similarity	100.0%; Pred. No. 2.9e-314;
ID	ADH57381 standard; protein; 335 AA.	RESULT 541	
DE	Novel human secreted and transmembrane protein PRO1138.	ID	ADH57381 standard; protein; 335 AA.
PN	US2003180920-A1.	DE	Novel human secreted and transmembrane protein PRO1138.
PD	25-SEP-2003.	PN	US2003180920-A1.
PA	(GETH) GENENTECH INC.	PD	25-SEP-2003.
Query Match	100.0%; Score 335; DB 7; Length 335;	PA	(GETH) GENENTECH INC.
Best Local Similarity	100.0%; Pred. No. 2.9e-314;	Query Match	100.0%; Score 335; DB 7; Length 335;
RESULT 542		Best Local Similarity	100.0%; Pred. No. 2.9e-314;
ID	ADH53523 standard; protein; 335 AA.	RESULT 542	
DE	Novel human secreted and transmembrane protein PRO1138.	ID	ADH53523 standard; protein; 335 AA.
PN	US2003181636-A1.	DE	Novel human secreted and transmembrane protein PRO1138.
PD	25-SEP-2003.	PN	US2003181636-A1.
PA	(GETH) GENENTECH INC.	PD	25-SEP-2003.
Query Match	100.0%; Score 335; DB 7; Length 335;	PA	(GETH) GENENTECH INC.
Best Local Similarity	100.0%; Pred. No. 2.9e-314;	Query Match	100.0%; Score 335; DB 7; Length 335;
RESULT 543		Best Local Similarity	100.0%; Pred. No. 2.9e-314;
ID	ADH53563 standard; protein; 335 AA.	RESULT 543	
DE	Novel human secreted and transmembrane protein PRO1138.	ID	ADH53563 standard; protein; 335 AA.
PN	US2003181641-A1.	DE	Novel human secreted and transmembrane protein PRO1138.
PD	25-SEP-2003.	PN	US2003181641-A1.
PA	(GETH) GENENTECH INC.	PD	25-SEP-2003.
Query Match	100.0%; Score 335; DB 7; Length 335;	PA	(GETH) GENENTECH INC.
Best Local Similarity	100.0%; Pred. No. 2.9e-314;	Query Match	100.0%; Score 335; DB 7; Length 335;
RESULT 544		Best Local Similarity	100.0%; Pred. No. 2.9e-314;
ID	ADH52029 standard; protein; 335 AA.	RESULT 544	
DE	Novel human secreted and transmembrane protein PRO1138.	ID	ADH52029 standard; protein; 335 AA.
PN	US2003181638-A1.	DE	Novel human secreted and transmembrane protein PRO1138.
PD	25-SEP-2003.	PN	US2003181638-A1.
PA	(GETH) GENENTECH INC.	PD	25-SEP-2003.

PA	(GETH) GENENTECH INC.	100.0%;	Score 335;	DB 7;	Length 335;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 545					
ID	ADH49684 standard; protein; 335 AA.				
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003181639-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.	100.0%;	Score 335;	DB 7;	Length 335;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 546					
ID	AD125394 standard; protein; 335 AA.				
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003181696-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.	100.0%;	Score 335;	DB 7;	Length 335;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 547					
ID	ADH90187 standard; protein; 335 AA.				
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003181698-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.	100.0%;	Score 335;	DB 7;	Length 335;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 548					
ID	AD125564 standard; protein; 335 AA.				
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003181669-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.	100.0%;	Score 335;	DB 7;	Length 335;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 549					
ID	ADH97738 standard; protein; 335 AA.				
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003181672-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.	100.0%;	Score 335;	DB 7;	Length 335;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 550					
ID	AD135434 standard; protein; 335 AA.				
DE	Human PRO polypeptide #71.				
PN	US2003050457-A1.				
PD	13-MAR-2003.				
PA	(GETH) GENENTECH INC.	100.0%;	Score 335;	DB 7;	Length 335;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 551					
ID	AD103586 standard; protein; 335 AA.				
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003181656-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.	100.0%;	Score 335;	DB 7;	Length 335;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 552					
ID	AD111943 standard; protein; 335 AA.				
DE	Human PRO polypeptide #23.				
PN	US2003181686-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.	100.0%;	Score 335;	DB 7;	Length 335;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 553					
ID	ADH90017 standard; protein; 335 AA.				
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003181697-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.	100.0%;	Score 335;	DB 7;	Length 335;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		
RESULT 554					
ID	ADH90017 standard; protein; 335 AA.				
DE	Novel human secreted and transmembrane protein PRO1138.				
PN	US2003181697-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.	100.0%;	Score 335;	DB 7;	Length 335;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 2.9e-314;		

Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 554
ID ADH9926 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 555
ID ADH9418 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181707-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 556
ID ADI1093 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181682-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 557
ID ADI11603 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181684-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 558
ID ADH9248 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181709-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 559
ID ADH9658 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181708-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 560
ID ADH9078 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181673-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 561
ID ADI05066 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180848-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 562
ID ADI01988 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181654-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 563
ID ADI03246 standard; protein; 335 AA.

ID ADI04811 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181657-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 564
ID ADH78265 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181668-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 565
ID ADI19609 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181676-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 566
ID ADH90357 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181699-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 567
ID ADI03076 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181653-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 568
ID ADH77925 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181666-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 569
ID ADH97908 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181674-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 570
ID ADI01293 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003190669-A1.
PD 09-OCT-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 571
ID ADI01988 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181652-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 572
ID ADI03246 standard; protein; 335 AA.

DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 573
ID AD11433 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 574
ID AD10235 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 575
ID AD11773 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 576
ID AD105410 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 577
ID ADH79482 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 578
ID AD119439 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 579
ID AD105240 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 580
ID ADH79652 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 581
ID AD101478 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 582
ID AD101648 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 583
ID AD101818 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 584
ID ADH79822 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 585
ID AD104640 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 586
ID AD102776 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 587
ID ADH78095 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 588
ID AD125734 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 589
ID AD125904 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 590
ID ADK65416 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003073821-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 591
ID ADH98758 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 592
ID ADH79999 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 593
ID ADL3798 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 594
ID ADM30332 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 595
ID ADL93730 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 596
ID ADC52184 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 597
ID ADE74329 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 598
ID ADE74941 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 599
ID ADF35379 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;

RESULT 600
ID ADG11629 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 601
ID ADF96154 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 602
ID ADG04425 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 603
ID ADG00585 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 604
ID ADH06616 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 605
ID ADH06446 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 606
ID ADG68667 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 607
ID ADH27757 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 608
ID ADH25098 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 609
ID ADH33730 standard; protein; 335 AA.

DE Human PRO polypeptide #23.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 610
ID ADG82841 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 611
ID ADH02373 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 612
ID ADH07980 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 613
ID ADG6977 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 614
ID ADH3198 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 615
ID ADH26122 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 616
ID ADG83938 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 617
ID ADH19499 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 618
ID ADG85482 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.

PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 619
ID ADH06276 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 620
ID ADH31016 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 621
ID ADH24418 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 622
ID ADH33091 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 623
ID ADG69547 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 624
ID ADH07810 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 625
ID ADG85822 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 626
ID ADH3968 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 627
ID ADH33560 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181637-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 628
ID ADH33900 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 629
ID ADH01110 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 630
ID ADG69717 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 631
ID ADH20992 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN 04-DEC-2003.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 632
ID ADH02203 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 633
ID ADG69207 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 634
ID ADG85992 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 635
ID ADH24928 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 636
ID ADH3545 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 637
ID ADH20032 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 638
ID ADH02543 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 639
ID ADG69037 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 640
ID ADH07640 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 641
ID ADG86162 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 642
ID ADH24758 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 643
ID ADH25806 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 644
ID ADH38372 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 645
ID ADH57211 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;


```
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 646
ID ADH5199 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 647
ID ADH4565 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 648
ID ADH90527 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 649
ID ADI11263 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 650
ID ADH98928 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 651
ID ADI02158 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 652
ID ADH90697 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 653
ID ADJ54830 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 654
ID ADJ98572 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 655
ID ADJ98742 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 656
ID ADH78901 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 657
ID ADJ99135 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 658
ID ADJ99305 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 659
ID ADJ98923 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 660
ID ADH79071 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 661
ID ADK00931 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 662
ID ADK14452 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 663
ID ADJ64601 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 664
```

ID ADM31497 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 665
ID ADM3544 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 666
ID ADM40349 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 667
ID ADM80901 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 668
ID ADN37957 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 669
ID ADU87689 standard; protein; 335 AA.
DE Human C91 (SLMF7) protein.
PN WO2004100898-A2.
PD 25-NOV-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 100.0%; Score 335; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 670
ID ADY19131 standard; protein; 335 AA.
DE PRO polypeptide SEQ ID NO 4937.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 671
ID ADY77741 standard; protein; 335 AA.
DE Neoplastic disease detection protein PRO1138.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (BATO) EATON D L.
PA (FILV) FILVAROEF E.
PA (GERR) GERRITSEN M E.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GRIM) GRIMALDI V C.
PA (GURN) GURNEY A L.
PA (WATA) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 672
ID AEA38506 standard; protein; 335 AA.

DE Human secreted/transmembrane protein, #139.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 673
ID AAB32373 standard; protein; 336 AA.
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:59.
PN WO200047602-A1.
PD 17-AUG-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 335; DB 3; Length 336;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 674
ID ADS98579 standard; protein; 340 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 843.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 100.0%; Score 335; DB 8; Length 340;
Best Local Similarity 100.0%; Pred. No. 2.9e-314;
RESULT 675
ID AAY44610 standard; protein; 312 AA.
DE Mature human myocardium protein-7.
PN WO9967387-A2.
PD 29-DEC-1999.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 93.1%; Score 312; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 4.2e-292;
RESULT 676
ID ADS97998 standard; protein; 296 AA.
DE Protein factor discovery related isolated human polypeptide, SEQ ID 262.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 76.7%; Score 257; DB 8; Length 296;
Best Local Similarity 100.0%; Pred. No. 4.7e-239;
RESULT 677
ID ABB97473 standard; protein; 328 AA.
DE Novel human protein SEQ ID NO: 741.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 76.7%; Score 257; DB 5; Length 328;
Best Local Similarity 100.0%; Pred. No. 5.1e-239;
RESULT 678
ID ADS98765 standard; protein; 328 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 1029.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 76.7%; Score 257; DB 8; Length 328;
Best Local Similarity 100.0%; Pred. No. 5.1e-239;
RESULT 679
ID ADD16672 standard; protein; 335 AA.
DE Human disease related protein Segid103.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 69.9%; Score 234; DB 7; Length 335;
Best Local Similarity 99.7%; Pred. No. 8e-217;
RESULT 680
ID ADU69599 standard; protein; 335 AA.
DE Human heat mitochondrial protein as a therapeutic target Segid1405.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 69.9%; Score 234; DB 7; Length 335;

Best Local Similarity 99.7%; Pred. No. 8e-217;
RESULT 681
ID ABR58418 standard; protein; 348 AA.
DE Human NOV27D.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 64.8%; Score 217; DB 6; Length 348;
Best Local Similarity 100.0%; Pred. No. 2.1e-200;
RESULT 682
ID ABR20055 standard; protein; 165 AA.
DE Human immune response associated protein (IRAP), seq id 15.
PN WO2004048550-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 37.6%; Score 126; DB 8; Length 165;
Best Local Similarity 100.0%; Pred. No. 6.9e-113;
RESULT 683
ID ADN02731 standard; protein; 204 AA.
DE Human receptor and membrane-associated protein #34.
PN WO2004029218-A2.
PD 08-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 37.6%; Score 126; DB 8; Length 204;
Best Local Similarity 100.0%; Pred. No. 8.2e-113;
RESULT 684
ID AAM67911 standard; protein; 110 AA.
DE Human secreted protein encoded by gene 5 clone HSA5AV70.
PN WO9842738-A1.
PD 01-OCT-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 110; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.3e-97;
RESULT 685
ID AAB32405 standard; protein; 110 AA.
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:91.
PN WO20047602-A1.
PD 17-AUG-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 110; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.3e-97;
RESULT 686
ID ADA57321 standard; protein; 110 AA.
DE Human secreted protein #32.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 110; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.3e-97;
RESULT 687
ID ADA56750 standard; protein; 110 AA.
DE Human secreted protein #32.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 110; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.3e-97;
RESULT 688
ID ADA40601 standard; protein; 110 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 110; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.3e-97;
RESULT 689
ID ADA41198 standard; protein; 110 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 110; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.3e-97;
RESULT 690
ID AAG00391 standard; protein; 97 AA.
DE Human secreted protein, SEQ ID NO: 4472.
PN EPI033401-A2.
PD 06-SEP-2000.
PA (GEST-) GENSET.
Query Match 29.0%; Score 97; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 4.2e-85;
RESULT 691
ID AAV11662 standard; protein; 98 AA.
DE Human 5' EST secreted protein SEQ ID NO:314.
PN WO9906439-A2.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 29.0%; Score 97; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.2e-85;
RESULT 692
ID ABG11697 standard; protein; 684 AA.
DE Novel human diagnostic protein #11688.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 27.5%; Score 92; DB 4; Length 684;
Best Local Similarity 100.0%; Pred. No. 1.5e-79;
RESULT 693
ID ABG12169 standard; protein; 684 AA.
DE Novel human diagnostic protein #12160.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 27.5%; Score 92; DB 4; Length 684;
Best Local Similarity 100.0%; Pred. No. 1.5e-79;
RESULT 694
ID ADS98714 standard; protein; 684 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 978.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 27.5%; Score 92; DB 8; Length 684;
Best Local Similarity 100.0%; Pred. No. 1.5e-79;
RESULT 695
ID AAM21122 standard; protein; 91 AA.
DE Peptide #7556 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 27.2%; Score 91; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.4e-79;
RESULT 696
ID ABB43438 standard; peptide; 91 AA.
DE Peptide #10944 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 27.2%; Score 91; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.4e-79;
RESULT 697
ID AAM37326 standard; protein; 91 AA.
DE Peptide #11363 encoded by probe for measuring placental gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 27.2%; Score 91; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.4e-79;
RESULT 698
ID ABB26408 standard; protein; 91 AA.
DE Protein #8407 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 27.2%; Score 91; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.4e-79;

RESULT 699
ID AAM77190 standard; protein; 91 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 37496.
PN W0200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 27.2%; Score 91; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.4e-79;
RESULT 700
ID AAM64367 standard; protein; 91 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 36472.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 27.2%; Score 91; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.4e-79;
RESULT 701
ID ABG58815 standard; peptide; 91 AA.
DE Human liver peptide, SEQ ID No 37463.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 27.2%; Score 91; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.4e-79;
RESULT 702
ID ABG46203 standard; peptide; 91 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 35868.
PN W0200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 27.2%; Score 91; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.4e-79;
RESULT 703
ID AAB32404 standard; protein; 90 AA.
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:90.
PN W0200047602-A1.
PD 17-AUG-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.7%; Score 86; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-74;
RESULT 704
ID AAY12645 standard; protein; 124 AA.
DE Human 5' EST secreted protein SEQ ID NO: 310 from W0 9906553.
PN W09906553-A2.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 20.3%; Score 68; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
RESULT 705
ID ADR20041 standard; protein; 91 AA.
DE Human immune response associated protein (IRAP), seq id 1.
PN W02004048550-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.2%; Score 51; DB 8; Length 91;
Best Local Similarity 100.0%; Pred. No. 9.4e-41;
RESULT 706
ID AAM67933 standard; protein; 33 AA.
DE Fragment of human secreted protein encoded by gene 5.
PN W09842738-A1.
PD 01-OCT-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.9%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.2e-24;
RESULT 707
ID AAM67932 standard; protein; 28 AA.
DE Fragment of human secreted protein encoded by gene 5.
PN W09842738-A1.
PD 01-OCT-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.1%; Score 27; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e-18;
RESULT 708

ID AAM87990 standard; protein; 114 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:15583.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.7%; Score 19; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 8.5e-10;
RESULT 709
ID ADC89505 standard; peptide; 11 AA.
DE Human natural killer cell surface receptor CSI antigenic peptide #2.
PN US2003113332-A1.
PD 19-JUN-2003.
PA (UNVT-) UNIV NORTH TEXAS HEALTH SCI CENT.
Query Match 3.3%; Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0061;
RESULT 710
ID ADC89504 standard; peptide; 12 AA.
DE Human natural killer cell surface receptor CSI antigenic peptide #1.
PN US2003113332-A1.
PD 19-JUN-2003.
PA (UNVT-) UNIV NORTH TEXAS HEALTH SCI CENT.
Query Match 3.3%; Score 11; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0065;
RESULT 711
ID ADC89506 standard; peptide; 16 AA.
DE Human natural killer cell surface receptor CSI antigenic peptide #3.
PN US2003113332-A1.
PD 19-JUN-2003.
PA (UNVT-) UNIV NORTH TEXAS HEALTH SCI CENT.
Query Match 3.3%; Score 11; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0064;
RESULT 712
ID AAG25088 standard; protein; 66 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29010.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.7%; Score 9; DB 3; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.4;
RESULT 713
ID AAG35118 standard; protein; 66 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 42854.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.7%; Score 9; DB 3; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.4;
RESULT 714
ID ABG25025 standard; protein; 456 AA.
DE Novel human diagnostic protein #25016.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 9; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 12;
RESULT 715
ID AAY13308 standard; peptide; 15 AA.
DE Naturally occurring variant of the glutenin epitope Y13221.
PN EP905518-A1.
PD 31-MAR-1999.
PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
Query Match 2.4%; Score 8; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.2;
RESULT 716
ID AAB74404 standard; peptide; 26 AA.
DE Desmoglein sequence transmembrane domain.
PN W0200118056-A2.
PD 15-MAR-2001.
PA (GENE-) GENENIA LTD.
Query Match 2.4%; Score 8; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.9;
RESULT 717
ID AAB80619 standard; protein; 105 AA.
DE Environmental stress tolerant protein SEQ ID 24.

PN W0200106006-A1.
PD 25-JAN-2001.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 2.4%; Score 8; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
RESULT 718
ID AAM37871 standard; protein; 122 AA.
DE Human protein comprising secretory signal amino acid sequence 8.
PN W09811217-A2.
PD 19-MAR-1998.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (PROT-) PROTEGENE INC.
Query Match 2.4%; Score 8; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 37;
RESULT 719
ID ADT58961 standard; protein; 130 AA.
DE Plant polypeptide; SEQ ID 9038.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 2.4%; Score 8; DB 8; Length 130;
Best Local Similarity 100.0%; Pred. No. 39;
RESULT 720
ID AAB27244 standard; protein; 172 AA.
DE Human EXMAD-22 SEQ ID NO: 22.
PN W0200068380-A2.
PD 16-NOV-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 8; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 49;
RESULT 721
ID AAM40751 standard; protein; 194 AA.
DE Human polypeptide SEQ ID NO 5682.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSB-) HYSBQ INC.
Query Match 2.4%; Score 8; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 55;
RESULT 722
ID AEA20940 standard; protein; 194 AA.
DE Novel human polypeptide SEQ ID NO 1634.
PN W02005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 2.4%; Score 8; DB 9; Length 194;
Best Local Similarity 100.0%; Pred. No. 55;
RESULT 723
ID ADM80804 standard; protein; 259 AA.
DE Human CADECM-33 protein SEQ ID NO:33.
PN W02004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.4%; Score 8; DB 8; Length 259;
Best Local Similarity 100.0%; Pred. No. 70;
RESULT 724
ID ADT99536 standard; protein; 270 AA.
DE Human DSG2.
PN W02004093788-A2.
PD 04-NOV-2004.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 2.4%; Score 8; DB 8; Length 270;
Best Local Similarity 100.0%; Pred. No. 73;
RESULT 725
ID AAY93912 standard; protein; 289 AA.
DE A human hyaluronan-binding protein, designated OE-HAMP.
PN W0200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RBD CROSG.
Query Match 2.4%; Score 8; DB 3; Length 289;
Best Local Similarity 100.0%; Pred. No. 77;
RESULT 726
ID ABU24508 standard; protein; 306 AA.

DE Protein encoded by prokaryotic essential gene #10035.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.4%; Score 8; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 81;
RESULT 727
ID ADA55489 standard; protein; 310 AA.
DE Human protein, SEQ ID 3057.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELT-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.4%; Score 8; DB 6; Length 310;
Best Local Similarity 100.0%; Pred. No. 82;
RESULT 728
ID AAY13381 standard; protein; 360 AA.
DE Amino acid sequence of protein PRO271.
PN W09914328-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Query Match 2.4%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 729
ID ADC78533 standard; protein; 360 AA.
DE Human PRO271 protein.
PN W0200015796-A2.
PD 23-MAR-2000.
PA (GETH-) GENENTECH INC.
Query Match 2.4%; Score 8; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 730
ID AAB80249 standard; protein; 360 AA.
DE Human PRO271 protein.
PN W0200104311-A1.
PD 18-JAN-2001.
PA (GETH-) GENENTECH INC.
Query Match 2.4%; Score 8; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 731
ID AAV29037 standard; protein; 360 AA.
DE Human PRO polypeptide sequence #14.
PN W0200168848-A2.
PD 20-SEP-2001.
PA (GETH-) GENENTECH INC.
Query Match 2.4%; Score 8; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 732
ID AAM38965 standard; protein; 360 AA.
DE Human polypeptide SEQ ID NO 2110.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSB-) HYSBQ INC.
Query Match 2.4%; Score 8; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 733
ID ABUS8413 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 734
ID ABU71627 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH-) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 735
ID ABU87961 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.

[illegible]

Best Local Similarity 100.0%; Pred. No. 93;
RESULT 756
ID ABU86206 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 757
ID ABU67419 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 758
ID ABU80447 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 759
ID ABO01811 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 760
ID ABR93365 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 761
ID ABR98755 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 762
ID ABO16278 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 763
ID ABR92178 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 764
ID ABO18619 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 765
ID ABR78240 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054474-A1.
PD 20-MAR-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 766
ID ABU84976 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032114-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 767
ID ABO00115 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032101-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 768
ID ABO11447 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 769
ID ABO02092 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 770
ID ABU54384 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 771
ID ABU8666 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 772
ID ABU83361 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 773
ID ABO06162 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 774
ID ABR59198 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 775
ID ABO09260 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;


```
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 776
ID ABO15124 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 777
ID ABO11142 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 778
ID ABR66760 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 779
ID ABO15973 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 780
ID ABO13679 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 781
ID ABO47399 standard; protein; 360 AA.
DE Human secreted/transmembrane polypeptide PRO271.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 782
ID ABU65582 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, SEQ ID 28.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 783
ID ABO07430 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 784
ID ABO03617 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 785
ID ABR67065 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 786
ID ABO15668 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 787
ID ABU55949 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, PRO271.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 788
ID ABU65277 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 789
ID ABU95222 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 790
ID ABU71125 standard; protein; 360 AA.
DE Human PRO271 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 791
ID ABO07735 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 792
ID ABR69976 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 793
ID ABR69309 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 794
ID ABO01450 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 795
ID ABU81252 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
```

```
RESULT 796
ID ABR60049 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 797
ID ABR67784 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 798
ID ABR65172 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 799
ID ABR68394 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 800
ID ABR71806 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 801
ID ABU85286 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 802
ID ABU88976 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 803
ID ABU83056 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 804
ID ABU94912 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 805
ID ABU90460 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 806
ID ABU83971 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 807
ID ABU93622 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 808
ID ABR64867 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 809
ID ABR68699 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 810
ID ABO06515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 811
ID ABR39060 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 812
ID ABU56944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 813
ID ABU64536 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #40.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 814
ID ABU85896 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 815
ID ABU67382 standard; protein; 360 AA.
DE Human secreted protein PRO271.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93; Length 360;
RESULT 816
ID ABU82183 standard; protein; 360 AA.
```

DE Novel human secreted and transmembrane protein PRO271.
PN US2003036136-A1.
20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 817
ID ABU87194 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036138-A1.
20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 818
ID ABU83666 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032109-A1.
13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 819
ID ABO08040 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003040066-A1.
27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 820
ID ABO14902 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003036060-A1.
20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 821
ID ABU81751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032104-A1.
13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 822
ID ABU65915 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036157-A1.
20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 823
ID ABR59744 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032120-A1.
13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 824
ID ABU93932 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036155-A1.
20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 825
ID ABU99785 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022296-A1.
30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 826
ID ABR66455 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027281-A1.

PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 827
ID ABR90873 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040058-A1.
27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 828
ID ABU94300 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017540-A1.
23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 829
ID ABU79182 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032106-A1.
13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 830
ID ABU86511 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032129-A1.
13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 831
ID ABU86816 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032131-A1.
13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 832
ID ABU94605 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032103-A1.
13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 833
ID ABO04532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032107-A1.
13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 834
ID ABR70281 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032139-A1.
13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 835
ID ABU98446 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022301-A1.
30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
Pred. No. 93;
RESULT 836
ID ABR65845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036165-A1.
20-FEB-2003.
PA (GETH) GENENTECH INC.

```
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 837
ID ABR64562 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 838
ID ABU79487 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 839
ID ABU92878 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 840
ID ABU95837 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 841
ID ABU91057 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 842
ID ABU90150 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 843
ID ABO09565 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 844
ID ABO10837 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 845
ID ABR70891 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 846
ID ABU87499 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 847
ID ABU91367 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 848
ID ABU84581 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 849
ID ABR69671 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 850
ID ABU80048 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 851
ID ABU69659 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017463-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 852
ID ABU93317 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 853
ID ABO09870 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 854
ID ABO08955 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 855
ID ABU10523 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 856
ID ABU95532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 360;
RESULT 857
ID ABU96741 standard; protein; 360 AA.
```

DE Novel human secreted and transmembrane protein PRO271.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 858
ID ABR70586 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 859
ID ABO04937 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003008352-A1.
PD 09-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 860
ID ABO08345 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 861
ID ABO14841 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 862
ID ABO05552 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 863
ID ABR73941 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 864
ID ABR9553 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 865
ID ABR80830 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 866
ID ABR81135 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;

Best Local Similarity 100.0%; Pred. No. 93;
RESULT 867
ID ABM00831 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 868
ID ABR88433 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 869
ID ABM77254 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 870
ID ABO28738 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 871
ID ABO31483 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 872
ID ABM07900 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 873
ID ABO40380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 874
ID ABO35605 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 875
ID ABO43944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;

RESULT 876
ID ADA77780 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 877
ID ABM24739 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 878
ID ADB29418 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 879
ID ABO03007 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 880
ID ABR90263 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 881
ID ABM17177 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 882
ID ABR94923 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 883
ID ABR95228 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 884
ID ABO21466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 885
ID ABR97730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 886
ID ABR87518 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 887
ID ABM77559 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 888
ID ABM27789 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 889
ID ABM06070 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 890
ID ABM03576 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 891
ID ABM35027 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 892
ID ABM26264 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 893
ID ABO48046 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 894
ID ABR92788 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;

Best Local Similarity 100.0%; Pred. No. 93;
RESULT 895
ID ABO24549 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 896
ID ABM1560 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 897
ID ABM02661 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 898
ID ABM15957 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 899
ID ABO27518 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 900
ID ABM2909 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 901
ID ABM06985 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 902
ID ABM21079 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 903
ID ABM09425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 904
ID ABO41295 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 905
ID ABO36110 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 906
ID ABO43639 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 907
ID ABM76339 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 908
ID ABM76035 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 909
ID ABM25654 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 910
ID ABM25959 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 911
ID ABO03312 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 912
ID ABO02397 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 913
ID ABR90568 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;


```
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 914
ID ABR73636 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 915
ID ABO1688 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 916
ID ABR94313 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 917
ID ABR75820 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 918
ID ADA18274 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003038971-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 919
ID ABO32793 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 920
ID ABR71196 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 921
ID ABR933093 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 922
ID ABR93398 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 923
ID ABR87823 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 924
ID ABO27823 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 925
ID ABO29958 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 926
ID ABO33167 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 927
ID ABO4855 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 928
ID ABO08815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 929
ID ABO36415 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 930
ID ABO35500 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 931
ID ABO39465 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 932
ID ABO10340 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
```

PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 933
ID ABM11865 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 934
ID ABO52011 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 935
ID ABO52316 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 936
ID ABO23634 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 937
ID ABR97120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 938
ID ABR86908 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 939
ID ABM10950 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 940
ID AMM28094 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 941
ID ABO32093 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068733-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 942
ID AMM15220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 943
ID ABM06375 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 944
ID ABM04186 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 945
ID ABM22299 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 946
ID ABM07595 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 947
ID ABO40685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 948
ID ABM35332 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 949
ID ABM33095 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 950
ID ABO52621 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;

```
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 951
ID ABO50181 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 952
ID ABU99175 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 953
ID ABO04227 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 954
ID ABO05857 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 955
ID ABO34853 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 956
ID ABM18397 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 957
ID ADA16249 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 958
ID ABR97425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 959
ID ABR80525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 960
ID ABM01136 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PD 08-MAY-2003.
PN US2003049770-A1.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 961
ID ABR88738 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 962
ID ABM13390 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 963
ID ABM20774 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 964
ID ABO41905 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 965
ID ABO42515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 966
ID ABM10035 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 967
ID ABO38550 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 968
ID ABM32790 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 969
ID ABM22604 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087373-A1.
PD 08-MAY-2003.
```

```
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 970
ID ABR74815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 971
ID ADA79572 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 972
ID ABR96205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 973
ID ABR02356 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 974
ID ABR86298 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 975
ID ABR86603 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 976
ID ABR16567 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 977
ID ABR29619 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 978
ID ABR029043 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 979
ID ABR23824 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003100061-A1.
PD 29-MAY-2003.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 980
ID ABR23214 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 981
ID ABR21994 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 982
ID ABR037635 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 983
ID ABR28399 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 984
ID ABR28704 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 985
ID ABR66348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 986
ID ABR75730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 987
ID ABR34010 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 8; DB 6; Length 360;
RESULT 988
ID ABR34315 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003100061-A1.
PD 29-MAY-2003.
```

PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 989
ID ABO20246 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 990
ID ABO21161 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 991
ID ABO22076 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 992
ID ABR96510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 993
ID ABR8568 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 994
ID ABR9670 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 995
ID ABM00221 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 996
ID ABM00526 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 997
ID ABO29653 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 998
ID ABM23519 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 999
ID ABM29314 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1000
ID ABO38245 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1001
ID ABO45545 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1002
ID ABM20469 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1003
ID ADA42394 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1004
ID ADA81299 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1005
ID ABO16583 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1006
ID ABO18209 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1007
ID ABO22636 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027265-A1.
PD 06-FEB-2003.

Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1008
ID ABO22941 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1009
ID ABR92483 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1010
ID ABR81440 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1011
ID ABO17531 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1012
ID ABM77864 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1013
ID ABR89653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1014
ID AMM26569 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1015
ID AMM13695 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1016
ID ABO28433 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1017
ID ABO30263 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1018
ID ABM07290 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1019
ID ABM03881 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1020
ID ABO37025 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1021
ID ABO41600 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1022
ID ABO35195 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1023
ID ABM25044 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1024
ID ABO47436 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1025
ID ABO47741 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1026
ID ABO48351 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.

PN	US2003049750-A1.
PA	(GETH) GENENTECH INC.
Query Match	2.4%; Score 8; DB 6; Length 360;
Best Local Similarity	100.0%; Pred. No. 93;
RESULT 1027	
ID	ABO51401 standard; protein, 360 AA.
DE	Human PRO polypeptide #14.
FN	US2003049766-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	2.4%; Score 8; DB 6; Length 360;
Best Local Similarity	100.0%; Pred. No. 93;
RESULT 1028	
ID	ABO51706 standard; protein, 360 AA.
DE	Human PRO polypeptide #14.
FN	US2003049767-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	2.4%; Score 8; DB 6; Length 360;
Best Local Similarity	100.0%; Pred. No. 93;
RESULT 1029	
ID	ABO50486 standard; protein, 360 AA.
DE	Human secreted/transmembrane protein (PRO) #14.
FN	US2003049779-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	2.4%; Score 8; DB 6; Length 360;
Best Local Similarity	100.0%; Pred. No. 93;
RESULT 1030	
ID	ABR79610 standard; protein, 360 AA.
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.
FN	US2003040059-A1.
PD	27-FEB-2003.
PA	(GETH) GENENTECH INC.
Query Match	2.4%; Score 8; DB 6; Length 360;
Best Local Similarity	100.0%; Pred. No. 93;
RESULT 1031	
ID	ABM16872 standard; protein, 360 AA.
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.
FN	US2003040078-A1.
PD	27-FEB-2003.
PA	(GETH) GENENTECH INC.
Query Match	2.4%; Score 8; DB 6; Length 360;
Best Local Similarity	100.0%; Pred. No. 93;
RESULT 1032	
ID	ABO17904 standard; protein, 360 AA.
DE	Human secreted/transmembrane protein (PRO) #14.
FN	US2003044518-A1.
PD	06-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	2.4%; Score 8; DB 6; Length 360;
Best Local Similarity	100.0%; Pred. No. 93;
RESULT 1033	
ID	ABO20856 standard; protein, 360 AA.
DE	Human secreted/transmembrane protein (PRO) #14.
FN	US2003032132-A1.
PD	13-FEB-2003.
PA	(GETH) GENENTECH INC.
Query Match	2.4%; Score 8; DB 6; Length 360;
Best Local Similarity	100.0%; Pred. No. 93;
RESULT 1034	
ID	ABR96815 standard; protein, 360 AA.
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.
FN	US2003054462-A1.
PD	20-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	2.4%; Score 8; DB 6; Length 360;
Best Local Similarity	100.0%; Pred. No. 93;
RESULT 1035	
ID	ABM12170 standard; protein, 360 AA.
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.
FN	US2003064445-A1.
PD	03-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	2.4%; Score 8; DB 6; Length 360;

Best Local Similarity	100.0%;	Pred. No. 93;
RESULT 1036		
ID	ABM16262 standard; protein, 360 AA.	
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.	
PN	US2003064449-A1.	
PD	03-APR-2003.	
PA	(GENET) GENENTECH INC.	
Query Match	2.4%;	Score 8; DB 6; Length 360;
Best Local Similarity	100.0%;	Pred. No. 93;
RESULT 1037		
ID	ABM24129 standard; protein, 360 AA.	
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.	
PN	US2003064441-A1.	
PD	03-APR-2003.	
PA	(GENET) GENENTECH INC.	
Query Match	2.4%;	Score 8; DB 6; Length 360;
Best Local Similarity	100.0%;	Pred. No. 93;
RESULT 1038		
ID	ABM14610 standard; protein, 360 AA.	
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.	
PN	US2003068696-A1.	
PD	10-APR-2003.	
PA	(GENET) GENENTECH INC.	
Query Match	2.4%;	Score 8; DB 6; Length 360;
Best Local Similarity	100.0%;	Pred. No. 93;
RESULT 1039		
ID	ABM04491 standard; protein, 360 AA.	
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.	
PN	US2003068712-A1.	
PD	10-APR-2003.	
PA	(GENET) GENENTECH INC.	
Query Match	2.4%;	Score 8; DB 6; Length 360;
Best Local Similarity	100.0%;	Pred. No. 93;
RESULT 1040		
ID	ABM06680 standard; protein, 360 AA.	
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.	
PN	US2003068730-A1.	
PD	10-APR-2003.	
PA	(GENET) GENENTECH INC.	
Query Match	2.4%;	Score 8; DB 6; Length 360;
Best Local Similarity	100.0%;	Pred. No. 93;
RESULT 1041		
ID	ABM09120 standard; protein, 360 AA.	
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.	
PN	US2003073174-A1.	
PD	17-APR-2003.	
PA	(GENET) GENENTECH INC.	
Query Match	2.4%;	Score 8; DB 6; Length 360;
Best Local Similarity	100.0%;	Pred. No. 93;
RESULT 1042		
ID	ABO39160 standard; protein, 360 AA.	
DE	Human secreted (transmembrane protein (PRO) #14.	
PN	US2003068775-A1.	
PD	10-APR-2003.	
PA	(GENET) GENENTECH INC.	
Query Match	2.4%;	Score 8; DB 6; Length 360;
Best Local Similarity	100.0%;	Pred. No. 93;
RESULT 1043		
ID	ABM75425 standard; protein, 360 AA.	
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.	
PN	US2003104545-A1.	
PD	05-JUN-2003.	
PA	(GENET) GENENTECH INC.	
Query Match	2.4%;	Score 8; DB 6; Length 360;
Best Local Similarity	100.0%;	Pred. No. 93;
RESULT 1044		
ID	ABM25349 standard; protein, 360 AA.	
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.	
PN	US2003104541-A1.	
PD	05-JUN-2003.	
PA	(GENET) GENENTECH INC.	
Query Match	2.4%;	Score 8; DB 6; Length 360;
Best Local Similarity	100.0%;	Pred. No. 93;
RESULT 1045		
ID	ABM19859 standard; protein, 360 AA.	
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.	

PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1046
ID ABO46765 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1047
ID ABO47070 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1048
ID ADA83097 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1049
ID ABR71501 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1050
ID ABR72111 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1051
ID ABR98450 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1052
ID ABO06820 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1053
ID ABR84773 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1054
ID ABR73331 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1055

ID ABR76425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1056
ID ABR73026 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1057
ID ABR18092 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1058
ID ABO20551 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1059
ID ABO25294 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1060
ID ABO25599 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1061
ID ABR94008 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1062
ID ABR79915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1063
ID ABR11255 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1064
ID ABO32862 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

```
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1065
ID ABO30568 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1066
ID ABO30873 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1067
ID ABM27179 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1068
ID ABM29924 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1069
ID ABM05460 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1070
ID ABM15525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1071
ID ABM08510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1072
ID ABO42210 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1073
ID ABO37940 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1074
ID ABO45850 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1075
ID ABM66653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1076
ID ADB20140 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1077
ID ABM19554 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1078
ID ABO49266 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1079
ID ABO49571 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1080
ID ADA78392 standard; protein; 360 AA.
DE Human secreted/cranmembrane protein (PRO) #14.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1081
ID ABR88128 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1082
ID ABM26874 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1083
```

ID ABO03271 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1084
ID ABO39770 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1085
ID ABO49876 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003048776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1086
ID ABO50791 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1087
ID ABO05247 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1088
ID ABR74551 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1089
ID ABR77030 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1090
ID ADA16673 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1091
ID ABR17787 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1092
ID ABR95838 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;

Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1093
ID ADA13102 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1094
ID ABO21771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1095
ID ABO19941 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1096
ID ABO24244 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1097
ID ABR85993 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1098
ID ABR10645 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1099
ID ABR76644 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1100
ID ABR89348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1101
ID ABR12475 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1102
ID ABR05765 standard; protein; 360 AA.

```
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1103
ID ABO34890 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1104
ID ABO2966 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1105
ID ABO1894 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1106
ID ABO19249 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1107
ID ABO46460 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1108
ID ABO48961 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1109
ID ADA41970 standard; protein; 360 AA.
DE Human secreted/transmembrane protein. #42.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1110
ID ABO69004 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1111
ID ABO89043 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1112
ID ABO72416 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1113
ID ABO74246 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1114
ID ABO18514 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1115
ID ADA17317 standard; protein; 360 AA.
DE Human secreted/transmembrane protein. #42.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1116
ID ABO80220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1117
ID ABO01441 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1118
ID ABO2051 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1119
ID ABO87213 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1120
ID ABO12780 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
```

RESULT 1121
ID ABO30534 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1122
ID ABO24434 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1123
ID ABO29348 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1124
ID ABO31178 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1125
ID ABO14305 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1126
ID ABO09730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1127
ID ABO38855 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1128
ID ABO34620 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1129
ID ABO51096 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1130
ID ADA42820 standard; protein; 360 AA.

DE Human secreted/transmembrane protein, #42.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1131
ID ABO03922 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1132
ID ABO10392 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1133
ID ABR77635 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1134
ID ABR78845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1135
ID ABO23939 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1136
ID ABR93703 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1137
ID ABO1746 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1138
ID ABR78169 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1139
ID ABR8958 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;

Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1140
ID ABM27484 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1141
ID ABM13085 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1142
ID ABO31788 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1143
ID ABM14000 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1144
ID ABM08205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1145
ID ABO40075 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1146
ID ABM74510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1147
ID ABM33705 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1148
ID ABM20164 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1149
ID ABO48656 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1150
ID ABR72721 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1151
ID ABO15363 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1152
ID ABR85078 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1153
ID ABO15058 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1154
ID ABO17193 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1155
ID ABM17482 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1156
ID ABR85383 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1157
ID ABO17592 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1158
ID ABM76949 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;

RESULT 1159
ID ABO28128 standard; protein: 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1160
ID ABM22909 standard; protein: 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1161
ID ABM30229 standard; protein: 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1162
ID ABM21689 standard; protein: 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1163
ID ABM21384 standard; protein: 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1164
ID ABM14915 standard; protein: 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1165
ID ABO40990 standard; protein: 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1166
ID ABO36720 standard; protein: 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1167
ID ABO37330 standard; protein: 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1168

ID ABM75120 standard; protein: 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1169
ID ABM33400 standard; protein: 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1170
ID ABO46155 standard; protein: 360 AA.
DE Human PRO polypeptide #14.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1171
ID ADA82463 standard; protein: 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1172
ID ABM31754 standard; protein: 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1173
ID ABM31144 standard; protein: 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1174
ID ADB77739 standard; protein: 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1175
ID ADB74875 standard; protein: 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1176
ID ADB85771 standard; protein: 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1177
ID ABM32059 standard; protein: 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 8; DB 7; Length 360;
RESULT 1178
ID ABM32364 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1179
ID ABM31449 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1180
ID ABM30839 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1181
ID ADC28521 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1182
ID ADC39721 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1183
ID ADC40235 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1184
ID ADC19059 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1185
ID ADC34359 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1186
ID ADC29414 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049676-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1187
ID ADC28945 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1188
ID ADC40830 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1189
ID ADC19487 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1190
ID ADC33935 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1191
ID ADC13005 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1192
ID ADC12457 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1193
ID ADD05501 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1194
ID ADD05012 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 93;
Length 360;
RESULT 1195
ID ADD04018 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104381-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1196
ID ADD03594 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1197
ID ADE34846 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1198
ID ADG02496 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1199
ID ADG01203 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1200
ID ADF93378 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1201
ID ADG12193 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1202
ID ADH08853 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1203
ID ADH59329 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1204
ID ADI38108 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;

Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1205
ID ADJ26376 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1206
ID ADJ32634 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1207
ID ADM30168 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 7; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1208
ID ADE79291 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1209
ID ADE79715 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1210
ID ADE73391 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1211
ID ADE74165 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1212
ID ADE73926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1213
ID ADE74777 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1214
ID ADE99480 standard; protein; 360 AA.

```
DE Human secreted/transmembrane protein, #42.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1215
ID ADE98599 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1216
ID ADE99026 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1217
ID ADG40496 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1218
ID ADF73890 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1219
ID ADF93990 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1220
ID ADF73466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1221
ID ADG04261 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215812-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1222
ID ADG040421 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1223
ID ADG82677 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1224
ID ADG92309 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1225
ID ADG92736 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1226
ID ADH25958 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1227
ID ADH32927 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1228
ID ADH20525 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1229
ID ADH07380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1230
ID ADH59925 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1231
```

ID ADH06953 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODD/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1233
ID ADI18695 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1233
ID ADI65415 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1233
ID ADI37678 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1234
ID ADI37678 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1235
ID ADH97474 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1236
ID ADI65842 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1237
ID ADH60585 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODD/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1238
ID ADJ99642 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GERTH) GENENTECH INC.

Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1239
ID ADL08835 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1240
ID ADI54666 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1241
ID ADM25176 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1242
ID ADM29926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1243
ID ADI64437 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1244
ID ADM31333 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1245
ID ADM36380 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1246
ID ADM440185 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1247
ID ADI91793 standard; protein; 360 AA.
DE Human PRO271 protein SEQ ID NO:14.
PN WO2004024076-A2.
PD 25-MAR-2004.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;

Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1248
ID ADO06248 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1249
ID ADN37793 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1250
ID ADR1100 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1251
ID ADR18009 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FLIV/) FLIVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLAJ/) KLJAVIN I J.
PA (KLAJ/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1252
ID AD574648 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #42.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FLIV/) FLIVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1253
ID ADR60851 standard; protein; 404 AA.
DE Plant polypeptide, SEQ ID 10928.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 2.4%; Score 8; DB 8; Length 404;
Best Local Similarity 100.0%; Pred. No. 1e+02;
RESULT 1256
ID ABO82428 standard; protein; 410 AA.
DE Pseudomonas aeruginosa polypeptide #14603.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 8; DB 7; Length 410;
Best Local Similarity 100.0%; Pred. No. 1e+02;
RESULT 1257
ID ADX75594 standard; protein; 419 AA.
DE Plant full length insert polypeptide seqid 44960.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match 2.4%; Score 8; DB 8; Length 419;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1258
ID AEA20028 standard; protein; 422 AA.
DE Novel human polypeptide SEQ ID NO 722.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NOVE-) NOVELO INC.
Query Match 2.4%; Score 8; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1259
ID ADX88402 standard; protein; 438 AA.
DE Plant full length insert polypeptide seqid 51066.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLAJ/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1253
ID ADT03685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1254
ID AEA37923 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GERTH) GENENTECH INC.
Query Match 2.4%; Score 8; DB 9; Length 360;
Best Local Similarity 100.0%; Pred. No. 93;
RESULT 1255
ID ADR60851 standard; protein; 404 AA.
DE Plant polypeptide, SEQ ID 10928.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 2.4%; Score 8; DB 8; Length 404;
Best Local Similarity 100.0%; Pred. No. 1e+02;
RESULT 1256
ID ABO82428 standard; protein; 410 AA.
DE Pseudomonas aeruginosa polypeptide #14603.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 8; DB 7; Length 410;
Best Local Similarity 100.0%; Pred. No. 1e+02;
RESULT 1257
ID ADX75594 standard; protein; 419 AA.
DE Plant full length insert polypeptide seqid 44960.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match 2.4%; Score 8; DB 8; Length 419;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1258
ID AEA20028 standard; protein; 422 AA.
DE Novel human polypeptide SEQ ID NO 722.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NOVE-) NOVELO INC.
Query Match 2.4%; Score 8; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1259
ID ADX88402 standard; protein; 438 AA.
DE Plant full length insert polypeptide seqid 51066.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.

PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1260
ID ADY09988 standard; protein; 462 AA.
DE Plant full length insert polypeptide seqid 65803.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUT/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1261
ID AAG74913 standard; protein; 486 AA.
DE Human colon cancer antigen protein SEQ ID NO:5677.
PN WO2001292920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
RESULT 1262
ID ADU02541 standard; protein; 500 AA.
DE Novel human polypeptide seqid 1008.
PN WO2004093804-A2.
PD 04-NOV-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
RESULT 1263
ID AAE38765 standard; protein; 585 AA.
DE Human 69624 protein sodium sulphate symporter domain.
PN US2002193582-A1.
PD 19-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
RESULT 1264
ID ADO55650 standard; protein; 688 AA.
DE Wheat storage protein #8.
PN WO2004044208-A2.
PD 27-MAY-2004.
PA (PLAN-) PLANTECHNO SRL.
PA (PROG-) PROGEO SCRL.
PA (TECN-) TECNALIMENTI SCPA.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
RESULT 1265
ID ABG10285 standard; protein; 808 AA.
DE Novel human diagnostic protein #10276.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
RESULT 1266
ID ABB63905 standard; protein; 868 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18507.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 100.0%; Pred. No. 2e+02;
RESULT 1267
ID AAM39436 standard; protein; 940 AA.
DE Human polypeptide SEQ ID NO 2581.

PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
RESULT 1268
ID AAV78053 standard; protein; 1117 AA.
DE Human desmoglein 2 protein sequence.
PN WO200210767-A2.
PD 07-FEB-2002.
PA (TUIA-) TULANE EDUCATIONAL FUND.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1269
ID ADR9232 standard; protein; 1117 AA.
DE Clone IMAGE:4242700, SEQ ID 238.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (PARB-) BAYER PHARM CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1270
ID ADU06431 standard; protein; 1117 AA.
DE Novel bronchial cancer-associated human protein SeqID655.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ B.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1271
ID AAE20266 standard; protein; 1118 AA.
DE Human lung specific gene (LSG) protein #4.
PN WO200208278-A2.
PD 31-JAN-2002.
PA (DIAD-) DIADEXUS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1272
ID ABG10284 standard; protein; 1120 AA.
DE Novel human diagnostic protein #10275.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1273
ID AAM41222 standard; protein; 1121 AA.
DE Human polypeptide SEQ ID NO 6153.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1274
ID ADO55146 standard; protein; 1235 AA.
DE Protein #48 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
RESULT 1275
ID ABR58408 standard; protein; 1280 AA.
DE Human NOV22a.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
RESULT 1276
ID ADY40906 standard; peptide; 24 AA.

DE hSARS virus peptide, SEQ ID 1895.
PN WO2004085650-A1.
PD 07-OCT-2004.
PA (UYHK-) UNIV HONG KONG.
Query Match 2.1%; Score 7; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 85;
RESULT 1277
ID ADB580323 standard; protein; 24 AA.
DE SARS virus complementary DNA strand reading frame 2 protein #305.
PN WO2004085455-A1.
PD 07-OCT-2004.
PA (UYHK-) UNIV HONG KONG.
Query Match 2.1%; Score 7; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 85;
RESULT 1278
ID ADP38436 standard; peptide; 24 AA.
DE hSARS virus peptide, SEQ ID 1895.
PN WO2004085633-A1.
PD 07-OCT-2004.
PA (UYHK-) UNIV HONG KONG.
Query Match 2.1%; Score 7; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 85;
RESULT 1279
ID AAB52107 standard; peptide; 31 AA.
DE Human secreted protein encoded by cDNA #4.
PN WO200061624-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1280
ID AAB19733 standard; peptide; 31 AA.
DE Human secreted protein amino acid sequence - SEQ ID NO 201.
PN WO200277188-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1281
ID AAB99811 standard; protein; 31 AA.
DE Human secreted protein SEQ ID NO 755.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1282
ID ADC20544 standard; protein; 31 AA.
DE Human secreted protein - amino acid sequence #225.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 7; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1283
ID ADB04547 standard; protein; 47 AA.
DE Staphylococcus epidermis polypeptide seqid 3842.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 2.1%; Score 7; DB 8; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
RESULT 1284
ID AAB59891 standard; protein; 64 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77517.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 64;
Best Local Similarity 100.0%; Pred. No. 2e+02;
RESULT 1285
ID AAB82439 standard; protein; 65 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:10032.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 2e+02;
RESULT 1286
ID ADF04448 standard; protein; 67 AA.
DE Bacterial polypeptide #561.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.1%; Score 7; DB 7; Length 67;
Best Local Similarity 100.0%; Pred. No. 2e+02;
RESULT 1287
ID AAU54392 standard; protein; 72 AA.
DE Propionibacterium acnes immunogenic protein #15288.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.1%; Score 7; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 1288
ID ABB34821 standard; protein; 72 AA.
DE Human ORF3794 protein, SEQ ID NO:7588.
PN WO200190366-A2.
PD 29-NOV-2001.
PA (CURA-) CURAGEN CORP.
Query Match 2.1%; Score 7; DB 5; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 1289
ID AAM50911 standard; protein; 72 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #15587.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 2.1%; Score 7; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 1290
ID AAG05240 standard; protein; 75 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1571.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 1291
ID ADM26879 standard; protein; 75 AA.
DE Hyperthermophile Methanopyrus kandleri protein #1485.
PN WO2003076575-A2.
PD 18-SEP-2003.
PA (FIDE-) FIDELITY SYSTEMS INC.
PA (MALY/) MALYKH A.
Query Match 2.1%; Score 7; DB 7; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 1292
ID AAU5764 standard; protein; 76 AA.
DE Propionibacterium acnes immunogenic protein #16660.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.1%; Score 7; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
RESULT 1293
ID AAM52283 standard; protein; 76 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #16959.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 2.1%; Score 7; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
RESULT 1294
ID ADK15830 standard; protein; 76 AA.
DE Human ABCA10 N-terminal peptide fragment SEQ ID NO:39.
PN WO2004018633-A2.

PD 04-MAR-2004.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 2.1%; Score 7; DB 8; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
RESULT 1295
ID ABP32005 standard; protein; 85 AA.
DE Human ORF978 protein, SEQ ID NO:1956.
PN WO200190366-A2.
PD 29-NOV-2001.
PA (CURA-) CURAGEN CORP.
Query Match 2.1%; Score 7; DB 5; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 1296
ID AAG11654 standard; protein; 86 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 10452.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 1297
ID AAG14682 standard; protein; 92 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14638.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
RESULT 1298
ID AAG1533 standard; protein; 92 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 15546.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
RESULT 1299
ID AAG07776 standard; protein; 93 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 5059.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
RESULT 1300
ID AAG39872 standard; protein; 93 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49396.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
RESULT 1301
ID AAM69995 standard; protein; 97 AA.
DE Revised complete rodent chemokine MCP243 amino acid sequence.
PN WO9832858-A2.
PD 30-JUL-1998.
PA (SCHE) SCHERING CORP.
Query Match 2.1%; Score 7; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1302
ID AAV39480 standard; protein; 97 AA.
DE Propionibacterium acnes immunogenic protein #376.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.1%; Score 7; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1303
ID ADZ58701 standard; protein; 97 AA.
DE Mouse MCP-2 protein SEQ ID NO:29.
PN CA2351275-A1.
PD 20-DEC-2001.
PA (SWIT-) SWITCH BIOTECH AG.
Query Match 2.1%; Score 7; DB 5; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1304
ID AAM35999 standard; protein; 97 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #675.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 2.1%; Score 7; DB 6; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1305
ID ADS85069 standard; protein; 97 AA.
DE Mouse atopic dermatitis-related protein sequence SegID71.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UTUT-) UNIV JUNTENDO.
Query Match 2.1%; Score 7; DB 8; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1306
ID AAR93087 standard; protein; 98 AA.
DE Human chemokine beta-10.
PN WO9605856-A1.
PD 29-FEB-1996.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1307
ID AAM2670 standard; protein; 98 AA.
DE Human chemokine beta10 or monocyte chemotactic protein 4.
PN WO9731098-A1.
PD 28-AUG-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1308
ID AAM30191 standard; protein; 98 AA.
DE Monocyte chemotactic protein 5.
PN WO9735982-A2.
PD 02-OCT-1997.
PA (ICOS-) ICOS CORP.
Query Match 2.1%; Score 7; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1309
ID AAM56087 standard; protein; 98 AA.
DE Human monocyte chemoattractant protein 4.
PN WO9814573-A1.
PD 09-APR-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 2.1%; Score 7; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1310
ID AAV41164 standard; protein; 98 AA.
DE Human chemokine beta-10 (Ckbeta-10) polypeptide.
PN US5981230-A.
PD 09-NOV-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1311
ID AAB15831 standard; protein; 98 AA.
DE Human chemokine MIP1beta SEQ ID NO: 83.
PN WO200042071-A2.
PD 20-JUL-2000.
PA (NEOR-) NEORX CORP.
Query Match 2.1%; Score 7; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1312
ID AAB15808 standard; protein; 98 AA.
DE Human chemokine CCR-2 SEQ ID NO: 50.
PN WO200042071-A2.
PD 20-JUL-2000.
PA (NEOR-) NEORX CORP.
Query Match 2.1%; Score 7; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1313

ID AAY95534 standard; protein; 98 AA.
DE Human chemokine beta-10.
PN WO200040726-A1.
PD 13-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (SMITK) SMITHKLINE BEECHAM CORP.
Query Match 2.1%; Score 7; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1314
ID AAB31795 standard; protein; 98 AA.
DE Amino acid sequence of a human chemokine beta-10 polypeptide.
PN US6174995-B1.
PD 16-JAN-2001.
PA (LIHM/) LI H.
PA (ADAM/) ADAMS M.
PA (LIMA/) LIMA S H.
PA (ALDE/) ALDERSON R.
PA (LITY/) LI Y.
PA (PARM/) PARMELEE D.
PA (WHIT/) WHITE J.
PA (APPL/) APPLEBAUM E.
Query Match 2.1%; Score 7; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1315
ID AAO19997 standard; protein; 98 AA.
DE Protein of human chemokine beta-10 (Ckbeta-10) .
PN US20026044-A1.
PD 28-FEB-2002.
PA (LIHM/) LI H.
PA (ADAM/) ADAMS M D.
Query Match 2.1%; Score 7; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1316
ID AAB15751 standard; protein; 98 AA.
DE Human chemokine beta-10 (ckb-10) protein.
PN WO200194557-A1.
PD 13-DEC-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (GLAX) GLAXOSMITHKLINE.
Query Match 2.1%; Score 7; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1317
ID AAU77180 standard; protein; 98 AA.
DE Human chemokine MCP-4 (hmcp-4) polypeptide.
PN US2002034494-A1.
PD 21-MAR-2002.
PA (VICA/) VICARI A P.
PA (CAUX/) CAUX C.
PA (LAFA/) LAFACE D.
Query Match 2.1%; Score 7; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1318
ID ADD46371 standard; protein; 98 AA.
DE Human Protein Q99616, SEQ ID NO 12051.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 2.1%; Score 7; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1319
ID AAD339903 standard; protein; 98 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C273.
PN WO2003042861-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 2.1%; Score 7; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1320
ID ADU66672 standard; protein; 98 AA.
DE Human chemokine MCP-4.
PN US2004037805-A1.
PD 26-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 8; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1321
ID ADO32066 standard; protein; 98 AA.
DE Chemokine monocyte chemotactic protein (MCP-4) .
PN US6673344-B1.
PD 06-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 8; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1322
ID ADO20884 standard; protein; 98 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3704.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.1%; Score 7; DB 8; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1323
ID ADW20982 standard; protein; 98 AA.
DE Human chemokine (Ck) beta-10 protein.
PN US2004265974-A1.
PD 30-DEC-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 1324
ID AAG26647 standard; protein; 100 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 31182.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 1325
ID ABB42869 standard; peptide; 100 AA.
DE Peptide #10175 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 1326
ID AAM36482 standard; protein; 100 AA.
DE Peptide #10519 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 1327
ID ABB26006 standard; protein; 100 AA.
DE Protein #8005 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 1328
ID AAM76374 standard; protein; 100 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 36680.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 1329
ID AAM63559 standard; protein; 100 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 35664.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 100;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 1330
ID ABG58080 standard; peptide; 100 AA.
DE Human liver peptide, SEQ ID No 36728.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 1331
ID ABG45662 standard; peptide; 100 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 35327.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 5; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 1332
ID AAB40922 standard; protein; 101 AA.
DE Human ORFX ORF686 polypeptide sequence SEQ ID NO:1372.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 2.1%; Score 7; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 1333
ID AAY16779 standard; protein; 104 AA.
DE Human secreted protein (clone aez20_2).
PN WO9924469-A1.
PD 20-MAY-1999.
PA (GEMV-) GENETICS INST INC.
Query Match 2.1%; Score 7; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 1334
ID AAG14713 standard; protein; 105 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14679.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 1335
ID ABG13572 standard; protein; 106 AA.
DE Novel human diagnostic protein #13563.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.1%; Score 7; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 1336
ID AAY75273 standard; protein; 120 AA.
DE Neisseria meningitidis ORF 628 protein sequence SEQ ID NO:2020.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR-) CHIRON CORP.
Query Match 2.1%; Score 7; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
RESULT 1337
ID ABB69393 standard; protein; 120 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 34971.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 2.1%; Score 7; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
RESULT 1338
ID AAG14712 standard; protein; 134 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14678.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1339

ID ABG01162 standard; protein; 135 AA.
DE Novel human diagnostic protein #1153.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.1%; Score 7; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1340
ID AAG19471 standard; protein; 137 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21286.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 137;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
RESULT 1341
ID ABW88501 standard; protein; 140 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:6747.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (STGN-) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 7; DB 7; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
RESULT 1342
ID ADM25851 standard; protein; 145 AA.
DE Hyperthermophile Methanopyrus kandleri protein #457.
PN WO2003076575-A2.
PD 18-SEP-2003.
PA (FIDE-) FIDELITY SYSTEMS INC.
Query Match 2.1%; Score 7; DB 7; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
RESULT 1343
ID AAB58938 standard; protein; 153 AA.
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 646.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 3; Length 153;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
RESULT 1344
ID ADI21209 standard; protein; 159 AA.
DE Novel human protein #184.
PN WO2003025146-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 2.1%; Score 7; DB 7; Length 159;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1345
ID ADI214578 standard; protein; 159 AA.
DE Human tumor associated antigenic protein MGC71744 Seg 94.
PN WO2003030250-A2.
PD 07-APR-2005.
PA (GANV-) GANVYED PHARM AG.
Query Match 2.1%; Score 7; DB 9; Length 159;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1346
ID AAG19470 standard; protein; 162 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21285.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1347
ID AEA49191 standard; protein; 163 AA.
DE L. rhamosus polypeptide #55.
PN WO2005056801-A1.
PD 23-JUN-2005.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 2.1%; Score 7; DB 9; Length 163;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
RESULT 1348
ID ADR09266 standard; protein; 170 AA.

DE Human protein useful for treating neurological disease Seq 2772.
PN BPI447413-A2.
PD 18-AUG-2004.
PA (MOLFE-) RBS ASSOC BIOTECHNOLOGY.
Query Match 2.1%; Score 7; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
RESULT 1349
ID AB023743 standard; protein; 179 AA.
DE Protein encoded by Prokaryotic essential gene #9270.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (EITR-) EITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 179;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 1350
ID AB010263 standard; protein; 192 AA.
DE Mason-Pfizer monkey virus enveloped protein gp20.
PN US6518013-B1.
PD 11-FEB-2003.
PA (TRIM-) TRIMERIS INC.
Query Match 2.1%; Score 7; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 5e+02;
RESULT 1351
ID AAU14098 standard; peptide; 193 AA.
DE Simian Mason-Pfizer monkey virus enveloped protein gp20.
PN WO200151673-A2.
PD 19-JUL-2001.
PA (TRIM-) TRIMERIS INC.
Query Match 2.1%; Score 7; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 5e+02;
RESULT 1352
ID AAU33258 standard; protein; 194 AA.
DE Novel human secreted protein #3749.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.1%; Score 7; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 5e+02;
RESULT 1353
ID AAM17341 standard; protein; 201 AA.
DE Peptide #3775 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLFE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 1354
ID ABB36350 standard; peptide; 201 AA.
DE Peptide #3856 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLFE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 1355
ID AAM29848 standard; protein; 201 AA.
DE Peptide #3885 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLFE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 1356
ID ABB31155 standard; peptide; 201 AA.
DE Peptide #3806 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLFE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 1357
ID ABB21708 standard; protein; 201 AA.
DE Protein #3707 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLFE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 1358
ID AAM69509 standard; protein; 201 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29815.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLFE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 1359
ID AAM57117 standard; protein; 201 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29222.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLFE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 1360
ID ABB51183 standard; peptide; 201 AA.
DE Human liver peptide, SEQ ID No 29831.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLFE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 1361
ID AAM05030 standard; protein; 201 AA.
DE Peptide #3712 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLFE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 1362
ID ABB39134 standard; peptide; 201 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 28799.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLFE-) MOLECULAR DYNAMICS INC.
Query Match 2.1%; Score 7; DB 5; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 1363
ID AD75735 standard; protein; 202 AA.
DE Xanthomonas campestris XCCU3_1220, SEQ ID 78.
PN US2005100892-A1.
PD 12-MAY-2005.
PA (SHEA/) SHEA T P.
PA (SIAT/) SIATER S C.
Query Match 2.1%; Score 7; DB 9; Length 202;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 1364
ID ABB04730 standard; protein; 205 AA.
DE Human mper3-23 protein SEQ ID NO:2.
PN CN1311206-A.
PD 05-SEP-2001.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 2.1%; Score 7; DB 5; Length 205;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1365
ID AAM23009 standard; protein; 208 AA.
DE Canine herpesvirus PCICP4-208 protein.
PN WO9729772-A1.
PD 21-AUG-1997.
PA (HESK-) HESKA CORP.
Query Match 2.1%; Score 7; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1366
ID AAM72665 standard; protein; 208 AA.
DE Canine herpes virus protein sequence PCICP4-208.

PN USS804197-A.
PD 08-SEP-1998.
PA (HESK-) HESKA CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1367
ID AAB51322 standard; protein; 208 AA.
DE Canine herpes virus protein sequence SEQ ID NO:72.
PN US6159478-A.
PD 12-DEC-2000.
PA (HESK-) HESKA CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1368
ID AAB3193 standard; protein; 208 AA.
DE CHV PCICP4 208 protein.
PN US2003049844-A1.
PD 13-MAR-2003.
PA (HESK-) HESKA CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1369
ID ABG13573 standard; protein; 211 AA.
DE Novel human diagnostic protein #13564.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1370
ID AAG55192 standard; protein; 220 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 70733.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
RESULT 1371
ID ABP29523 standard; protein; 226 AA.
DE Streptococcus polypeptide SEQ ID NO 8222.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1372
ID ADT58027 standard; protein; 227 AA.
DE Plant polypeptide, SEQ ID 8104.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1373
ID AAG19469 standard; protein; 228 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21284.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1374
ID AAY05733 standard; protein; 229 AA.
DE Streptococcus pneumoniae MurB protein.
PN EP911403-A2.
PD 28-APR-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1375
ID AAU43422 standard; protein; 230 AA.
DE Propionibacterium acnes immunogenic protein #4318.
PN WO200181581-A2.

PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1376
ID ABW39941 standard; protein; 230 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4617.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1377
ID AAB63119 standard; protein; 234 AA.
DE Gene 41 human secreted protein homologous amino acid sequence #129.
PN WO200061748-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
RESULT 1378
ID ABG25117 standard; protein; 235 AA.
DE Novel human diagnostic protein #25108.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
RESULT 1379
ID ADK67601 standard; protein; 237 AA.
DE Plant full length insert polypeptide seqid 38444.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TBBA/) TABASKA J E.
PA (CMOV/) CAO Y.
Query Match
Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 1380
ID ADA33029 standard; protein; 244 AA.
DE Actinobacter Baumannii protein #190.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
RESULT 1381
ID ABP28316 standard; protein; 246 AA.
DE Streptococcus polypeptide SEQ ID NO 5808.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1382
ID ABP65401 standard; protein; 246 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:145.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Query Match
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1383
ID ADV88876 standard; protein; 246 AA.
DE Streptococcus agalactiae protein sequence, SEQ ID 1270.
PN FR2824074-A1.
PD 31-OCT-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.

Query Match 2.1%; Score 7; DB 8; Length 246;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1384
ID ADV80129 standard; protein; 246 AA.
DE Streptococcus agalactiae protein, SEQ ID 1270.
PN W0200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCT.
Query Match 2.1%; Score 7; DB 8; Length 246;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1385
ID ADV82261 standard; protein; 246 AA.
DE Streptococcus agalactiae protein, SEQ ID 3402.
PN W0200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCT.
Query Match 2.1%; Score 7; DB 8; Length 246;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1386
ID ABB27486 standard; protein; 250 AA.
DE Protein encoded by Prokaryotic essential gene #13013.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 1387
ID AAM47576 standard; protein; 261 AA.
DE Drosophila cell cycle progression protein #5.
PN W0200172774-A2.
PD 04-OCT-2001.
PA (CYCL-) CYCLACEL LTD.
Query Match 2.1%; Score 7; DB 5; Length 261;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
RESULT 1388
ID ADB63852 standard; protein; 262 AA.
DE Human protein encoded by clone ASTRO20045840.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.1%; Score 7; DB 7; Length 262;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
RESULT 1389
ID ADR94265 standard; protein; 266 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 2900.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.1%; Score 7; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 1390
ID AEA58135 standard; protein; 266 AA.
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:2900.
PN US2005136404-A1.
PD 23-JUN-2005.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 2.1%; Score 7; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 1391
ID ABR92104 standard; protein; 276 AA.
DE M. xanthus protein sequence, seq id 11303.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 2.1%; Score 7; DB 9; Length 276;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
RESULT 1392
ID ADR46429 standard; protein; 277 AA.
DE Streptococcus pneumoniae protein, Seq ID No 2944.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.1%; Score 7; DB 8; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
RESULT 1393
ID ADS41825 standard; protein; 280 AA.
DE Bacterial polypeptide #20255.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.1%; Score 7; DB 8; Length 280;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
RESULT 1394
ID AAU33365 standard; protein; 283 AA.
DE Enterococcus faecalis cellular proliferation protein #1.
PN W0200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 7e+02;
RESULT 1395
ID AAM80665 standard; protein; 289 AA.
DE S. pneumoniae UDP-N-acetylglucosaminyl-3-enolpyruvate reductase.
PN W09826072-A1.
PD 18-JUN-1998.
PA (ELIL) LILLY & CO ELI.
Query Match 2.1%; Score 7; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1396
ID ADN23273 standard; protein; 290 AA.
DE Bacterial polypeptide #5926.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.1%; Score 7; DB 8; Length 290;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1397
ID ADN23272 standard; protein; 290 AA.
DE Bacterial polypeptide #5925.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.1%; Score 7; DB 8; Length 290;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1398
ID ADR95627 standard; protein; 290 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 4262.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.1%; Score 7; DB 8; Length 290;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1399
ID AEA59497 standard; protein; 290 AA.
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:4262.
PN US2005136404-A1.
PD 23-JUN-2005.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 2.1%; Score 7; DB 9; Length 290;

Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1400
ID AAV35025 standard; protein; 300 AA.
DE Enterococcus faecalis cellular proliferation protein #312.
PN W0200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 1401
ID ABP28072 standard; protein; 300 AA.
DE Streptococcus polypeptide SEQ ID NO 5320.
PN W0200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 2.1%; Score 7; DB 5; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 1402
ID AAO22108 standard; protein; 300 AA.
DE Protein of human CARD-3 SEQ ID NO 4.
PN US6369196-B1.
PD 09-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.1%; Score 7; DB 5; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 1403
ID AAV56270 standard; protein; 300 AA.
DE Human Caspase recruitment domain protein 3, kinase domain.
PN US6469140-B1.
PD 22-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 1404
ID ABU14645 standard; protein; 300 AA.
DE Protein encoded by Prokaryotic essential gene #172.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 1405
ID ADV88098 standard; protein; 300 AA.
DE Streptococcus agalactiae protein sequence, SEQ ID 492.
PN FR2824074-A1.
PD 31-OCT-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 2.1%; Score 7; DB 8; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 1406
ID ADV81529 standard; protein; 300 AA.
DE Streptococcus agalactiae protein, SEQ ID 2670.
PN W0200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 2.1%; Score 7; DB 8; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 1407
ID ADV79351 standard; protein; 300 AA.
DE Streptococcus agalactiae protein, SEQ ID 492.
PN W0200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 2.1%; Score 7; DB 8; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 1408
ID ADK47008 standard; protein; 301 AA.
DE Streptococcus pneumoniae protein, Seq ID No 3523.
PN US6699703-B1.

PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.1%; Score 7; DB 8; Length 301;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 1409
ID AAB46977 standard; protein; 303 AA.
DE B. subtilis Murb protein SEQ ID 5.
PN W020011054-A1.
PD 15-FEB-2001.
PA (PHAR) PHARMACIA & UPJOHN CO.
Query Match 2.1%; Score 7; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 1410
ID ADX79238 standard; protein; 303 AA.
DE Plant full length insert polypeptide seqid 48604.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 2.1%; Score 7; DB 8; Length 303;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 1411
ID ABU23861 standard; protein; 305 AA.
DE Protein encoded by Prokaryotic essential gene #9388.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 1412
ID ABU43927 standard; protein; 307 AA.
DE Protein encoded by Prokaryotic essential gene #29454.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 307;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
RESULT 1413
ID ABU29984 standard; protein; 311 AA.
DE Protein encoded by Prokaryotic essential gene #15511.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 311;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
RESULT 1414
ID ADE63290 standard; protein; 312 AA.
DE Rat Protein CAA28650, SEQ ID NO 9227.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 2.1%; Score 7; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1415
ID ADI82102 standard; protein; 312 AA.
DE Apolipoprotein E protein.
PN W02004005934-A2.
PD 15-JAN-2004.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match 2.1%; Score 7; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1416
ID AEA17430 standard; protein; 312 AA.
DE Rat Apolipoprotein E protein.
PN W02005047455-A2.
PD 26-MAY-2005.
PA (SEMB-) SEMBIOSIS GENETICS INC.
Query Match 2.1%; Score 7; DB 9; Length 312;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1417
ID AAM89165 standard; protein; 314 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7411.
PN WO2003008540-A2.
PD 30-JUN-2003.
PA (STGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 7; DB 7; Length 314;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1418
ID AAY05732 standard; protein; 316 AA.
DE Streptococcus pneumoniae MurB protein.
PN EP911403-A2.
PD 28-APR-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 2.1%; Score 7; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1419
ID AAN37701 standard; protein; 316 AA.
DE Streptococcus pneumoniae cellular proliferation protein #130.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1420
ID ABU01833 standard; protein; 316 AA.
DE S. pneumoniae type 4 strain protein from coding region #1409.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 2.1%; Score 7; DB 6; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1421
ID ABU46115 standard; protein; 316 AA.
DE Protein encoded by Prokaryotic essential gene #31642.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1422
ID AD226300 standard; protein; 316 AA.
DE Streptococcus UDP-N-acetylenolpyruvoylglucosamine reductase.
PN KR2004105416-A.
PD 16-DEC-2004.
PA (SONG/) SONG J H.
Query Match 2.1%; Score 7; DB 9; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1423
ID AAN37931 standard; protein; 317 AA.
DE Streptococcus pneumoniae cellular proliferation protein #360.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1424
ID ADN47056 standard; protein; 317 AA.
DE Thermococcus kodakarensis KOD1 protein sequence SeqID934.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 2.1%; Score 7; DB 8; Length 317;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1425
ID AAG8738 standard; protein; 318 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34069.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 318;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1426
ID AAB86957 standard; protein; 318 AA.
DE D. melanogaster peptide receptor SEQ ID 12.
PN DE10013618-A1.
PD 20-SEP-2001.
PA (FARB) BAYER AG.
Query Match 2.1%; Score 7; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1427
ID ADC96745 standard; protein; 318 AA.
DE E. faecium protein sequence SEQ ID 6372.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.1%; Score 7; DB 7; Length 318;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1428
ID AAG28737 standard; protein; 320 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34068.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1429
ID ABU11628 standard; protein; 330 AA.
DE Human MDP1 polypeptide SEQ ID 575.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.1%; Score 7; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
RESULT 1430
ID ADF06337 standard; protein; 332 AA.
DE Bacterial polypeptide #2450.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.1%; Score 7; DB 7; Length 332;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1431
ID ADX71573 standard; protein; 343 AA.
DE Plant full length insert polypeptide seqid 40939.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match 2.1%; Score 7; DB 8; Length 343;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
RESULT 1432
ID ADX68254 standard; protein; 343 AA.
DE Plant full length insert polypeptide seqid 39097.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match 2.1%; Score 7; DB 8; Length 343;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
RESULT 1433
ID AAB43522 standard; protein; 344 AA.
DE Human cancer associated protein sequence SEQ ID NO:967.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 3; Length 344;

Best Local Similarity 100.0%; Pred. No. 8.2e+02;
RESULT 1434
ID ABU19490 standard; protein; 344 AA.
DE Protein encoded by Prokaryotic essential gene #5017.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
RESULT 1435
ID ABJ26048 standard; protein; 345 AA.
DE Aspergillus fumigatus essential gene protein #706.
PN W0200286090-A2.
PD 31-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
RESULT 1436
ID ADX90108 standard; protein; 354 AA.
DE Plant full length insert polypeptide seqid 52772.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 2.1%; Score 7; DB 8; Length 354;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
RESULT 1437
ID ABU27576 standard; protein; 357 AA.
DE Protein encoded by Prokaryotic essential gene #13103.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 357;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
RESULT 1438
ID AB083519 standard; protein; 357 AA.
DE Pseudomonas aeruginosa polypeptide #15694.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.1%; Score 7; DB 7; Length 357;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
RESULT 1439
ID AAU18004 standard; protein; 361 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 149.
PN W0200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 4; Length 361;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 1440
ID ADB31628 standard; protein; 361 AA.
DE Human novel protein SEQ ID NO 149.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.1%; Score 7; DB 7; Length 361;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 1441
ID ADO07190 standard; protein; 362 AA.
DE Saccharomyces cerevisiae asparaginase.
PN W02004032648-A1.
PD 22-APR-2004.
PA (NOVO) NOVOZYMES AS.
Query Match 2.1%; Score 7; DB 8; Length 362;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 1442
ID AAM29662 standard; protein; 366 AA.
DE Homo sapiens CN483_2 clone secreted protein.
PN W09830695-A2.
PD 16-JUL-1998.
PA (GENY) GENETICS INST INC.
Query Match 2.1%; Score 7; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
RESULT 1443
ID ADN23206 standard; protein; 367 AA.
DE Bacterial polypeptide #5859.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.1%; Score 7; DB 8; Length 367;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
RESULT 1444
ID ADN23579 standard; protein; 369 AA.
DE Bacterial polypeptide #6232.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.1%; Score 7; DB 8; Length 369;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
RESULT 1445
ID ADY08632 standard; protein; 373 AA.
DE Plant full length insert polypeptide seqid 64447.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 2.1%; Score 7; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
RESULT 1446
ID ADH86933 standard; protein; 375 AA.
DE Enterococcus faecalis polypeptide #1413.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 2.1%; Score 7; DB 7; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
RESULT 1447
ID ABB61525 standard; protein; 376 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11367.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.1%; Score 7; DB 4; Length 376;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 1448
ID ADT61003 standard; protein; 376 AA.
DE Plant polypeptide, SEQ ID 11080.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 2.1%; Score 7; DB 8; Length 376;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 1449
ID ADN24357 standard; protein; 377 AA.
DE Bacterial polypeptide #7010.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.1%; Score 7; DB 8; Length 377;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 1450
ID AAG28736 standard; protein; 391 AA.
DE Arbidolopis chailana protein fragment SEQ ID NO: 34067.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.1%; Score 7; DB 3; Length 391;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
RESULT 1451
ID ADY60859 standard; protein; 403 AA.
DE RIPK2 isoform RIPK2v1.2, SEQ ID 4.
PN US200505908-A1.
PD 17-MAR-2005.
PA (ARMO/) ARMOUR C D.
PA (CAST/) CASTLE J C.
PA (GAR/) GARRETT-ENGLE P W.
PA (KAN/) KAN Z.
PA (LOER/) LOERCH P M.
PA (TSIN/) TSINOREMAS N P.
Query Match 2.1%; Score 7; DB 9; Length 403;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
RESULT 1452
ID AD63997 standard; protein; 403 AA.
DE Human cancer-linked gene RIPK2, protein, SEQ ID 38.
PN WO2005035724-A2.
PD 21-APR-2005.
PA (AVAL-) AVALON PHARM INC.
Query Match 2.1%; Score 7; DB 9; Length 403;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
RESULT 1453
ID AAU51026 standard; protein; 405 AA.
DE Propionibacterium acnes immunogenic protein #11922.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.1%; Score 7; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
RESULT 1454
ID ABA47545 standard; protein; 405 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #12221.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 2.1%; Score 7; DB 6; Length 405;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
RESULT 1455
ID AAW75856 standard; protein; 408 AA.
DE Human secretory protein of clone COL39-3.
PN WO9833916-A2.
PD 06-AUG-1998.
PA (GENY-) GENETICS INST INC.
Query Match 2.1%; Score 7; DB 2; Length 408;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
RESULT 1456
ID AA445161 standard; protein; 408 AA.
DE Human secreted protein clone COL39_3 protein sequence.
PN US965397-A.
PD 12-OCT-1999.
PA (GENY-) GENETICS INST INC.
Query Match 2.1%; Score 7; DB 2; Length 408;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
RESULT 1457
ID ABU27137 standard; protein; 410 AA.
DE Protein encoded by Prokaryotic essential gene #12664.
PN WO2002727183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.1%; Score 7; DB 6; Length 410;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;
RESULT 1458
ID AAB16533 standard; protein; 415 AA.
DE Bacteriophage 44AHD protein sequence 44HDF005.
PN WO20032825-A2.
PD 08-JUN-2000.
PA (PHAG-) PHAGETECH INC.
Query Match 2.1%; Score 7; DB 3; Length 415;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
RESULT 1459
ID AAM42401 standard; protein; 417 AA.
DE TRAF2 binding protein encoded by clone 15.
PN WO9737016-A1.
PD 09-OCT-1997.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 2.1%; Score 7; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
RESULT 1460
ID AAM60149 standard; protein; 419 AA.
DE M. vaccae antigen GV-38B 3' amino acid sequence.
PN WO9808542-A2.
PD 05-MAR-1998.
PA (GENE-) GENESIS RES & DEV CORP.
Query Match 2.1%; Score 7; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
RESULT 1461
ID AAY14896 standard; protein; 419 AA.
DE M. vaccae antigen GV-38B 3' amino acid sequence.
PN WO9932634-A2.
PD 01-JUL-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 2.1%; Score 7; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
RESULT 1462
ID ABB73502 standard; protein; 419 AA.
DE M vaccae GV-38B partial protein SEQ ID NO: 125.
PN US6328978-B1.
PD 11-DEC-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 2.1%; Score 7; DB 5; Length 419;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
RESULT 1463
ID ADH86952 standard; protein; 427 AA.
DE Enterococcus faecalis polypeptide #1432.
PN US617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSM/) BUSH D.
Query Match 2.1%; Score 7; DB 7; Length 427;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
RESULT 1464
ID AAE38166 standard; protein; 431 AA.
DE Fruit fly G protein-coupled receptor (GPCR) protein #15.
PN WO2003052078-A2.
PD 26-JUN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 7; DB 7; Length 431;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1465
ID ABG97421 standard; protein; 433 AA.
DE S. macromyceticus UNBU protein.
PN CA2387401-A1.
PD 04-SEP-2002.
PA (ECOP-) ECOPHA BIOSCIENCES INC.
Query Match 2.1%; Score 7; DB 5; Length 433;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1466
ID AEB12615 standard; protein; 433 AA.
DE Eneidiyne related UNBU, SEQ ID 11.
PN US2005142601-A1.
PD 30-JUN-2005.
PA (FARN/) FARNET C M.
PA (STAF/) STAFPA A.

PA (ZAZO/) ZAZOPOULOS E. 2.1%; Score 7; DB 9; Length 433;
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1467
ID AEG10208 standard; protein; 433 AA.
DE Streptomyces macromyceticus enediyne biosynthetic protein UNBU, SEQ:11.
PN US2005170411-A1.
PD 04-AUG-2005.
PA (FARM/) FARNET C. M.
PA (STAF/) STAFPA A.
PA (ZAZO/) ZAZOPOULOS E.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1468
ID AAY28799 standard; protein; 439 AA.
DE Maize histone deacetylase-3.
PN WO9951731-A2.
PD 14-OCT-1999.
PA (PRON-) PRONER HI-BRED INT INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1469
ID ADZ63998 standard; protein; 443 AA.
DE Human cancer-linked gene R1PK2, protein, SEQ ID 39.
PN WO2005035724-A2.
PD 21-APR-2005.
PA (AVAL-) AVALON PHARM INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1470
ID ABB66286 standard; protein; 444 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 25650.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (BEKE-) PE CORP NY.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1471
ID AAU38968 standard; protein; 444 AA.
DE Drosophila G-protein coupled receptor, GCPR #46.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (BEKE-) PE CORP NY.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1472
ID ADC3586 standard; protein; 444 AA.
DE Drosophila G protein coupled receptor seq id 48.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1473
ID ABU11985 standard; protein; 448 AA.
DE M. echinospora calicheamicin biosynthesis protein CalW.
PN WO200279465-A2.
PD 10-OCT-2002.
PA (SLOK-) SLOAN KETTERING INST CANCER RES.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1474
ID ADH71794 standard; protein; 457 AA.
DE Human protein of the invention NOV29m SEQ ID NO:690.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1475
ID ADH71790 standard; protein; 457 AA.
DE Human protein of the invention NOV29k SEQ ID NO:686.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1476
ID ADH71792 standard; protein; 460 AA.
DE Human protein of the invention NOV29l SEQ ID NO:688.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1477
ID AAU35054 standard; protein; 464 AA.
DE Enterococcus faecalis cellular proliferation protein #341.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1478
ID ABB49506 standard; protein; 464 AA.
DE Listeria monocytogenes protein #2210.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP-) INST PASTEUR.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1479
ID ABU14637 standard; protein; 464 AA.
DE Protein encoded by Prokaryotic essential gene #164.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1480
ID ABU32474 standard; protein; 464 AA.
DE Protein encoded by Prokaryotic essential gene #18001.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1481
ID ABU30009 standard; protein; 465 AA.
DE Protein encoded by Prokaryotic essential gene #15536.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1482
ID AAU33501 standard; protein; 467 AA.
DE Enterococcus faecalis cellular proliferation protein #137.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1483
ID ABO64627 standard; protein; 467 AA.
DE Klebsiella pneumoniae polypeptide seqid 11144.
PN US610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1484
ID ADC66490 standard; protein; 472 AA.
DE E. faecium protein sequence SEQ ID 6117.
PN US6583275-B1.
PD 24-JUN-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 2.1%; Score 7; DB 7; Length 472;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1485
 ID ADX74976 standard; protein; 472 AA.
 DE Plant full length insert polypeptide seqid 44342.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIU/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D. K.
 PA (SCRE/) SCREEN S. E.
 PA (TABAS/) TABASKA J. E.
 PA (CAOY/) CAO Y.
 Query Match 2.1%; Score 7; DB 8; Length 472;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1486
 ID ADH71800 standard; protein; 473 AA.
 DE Human protein of the invention NOV29p SEQ ID NO:696.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.1%; Score 7; DB 8; Length 473;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1487
 ID ADH71798 standard; protein; 473 AA.
 DE Human protein of the invention NOV29o SEQ ID NO:694.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.1%; Score 7; DB 8; Length 473;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1488
 ID ADH71796 standard; protein; 473 AA.
 DE Human protein of the invention NOV29n SEQ ID NO:692.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.1%; Score 7; DB 8; Length 473;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1489
 ID ADH71788 standard; protein; 473 AA.
 DE Human protein of the invention NOV29j SEQ ID NO:684.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.1%; Score 7; DB 8; Length 473;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1490
 ID ADH71802 standard; protein; 473 AA.
 DE Human protein of the invention NOV29q SEQ ID NO:698.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.1%; Score 7; DB 8; Length 473;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1491
 ID AA46847 standard; protein; 474 AA.
 DE Propionibacterium acnes immunogenic protein #7743.
 PN WO200181581-A2.
 PD 01-NOV-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.1%; Score 7; DB 4; Length 474;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1492
 ID ABM43366 standard; protein; 474 AA.
 DE Propionibacterium acnes membrane-related polypeptide #8042.
 PN WO2003033515-A1.
 PD 24-APR-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 2.1%; Score 7; DB 6; Length 474;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1493

ID ABB27131 standard; protein; 476 AA.
 DE Pinus radiata cell cycle protein SEQ ID NO 292.
 PN WO2005065339-A2.
 PD 21-JUL-2005.
 PA (ARBO-) ARBOGEN LLC.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 Query Match 2.1%; Score 7; DB 9; Length 476;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1494
 ID AAY59405 standard; protein; 478 AA.
 DE Human RICK protein sequence residues 54-531.
 PN WO9955134-A2.
 PD 04-NOV-1999.
 PA (UNMI) UNIV MICHIGAN.
 Query Match 2.1%; Score 7; DB 3; Length 478;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1495
 ID AAM91275 standard; protein; 478 AA.
 DE M. xanthus protein sequence, seq id 10474.
 PN US6833447-B1.
 PD 21-DEC-2004.
 PA (MONS) MONSANTO TECHNOLOGY LLC.
 Query Match 2.1%; Score 7; DB 9; Length 478;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1496
 ID ABB59096 standard; protein; 487 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 4080.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.1%; Score 7; DB 4; Length 487;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1497
 ID AAY58828 standard; protein; 493 AA.
 DE Rice histone deacetylase 1 (HD1) protein (C-terminal portion).
 PN WO200004177-A1.
 PD 27-JAN-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 Query Match 2.1%; Score 7; DB 3; Length 493;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1498
 ID ADQ37139 standard; protein; 493 AA.
 DE Cell proliferation-related polypeptide #133.
 PN WO2004061122-A2.
 PD 22-JUL-2004.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 2.1%; Score 7; DB 8; Length 493;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1499
 ID ADQ15723 standard; protein; 493 AA.
 DE Rice stress-related protein #66.
 PN WO2004061080-A2.
 PD 22-JUL-2004.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 2.1%; Score 7; DB 8; Length 493;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 RESULT 1500
 ID ABB64074 standard; protein; 496 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 19014.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.1%; Score 7; DB 4; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 11:18:06 ; Search time 70 Seconds

(without alignments)
1999.612 Million cell updates/secPerfect score: 1772
Sequence: 1 MAGSPCTLTLYIMQUTGS.....PHSLTTPDTPRLPAYENVI 335Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1772	100.0	335	US-09-732-524-2	Sequence 2, Appli
8	1772	100.0	335	US-09-745-605-4	Sequence 4, Appli
29	1772	100.0	335	US-09-997-428-253	Sequence 253, App
540	1772	100.0	335	US-10-021-741A-2	Sequence 2, Appli
565	1772	100.0	335	US-10-174-587-192	Sequence 192, App
629	1772	100.0	335	US-10-063-742-46	Sequence 46, Appl
739	1772	100.0	335	US-10-262-839-110	Sequence 110, App
745	1772	100.0	335	US-10-842-011-2	Sequence 11, App
746	1772	100.0	335	US-10-972-317-46	Sequence 46, Appl
748	1772	100.0	335	US-10-950-374-253	Sequence 253, App
751	1769	99.8	335	US-10-104-943-5	Sequence 5, Appli
752	1769	99.8	335	US-10-436-523-60	Sequence 60, Appl
753	1769	99.8	335	US-10-408-765A-1405	Sequence 1405, App
754	1755.5	99.1	348	US-10-262-839-112	Sequence 112, App
755	1653	93.3	312	US-09-732-524-4	Sequence 4, Appli
756	933.5	52.7	684	US-10-450-763-42056	Sequence 42056, A
757	933.5	52.7	684	US-10-450-763-42528	Sequence 42528, A
758	582	32.8	110	US-09-984-245-125	Sequence 125, App
759	582	32.8	110	US-09-966-262-125	Sequence 125, App
760	582	32.8	110	US-09-983-966-125	Sequence 125, App
761	582	32.8	110	US-10-059-395-125	Sequence 125, App
762	582	32.8	110	US-10-143-090-125	Sequence 125, App
763	582	32.8	110	US-10-960-251-125	Sequence 125, App
764	471	26.6	91	US-09-864-761-41706	Sequence 41706, A
765	362.5	20.5	328	US-10-104-943-30	Sequence 4, Appli
766	362.5	20.5	328	US-10-436-523-30	Sequence 30, Appl
767	362.5	20.5	328	US-10-723-860-1866	Sequence 1866, Ap
768	362.5	20.5	328	US-10-684-206-8	Sequence 8, Appli

769	362.5	20.5	328	US-10-756-149-5194	Sequence 5194, Ap
770	362.5	20.5	329	US-09-809-391-483	Sequence 483, App
771	362.5	20.5	329	US-09-882-171-483	Sequence 187, App
772	362.5	20.5	329	US-10-164-861-483	Sequence 483, App
773	345.5	19.5	301	US-10-311-829-11	Sequence 11, Appl
774	343	19.4	629	US-09-860-8368-9	Sequence 9, Appli
775	333.5	18.8	289	US-10-436-523-88	Sequence 88, Appl
776	330.5	18.7	289	US-10-220-946-18	Sequence 18, Appl
777	330.5	18.7	289	US-10-436-523-76	Sequence 76, Appl
778	330.5	18.7	289	US-10-436-523-91	Sequence 91, Appl
779	330.5	18.7	289	US-10-170-385-131	Sequence 131, App
780	327.5	18.5	289	US-10-436-523-89	Sequence 89, Appl
781	327.5	18.5	289	US-10-436-523-80	Sequence 80, Appl
782	327	18.5	270	US-10-436-523-77	Sequence 77, Appl
783	319.5	18.0	331	US-10-436-523-39	Sequence 39, Appl
784	318	17.9	615	US-10-659-004-48	Sequence 48, Appl
785	318	17.9	654	US-10-104-943-7	Sequence 7, Appli
786	318	17.9	654	US-10-310-612-2	Sequence 2, Appli
787	318	17.9	654	US-10-328-838-2	Sequence 2, Appli
788	316.5	17.9	331	US-10-377-413-2	Sequence 2, Appli
789	315.5	17.8	309	US-10-436-523-5	Sequence 5, Appli
790	315.5	17.8	331	US-10-104-943-2	Sequence 2, Appli
791	315.5	17.8	331	US-10-436-523-3	Sequence 3, Appli
792	315.5	17.8	331	US-10-264-237-2559	Sequence 2559, Ap
793	315.5	17.8	331	US-10-614-853-22	Sequence 22, Appl
794	315.5	17.8	331	US-10-484-139-2	Sequence 3, Appli
795	315.5	17.8	346	US-10-257-174-33	Sequence 33, Appl
796	314.5	17.7	331	US-10-436-523-41	Sequence 41, Appl
797	313.5	17.7	331	US-10-436-523-80	Sequence 40, Appl
798	312.5	17.6	610	US-09-860-8368-11	Sequence 11, Appl
799	311.5	17.6	331	US-10-436-523-42	Sequence 42, Appl
800	311	17.6	311	US-10-311-829-10	Sequence 10, Appl
809	311	17.6	332	US-10-237-535-76	Sequence 76, Appl
818	311	17.6	332	US-10-239-196-76	Sequence 76, Appl
822	311	17.6	332	US-10-104-943-41	Sequence 41, Appl
835	311	17.6	332	US-10-136-574-2	Sequence 2, Appli
836	311	17.6	332	US-10-471-449-8	Sequence 5, Appli
912	311	17.6	332	US-10-311-829-4	Sequence 4, Appli
913	307.5	17.4	285	US-10-436-523-100	Sequence 100, App
914	301.5	17.0	235	US-10-436-523-82	Sequence 82, Appl
915	298	16.8	217	US-10-436-523-79	Sequence 79, Appl
916	294.5	16.6	551	US-10-471-449-8	Sequence 8, Appli
917	282.5	15.9	526	US-10-659-004-45	Sequence 50, Appl
918	251	14.2	220	US-10-257-174-32	Sequence 32, Appl
919	247	13.9	310	US-10-258-951-48	Sequence 48, Appl
920	247	13.9	310	US-10-990-000-48	Sequence 48, Appl
921	245	13.8	195	US-10-436-523-15	Sequence 15, Appl
922	245	13.8	203	US-10-436-523-16	Sequence 16, Appl
923	236.5	13.3	229	US-10-258-951-47	Sequence 47, Appl
924	236.5	13.3	229	US-10-990-000-47	Sequence 47, Appl
925	225.5	12.7	351	US-10-436-523-11	Sequence 11, Appl
926	225.5	12.7	351	US-09-745-605-5	Sequence 5, Appli
927	225.5	12.7	351	US-10-104-943-3	Sequence 3, Appli
928	219	12.4	168	US-10-264-237-1621	Sequence 1621, Ap
929	206	11.6	220	US-10-104-943-33	Sequence 43, Appl
930	200.5	11.3	159	US-10-436-523-8	Sequence 8, Appli
931	199.5	11.3	221	US-10-471-449-4	Sequence 4, Appli
932	190.5	10.8	275	US-10-087-192-1485	Sequence 1485, Ap
933	182.5	10.3	335	US-09-731-449-10	Sequence 20, Appl
934	182.5	10.3	335	US-09-918-715-85	Sequence 285, App
935	182.5	10.3	335	US-09-369-248-3	Sequence 3, Appli
936	182.5	10.3	335	US-09-860-8368-1	Sequence 1, Appli
937	182.5	10.3	335	US-10-062-523-3	Sequence 3, Appli
938	182.5	10.3	335	US-10-254-426-20	Sequence 20, Appl
939	182.5	10.3	335	US-10-436-523-64	Sequence 64, Appl
940	182.5	10.3	335	US-10-464-469-3	Sequence 3, Appli
941	182.5	10.3	335	US-10-445-888A-3	Sequence 3, Appli
942	182.5	10.3	335	US-10-474-794-285	Sequence 285, App
943	182.5	10.3	335	US-10-892-171-3	Sequence 3, Appli
944	182.5	10.3	335	US-10-979-159-285	Sequence 285, App
945	179	10.1	278	US-09-731-449-25	Sequence 25, Appl
946	179	10.1	278	US-10-254-426-25	Sequence 25, Appl
947	177.5	10.0	258	US-09-731-449-28	Sequence 28, Appl

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 11:46:45 ; Search time 39 Seconds
(without alignments)
826.477 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 335
Sequence: 1 MAGSPCTLTLYILMQLTGS.....PHSLTWPPRPRLFAVENVI 335

Scoring table: Original
Gapop 60.0 , Gapept 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1500 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2.7	156	2	H72621	hypothetical prote
2	2.7	2464	1	QMSP1	microtubule-associ
3	2.4	173	2	S76681	hypothetical prote
4	2.4	286	2	A62159	hypothetical prote
5	2.4	705	2	S18733	glutenin high mole
6	2.4	1117	2	S38673	desmoglein 2 - hum
7	2.1	105	2	T29918	hypothetical prote
8	2.1	161	2	E71866	hypothetical prote
9	2.1	170	2	AB1817	hypothetical prote
10	2.1	179	2	F97283	ribosomal protein
11	2.1	179	2	F83305	hypothetical prote
12	2.1	182	2	F97499	hypothetical prote
13	2.1	184	2	I40220	hypothetical prote
14	2.1	189	2	H70416	hypothetical prote
15	2.1	199	2	T45543	hypothetical prote
16	2.1	220	2	E75285	hypothetical prote
17	2.1	228	2	T47847	hypothetical prote
18	2.1	238	2	G69830	hypothetical prote
19	2.1	238	2	C82884	conserved hypotet
20	2.1	239	2	F69996	amino acid ABC tra
21	2.1	239	2	T51270	hypothetical prote
22	2.1	266	2	C87367	flagellar biosynch
23	2.1	274	2	G84218	cysteine synthase
24	2.1	290	2	A88616	protein T2508.3 [i
25	2.1	301	2	DB3970	UDP-N-acetylenolp
26	2.1	301	2	T52549	probable chitosula
27	2.1	302	2	E75414	pecm-related prote
28	2.1	303	2	A43727	UDP-N-acetylenolp
29	2.1	305	2	G96962	UDP-N-acetylenolp

30	7	2.1	312	1	LPRT6
31	7	2.1	316	2	F98027
32	7	2.1	316	2	G95161
33	7	2.1	331	2	C89469
34	7	2.1	348	2	E84299
35	7	2.1	351	2	C82755
36	7	2.1	356	2	S14396
37	7	2.1	362	2	S68471
38	7	2.1	367	2	S41024
39	7	2.1	369	2	T21392
40	7	2.1	377	2	H89717
41	7	2.1	379	2	S49614
42	7	2.1	381	2	T11312
43	7	2.1	381	2	T11776
44	7	2.1	410	2	B81744
45	7	2.1	413	2	T48089
46	7	2.1	418	2	F64059
47	7	2.1	428	2	AD0675
48	7	2.1	433	2	S45856
49	7	2.1	443	2	AB2719
50	7	2.1	448	2	JC2305
51	7	2.1	454	2	T19380
52	7	2.1	458	2	F69123
53	7	2.1	463	2	A69905
54	7	2.1	464	2	AG1146
55	7	2.1	464	2	AG1505
56	7	2.1	467	2	A99498
57	7	2.1	475	2	T47480
58	7	2.1	480	2	F97500
59	7	2.1	492	2	D87606
60	7	2.1	501	2	H95859
61	7	2.1	508	2	E96804
62	7	2.1	513	2	B84391
63	7	2.1	572	2	AB2671
64	7	2.1	586	1	VCLDMP
65	7	2.1	587	1	VCLUSA
66	7	2.1	591	2	B54354
67	7	2.1	591	2	C54354
68	7	2.1	605	2	S52253
69	7	2.1	643	2	B72602
70	7	2.1	646	2	D82493
71	7	2.1	675	2	T22333
72	7	2.1	730	2	T13792
73	7	2.1	732	1	JC4655
74	7	2.1	797	2	T50072
75	7	2.1	799	2	H71255
76	7	2.1	829	2	T40239
77	7	2.1	914	2	I40529
78	7	2.1	943	2	C97893
79	7	2.1	943	2	F95021
80	7	2.1	954	2	AF2756
81	7	2.1	954	2	E97537
82	7	2.1	957	2	B85946
83	7	2.1	957	2	AC0873
84	7	2.1	957	2	F91100
85	7	2.1	957	2	S36834
86	7	2.1	958	2	E82994
87	7	2.1	959	2	AB0111
88	7	2.1	997	2	T32814
89	7	2.1	1002	2	S62035
90	7	2.1	1020	2	JN0124
91	7	2.1	1032	2	S53571
92	7	2.1	1070	2	T06733
93	7	2.1	1085	2	S55352
94	7	2.1	1166	2	T15628
95	7	2.1	1268	2	A49674
96	7	2.1	1277	2	T15109
97	7	2.1	1290	2	T00019
98	7	2.1	1291	2	T00019
99	7	2.1	1312	2	S68593
100	7	2.1	1345	2	T29080
101	7	2.1	1355	2	T22552
102	7	2.1	1487	2	S15904

apolipoprotein B p
UDP-N-acetylenolp
UDP-N-acetylenolp
protein F0766.1 [i
hypothetical prote
conserved hypotet
cytochrome-c oxid
asparaginase (BC 3
hypothetical prote
hypothetical prote
protein C18B12.2 [i
cyth protein - Rhi
ubiquinol-cytochro
ubiquinol-cytochro
poly(A) polymerase
hypothetical prote
hypothetical prote
tryptophan transpo
membrane transport
probable membrane
conserved hypotet
glucanate permease
hypothetical prote
efflux pump antibi
conserved hypotet
beta-glucosidase h
beta-glucosidase h
hypothetical prote
hypothetical prote
tolerance to colic
sensor histidine K
probable ABC trans
probable thioredox
DNA damage-inducib
cytochrome-c oxid
env polypeptin -
calnexin precursor
calnexin precursor
copper resistance
hypothetical prote
conserved hypotet
hypothetical prote
NMDH2 dehydrogenas
acylaminoacyl-pept
hypothetical prote
probable cell divi
probable helicase
penicillin-binding
exonuclease ABC c
exonuclease ABC,
glycine cleavage s
glycine cleavage s
hypothetical prote
glycine dehydrogen
glycine decarboxyl
glycine dehydrogen
glycine cleavage s
glycine dehydrogen
hypothetical prote
isolucine-CrNA 11
glycine dehydrogen
hypothetical prote
kinesin homolog F2
RHL protein - yea
hypothetical prote
flightless-I homol
hypothetical prote
period protein hom
period protein hom
DNA-directed DNA p
surface layer-asso
hypothetical prote
alpha-1 proteinase

103	7	2.1	1552	2	T05408	hypothetical prote
104	7	2.1	1560	2	T02885	peroxisome prolife
105	7	2.1	1585	2	AE2916	NAD-glutamate dehy
106	7	2.1	1585	2	H97690	NAD-glutamate dehy
107	7	2.1	1620	2	S61535	nucleotide-binding
108	7	2.1	2787	2	S45416	TRH1 protein - Yea
109	7	2.1	3973	2	B71612	hypothetical prote
110	7	2.1	4545	1	S25111	alpha-2-macroglobu
111	6	1.8	30	2	I57689	ubiquinol-cytochro
112	6	1.8	32	2	S21547	T-cell receptor al
113	6	1.8	36	2	H64607	hypothetical prote
114	6	1.8	39	2	C90523	hypothetical prote
115	6	1.8	52	2	C60232	T-cell surface gly
116	6	1.8	56	2	C69044	hypothetical prote
117	6	1.8	57	2	D95852	hypothetical prote
118	6	1.8	60	2	B28918	hypothetical prote
119	6	1.8	61	2	J01086	nodulin-14 precurs
120	6	1.8	66	2	C89925	hypothetical prote
121	6	1.8	70	2	A42155	GTP-binding, regula
122	6	1.8	72	2	C83219	hypothetical prote
123	6	1.8	73	2	T13199	hypothetical prote
124	6	1.8	73	2	T26110	hypothetical prote
125	6	1.8	74	2	E95204	hypothetical prote
126	6	1.8	75	2	C95959	hypothetical prote
127	6	1.8	77	2	AG2343	hypothetical prote
128	6	1.8	82	2	C81350	hypothetical prote
129	6	1.8	83	2	JC7607	prolactin-releasin
130	6	1.8	86	2	AC2117	hypothetical prote
131	6	1.8	92	2	I64109	mercury reductase
132	6	1.8	93	2	T45245	hypothetical prote
133	6	1.8	95	2	S68231	FBH22 protein prec
134	6	1.8	95	2	T49793	hypothetical prote
135	6	1.8	96	1	A42281	symblonin syms - p
136	6	1.8	96	1	ZEBCP4	gene B protein - p
137	6	1.8	96	2	A84932	10 kD chaperonin I
138	6	1.8	96	2	C92048	chaperonin, 10 kD
139	6	1.8	96	2	B64076	chaperonin groES -
140	6	1.8	96	2	JC4518	heat-shock protein
141	6	1.8	97	1	BVBCGS	chaperonin groES -
142	6	1.8	97	2	A48093	monocytic cytokine
143	6	1.8	97	2	JC5770	chaperonin groES-1
144	6	1.8	97	2	AD1045	GroES protein (imp
145	6	1.8	97	2	C91269	chaperonin GroES I
146	6	1.8	97	2	A86110	chaperonin mopB [s
147	6	1.8	97	2	E97266	glu-tRNA amidotran
148	6	1.8	98	2	S24920	NADH2 dehydrogenas
149	6	1.8	98	2	S41828	NADH2 dehydrogenas
150	6	1.8	98	2	T11488	NADH2 dehydrogenas
151	6	1.8	99	1	A32926	monocyte chemoattr
152	6	1.8	99	2	JC2336	monocyte chemoattr
153	6	1.8	99	2	A60299	monocyte chemoattr
154	6	1.8	99	2	JC5295	monocyte chemoattr
155	6	1.8	99	2	JC2136	monocyte chemoattr
156	6	1.8	99	2	JC2417	monocyte chemoattr
157	6	1.8	100	2	AE0796	NADH2 dehydrogenas
158	6	1.8	100	2	E64999	NADH2 dehydrogenas
159	6	1.8	100	2	D85868	NADH dehydrogenase
160	6	1.8	100	2	C91024	C91024
161	6	1.8	100	2	AH0310	NADH2 dehydrogenas
162	6	1.8	100	2	E69846	hypothetical prote
163	6	1.8	101	2	S37068	NADH2 dehydrogenas
164	6	1.8	101	2	S64222	probable membrane
165	6	1.8	102	2	F87993	protein ZC334.3 [1
166	6	1.8	103	2	S72692	probable membrane
167	6	1.8	105	2	B97734	hypothetical prote
168	6	1.8	107	2	PH0987	ig heavy chain V r
169	6	1.8	107	2	C70168	hypothetical prote
170	6	1.8	108	2	S73125	hypothetical prote
171	6	1.8	108	2	A55590	hypothetical prote
172	6	1.8	108	2	I40598	hypothetical prote
173	6	1.8	109	2	A54678	monocyte chemoact
174	6	1.8	109	2	H71142	hypothetical prote
175	6	1.8	111	2	F71940	probable ribosome-
176	6	1.8	111	2	G64650	ribose-binding f
177	6	1.8	111	2	G75009	hypothetical prote
178	6	1.8	111	2	B83101	hypothetical prote
179	6	1.8	112	2	S48472	probable membrane
180	6	1.8	113	2	S26263	T-cell receptor be
181	6	1.8	113	2	S26262	T-cell receptor be
182	6	1.8	113	2	S17385	T-cell receptor be
183	6	1.8	113	2	S26266	T-cell receptor be
184	6	1.8	113	2	JC4143	mol-t-inhibiting ho
185	6	1.8	113	2	AD2868	hypothetical prote
186	6	1.8	114	2	AC3033	hypothetical prote
187	6	1.8	115	2	AG3279	hypothetical prote
188	6	1.8	115	2	S09751	hypothetical prote
189	6	1.8	116	2	TS1028	hypothetical prote
190	6	1.8	118	2	AB2862	conserved hypotnet
191	6	1.8	118	2	A97639	hypothetical prote
192	6	1.8	118	2	H97644	hypothetical prote
193	6	1.8	120	2	I48147	monocyte chemoattr
194	6	1.8	122	2	AD5304	hemoglobin beta-1
195	6	1.8	122	2	A83283	hypothetical prote
196	6	1.8	123	2	E95940	conserved hypotnet
197	6	1.8	123	2	I48192	surface antigen -
198	6	1.8	123	2	G75336	hypothetical prote
199	6	1.8	124	2	A11647	hypothetical prote
200	6	1.8	125	2	I46857	monocyte chemoattr
201	6	1.8	125	2	T27519	hypothetical prote
202	6	1.8	126	2	S73081	hypothetical prote
203	6	1.8	126	2	AE0918	probable membrane
204	6	1.8	126	2	S30707	hypothetical 14.5K
205	6	1.8	126	2	C72650	hypothetical prote
206	6	1.8	128	2	C48552	hypothetical prote
207	6	1.8	128	2	D29504	hypothetical 14k p
208	6	1.8	128	2	C75462	hypothetical prote
209	6	1.8	128	2	AD1386	hypothetical prote
210	6	1.8	128	2	AF1761	hypothetical prote
211	6	1.8	129	2	F95987	conserved hypotnet
212	6	1.8	132	2	C87431	hypothetical prote
213	6	1.8	132	2	H75335	hypothetical prote
214	6	1.8	132	2	B83956	hypothetical prote
215	6	1.8	133	2	S57876	T cell receptor CK
216	6	1.8	133	2	C36886	hypothetical prote
217	6	1.8	134	2	D87021	probable DNA-bindi
218	6	1.8	135	2	A70659	hypothetical prote
219	6	1.8	135	2	B83440	hypothetical prote
220	6	1.8	135	2	F87156	hypothetical prote
221	6	1.8	136	2	AD0630	probable exported
222	6	1.8	136	2	T22797	hypothetical prote
223	6	1.8	137	1	F64961	hypothetical prote
224	6	1.8	137	2	S03489	T-cell receptor be
225	6	1.8	137	2	D90967	hypothetical prote
226	6	1.8	137	2	C85815	hypothetical prote
227	6	1.8	137	2	A44031	probable membrane
228	6	1.8	139	2	S36296	T-cell receptor ga
229	6	1.8	140	2	C81176	hypothetical prote
230	6	1.8	140	2	A99253	hypothetical prote
231	6	1.8	141	2	E32998	chorion protein S1
232	6	1.8	141	2	D81309	probable acetyltra
233	6	1.8	142	2	T27965	hypothetical prote
234	6	1.8	143	2	D75617	response regulator
235	6	1.8	144	2	T27945	hypothetical prote
236	6	1.8	145	2	G82617	Virk protein xR194
237	6	1.8	146	2	S26408	T-cell receptor be
238	6	1.8	146	2	T45385	ribosomal protein
239	6	1.8	146	2	T27964	hypothetical prote
240	6	1.8	149	2	AD3431	hypothetical prote
241	6	1.8	150	2	S43955	probable NADH2 deh
242	6	1.8	150	2	A87714	hypothetical prote
243	6	1.8	151	2	S48958	hypothetical prote
244	6	1.8	151	2	A83784	acetyltransferase
245	6	1.8	152	2	S21826	T-cell receptor be
246	6	1.8	152	2	F86318	protein F15H8.2 [
247	6	1.8	153	1	A28406	gastric inhibitory
248	6	1.8	153	2	E87306	hypothetical prote

249	6	1.8	153	2	C64373	hypothetical prote
250	6	1.8	157	2	S57451	cysteine proteinas
251	6	1.8	157	2	T24917	hypothetical prote
252	6	1.8	158	2	H96900	probable HD superf
253	6	1.8	159	2	D90586	hypothetical prote
254	6	1.8	161	2	B72339	hypothetical prote
255	6	1.8	162	1	CFKA	C-phycocyanin alph
256	6	1.8	162	1	CFMA	C-phycocyanin alph
257	6	1.8	162	1	S30940	phycocyanin alpha
258	6	1.8	162	2	H72351	phycocyanin alpha
259	6	1.8	163	2	A29674	phycocyanin alpha
260	6	1.8	163	2	AH1872	peptide methionine
261	6	1.8	166	2	G82910	MDH2 dehydrogenas
262	6	1.8	170	2	T11039	hypothetical prote
263	6	1.8	170	2	T30570	hypothetical prote
264	6	1.8	171	2	H87440	hypothetical prote
265	6	1.8	171	2	B75562	MUT/mudx family
266	6	1.8	172	1	DERING	MDH2 dehydrogenas
267	6	1.8	172	2	H72077	conserved hypotet
268	6	1.8	172	2	C81590	Ct006 hypothetical
269	6	1.8	172	2	H86545	hypothetical prote
270	6	1.8	174	2	T01466	hypothetical prote
271	6	1.8	176	2	S35949	eda protein - tre
272	6	1.8	176	2	JC6152	orphanin FQ precu
273	6	1.8	177	2	S45364	ribosomal protein
274	6	1.8	177	2	B91248	hypothetical prote
275	6	1.8	178	2	S54190	outer surface prot
276	6	1.8	179	2	S36295	T-cell receptor ga
277	6	1.8	179	2	S54186	outer surface prot
278	6	1.8	179	2	S54187	outer surface prot
279	6	1.8	179	2	S54188	outer surface prot
280	6	1.8	179	2	T35439	probable integral
281	6	1.8	180	2	S54189	outer surface prot
282	6	1.8	180	2	S54191	outer surface prot
283	6	1.8	181	2	G89799	hypothetical prote
284	6	1.8	181	2	I40146	outer surface prot
285	6	1.8	181	2	AC0686	hypothetical prote
286	6	1.8	184	2	S73640	inorganic diphosph
287	6	1.8	185	2	AG2026	hypothetical prote
288	6	1.8	186	1	HHFF23	heat shock protein
289	6	1.8	186	2	T11384	Arpase subunit 6 -
290	6	1.8	186	2	B20647	heat shock protein
291	6	1.8	186	2	T47804	hypothetical prote
292	6	1.8	187	2	G95076	conserved hypotet
293	6	1.8	187	2	H70450	lipoprotein nlpd h
294	6	1.8	188	2	S50158	RER1 protein - Yea
295	6	1.8	188	2	A69880	hypothetical prote
296	6	1.8	188	2	T33366	hypothetical prote
297	6	1.8	190	2	F82430	petriplasmic nitrat
298	6	1.8	191	2	S70262	outer surface prot
299	6	1.8	191	2	JC4663	T-cell receptor CD
300	6	1.8	192	2	S22981	T-cell surface gly
301	6	1.8	193	2	S70259	outer surface prot
302	6	1.8	193	2	S70274	outer surface prot
303	6	1.8	193	2	S70286	conserved hypotet
304	6	1.8	194	2	D97944	conserved hypotet
305	6	1.8	194	2	C83312	hypothetical prote
306	6	1.8	196	2	S54196	outer surface prot
307	6	1.8	197	2	E70642	probable ribosomal
308	6	1.8	197	2	G85521	hypothetical prote
309	6	1.8	197	2	C90671	hypothetical prote
310	6	1.8	197	2	B83768	hypothetical prote
311	6	1.8	200	2	B64756	membrane protein Y
312	6	1.8	200	2	A81295	probable membrane
313	6	1.8	201	2	D86912	conserved hypotet
314	6	1.8	201	2	T10016	hypothetical prote
315	6	1.8	202	2	D69046	conserved hypotet
316	6	1.8	202	2	B83375	hypothetical prote
317	6	1.8	203	2	AC0620	hypothetical proph
318	6	1.8	203	2	S32799	hypothetical prote
319	6	1.8	204	2	H70648	probable regulator
320	6	1.8	204	2	B72370	hypothetical prote
321	6	1.8	204	2	T51012	hypothetical prote
322	6	1.8	205	2	S42406	protein phosphatas
323	6	1.8	205	2	S10497	hypothetical prote
324	6	1.8	206	2	AE0891	probable membrane
325	6	1.8	206	2	S61705	hypothetical prote
326	6	1.8	206	2	AE2222	hypothetical prote
327	6	1.8	207	2	A35535	23k calcium-bindin
328	6	1.8	209	2	H69552	hypothetical prote
329	6	1.8	209	2	I40285	outer surface prot
330	6	1.8	209	2	S69926	outer surface prot
331	6	1.8	210	2	T50713	urease accessory p
332	6	1.8	210	2	G97037	hypothetical prote
333	6	1.8	211	2	S69932	outer surface prot
334	6	1.8	211	2	CS9091	hypothetical prote
335	6	1.8	212	2	B29010	alkylmercury lyase
336	6	1.8	212	2	S20543	outer surface prot
337	6	1.8	212	2	S69921	outer surface prot
338	6	1.8	213	2	C70346	UDP-N-acetoctolpyr
339	6	1.8	213	2	S74247	CMP diacylglycerol
340	6	1.8	213	2	S07573	amine oxidase (fla
341	6	1.8	214	1	S18729	adenyl-yl-sulfate k
342	6	1.8	214	2	T21585	hypothetical prote
343	6	1.8	215	2	G98036	conserved hypotet
344	6	1.8	215	2	G95170	hemolysin [import
345	6	1.8	215	2	T48789	trsl related prote
346	6	1.8	216	2	H72277	hypothetical prote
347	6	1.8	216	2	T00192	hypothetical prote
348	6	1.8	217	2	S65830	alpha fucosidase p
349	6	1.8	217	2	S49578	trypsin inhibitor
350	6	1.8	217	2	H72390	dihydroxotolate deh
351	6	1.8	217	2	F91246	PTS system, sorbos
352	6	1.8	218	2	B83862	endonuclease III (
353	6	1.8	218	2	G64673	DNA polymerase III
354	6	1.8	218	2	B71844	probable DNA polyme
355	6	1.8	218	2	S74867	hypothetical prote
356	6	1.8	219	2	S49428	hypothetical prote
357	6	1.8	221	1	S24328	glutathione peroxi
358	6	1.8	221	2	A47367	24k androgen-depen
359	6	1.8	221	2	B42719	O-methyltransferas
360	6	1.8	222	2	UC7697	beta-casein-like p
361	6	1.8	222	2	AD2999	thiol:disulfide in
362	6	1.8	222	2	E98284	histone H1 - mouse
363	6	1.8	223	2	S49492	conserved hypotet
364	6	1.8	224	2	F69444	hypothetical prote
365	6	1.8	225	2	G70721	hypothetical prote
366	6	1.8	227	2	F97276	CFSD/CAPA conserve
367	6	1.8	227	2	D84775	hypothetical prote
368	6	1.8	228	2	B90369	hypothetical prote
369	6	1.8	228	2	B90534	tna/tna methyltr
370	6	1.8	229	2	T18629	hypothetical prote
371	6	1.8	230	2	D84215	hypothetical prote
372	6	1.8	230	2	T36263	probable transcrip
373	6	1.8	231	2	AF1798	probable N-acetylM
374	6	1.8	231	2	B69392	ABC transporter. A
375	6	1.8	233	2	B64525	tblb protein - Hel
376	6	1.8	235	2	S48924	hypothetical prote
377	6	1.8	236	2	D84961	oxidative-5'-phosp
378	6	1.8	236	2	C75516	hypothetical prote
379	6	1.8	236	2	E75337	hypothetical prote
380	6	1.8	237	2	S08073	cyclic nucleotide
381	6	1.8	237	2	S34727	listeriolysin regu
382	6	1.8	237	2	AH1424	hypothetical prote
383	6	1.8	237	2	T05249	probable integral
384	6	1.8	239	2	A81437	hypothetical prote
385	6	1.8	239	2	T31881	hypothetical prote
386	6	1.8	240	2	AD1950	hypothetical prote
387	6	1.8	240	2	T47589	synapobrevin-like
388	6	1.8	240	2	AG0048	hypothetical prote
389	6	1.8	241	2	T33804	hypothetical prote
390	6	1.8	241	2	C86492	hypothetical prote
391	6	1.8	241	2	C72130	hypothetical prote
392	6	1.8	242	2	UC7517	caspace-14/a - hum
393	6	1.8	243	2	G81255	1-(5-phosphoribosy
394	6	1.8	244	2	T43764	Arpase chain 6 [im

395	6	1.8	245	2	B75340	transcription regu
396	6	1.8	245	2	D36145	precortrin-2 methyl
397	6	1.8	245	2	F83105	hypothetical prote
398	6	1.8	246	2	T00704	conserved hypotet
399	6	1.8	247	2	A75254	conserved hypotet
400	6	1.8	247	2	E86250	protein F25C20.16
401	6	1.8	247	2	S66064	conserved hypotet
402	6	1.8	248	2	D69034	phosphoribosylamin
403	6	1.8	249	2	S23902	genome polypeptid
404	6	1.8	249	2	C75156	hypothetical prote
405	6	1.8	250	2	B82821	MDH-ubiquinone ox
406	6	1.8	250	2	H83213	hypothetical prote
407	6	1.8	250	2	T40977	cdp-diacylglycerol
408	6	1.8	251	2	C84036	succinate dehydrog
409	6	1.8	251	2	AC2187	phospho-2-dehydro
410	6	1.8	251	2	G90810	flagellar rod prot
411	6	1.8	251	2	C85670	flagellar rod prot
412	6	1.8	251	2	B64851	flagellar basal bo
413	6	1.8	251	2	B72578	hypothetical prote
414	6	1.8	252	2	H90212	enoyl CoA hydratase
415	6	1.8	252	2	B47188	MHC class II histo
416	6	1.8	252	2	S05029	H+-transporting tw
417	6	1.8	253	2	D88427	protein R0785.15 [
418	6	1.8	253	2	T30928	hypothetical prote
419	6	1.8	254	1	VCCVY	coat protein - tob
420	6	1.8	254	2	S25281	gltF protein precu
421	6	1.8	255	2	F84244	proteaseome, subun
422	6	1.8	256	2	T22715	hypothetical prote
423	6	1.8	256	2	T00165	repressor - Staphy
424	6	1.8	257	2	B70246	outer surface prot
425	6	1.8	257	2	AC0087	probable flagellar
426	6	1.8	259	1	OMGAOL	ovulation hormone
427	6	1.8	260	2	I51542	MHC class II beta-
428	6	1.8	260	2	I51542	MHC class II beta-
429	6	1.8	260	2	S60480	low temperature-in
430	6	1.8	260	2	T29909	hypothetical prote
431	6	1.8	260	2	T33869	hypothetical prote
432	6	1.8	261	2	A83459	O-6-aloglycoprotei
433	6	1.8	261	2	S10321	31k protein - frog
434	6	1.8	262	1	D95271	hypothetical prote
435	6	1.8	262	1	CYFF3	cytochrome-c oxida
436	6	1.8	262	2	B72037	CT598 hypothetical
437	6	1.8	262	2	E86588	conserved hypotet
438	6	1.8	262	2	A81504	conserved hypotet
439	6	1.8	263	1	S23005	insulin-like growt
440	6	1.8	263	2	E72675	hypothetical prote
441	6	1.8	263	2	G69064	conserved hypotet
442	6	1.8	264	2	H81720	conserved hypotet
443	6	1.8	265	2	S16592	chlorophyll a/b-b1
444	6	1.8	265	2	F69742	hypothetical prote
445	6	1.8	265	2	A86891	hypothetical prote
446	6	1.8	267	2	H82201	probable bax prote
447	6	1.8	267	2	T29500	hypothetical prote
448	6	1.8	267	2	C75131	hypothetical prote
449	6	1.8	267	2	S70291	hypothetical prote
450	6	1.8	268	2	A71086	hypothetical prote
451	6	1.8	269	2	T04035	ribonuclease S hom
452	6	1.8	269	2	A75397	probable signal pe
453	6	1.8	269	2	I51539	MHC class II beta-
454	6	1.8	269	2	I51540	MHC class II beta-
455	6	1.8	269	2	S73999	hypothetical prote
456	6	1.8	269	2	H98273	iron(III) diclrat
457	6	1.8	270	2	I51543	MHC class II beta-
458	6	1.8	270	2	S57457	formylmethanofuran
459	6	1.8	271	2	D83059	phosphatidylserine
460	6	1.8	272	2	H87075	probable conserved
461	6	1.8	273	2	B64446	formylmethanofuran
462	6	1.8	274	2	A47639	OX-2 membrane gly
463	6	1.8	274	2	D97653	hypothetical prote
464	6	1.8	274	2	AB2877	conserved hypotet
465	6	1.8	275	2	S74417	hypothetical prote
466	6	1.8	275	2	S03967	intercellular adhe
467	6	1.8	276	1	PWYBAA	H+-transporting tw
468	6	1.8	276	2	A10565	11poreprotein [impor
469	6	1.8	276	2	UT0591	Alr1 protein - yea
470	6	1.8	276	2	E91117	hypothetical prote
471	6	1.8	276	2	F72342	conserved hypotet
472	6	1.8	276	2	T00923	hypothetical prote
473	6	1.8	277	2	T32460	hypothetical prote
474	6	1.8	277	2	B69479	conserved hypotet
475	6	1.8	278	1	TDRTOX	OX-2 membrane gly
476	6	1.8	279	2	E75472	ROK family protein
477	6	1.8	280	2	T02004	chitinase (EC 3.2.
478	6	1.8	280	2	B81100	2-dehydro-3-deoxyp
479	6	1.8	280	2	G81840	2-dehydro-3-deoxyp
480	6	1.8	280	2	B45537	viral coat protein
481	6	1.8	280	2	T32747	hypothetical prote
482	6	1.8	280	2	B87547	transcription regu
483	6	1.8	281	1	D69030	copy control prote
484	6	1.8	281	2	B47092	malodextrin ABC-t
485	6	1.8	281	2	B86820	malodextrin ABC-t
486	6	1.8	282	1	SAV654	UDP-N-acetylenolp
487	6	1.8	282	2	AC3084	probable DMSO redu
488	6	1.8	283	2	AH0726	probable DMSO redu
489	6	1.8	283	2	AC1340	probable dimethyls
490	6	1.8	283	2	A11710	probable transport
491	6	1.8	284	2	C72222	probable succinate
492	6	1.8	284	2	H90915	conserved hypotet
493	6	1.8	284	2	E85764	hypothetical prote
494	6	1.8	284	2	H64914	phosphotransferase
495	6	1.8	284	2	T36934	PTS enzyme IID, ma
496	6	1.8	285	2	E81388	mannose-specific P
497	6	1.8	285	2	B95241	mannose-5-dehydr
498	6	1.8	285	2	C98105	mucrein 3-oxoacyl
499	6	1.8	286	1	WQECWM	probable endo-1,
500	6	1.8	286	2	D85793	xyloglucan endo-1,
501	6	1.8	286	2	A98945	cytochrome-c oxida
502	6	1.8	286	2	H64053	gene PD-1 protein
503	6	1.8	287	1	A45168	sporulation protei
504	6	1.8	287	2	T04236	probable dehydroge
505	6	1.8	288	2	S36956	hypothetical prote
506	6	1.8	288	2	S28029	shikimate 5-dehydr
507	6	1.8	288	2	S18438	beta-lactamase (EC
508	6	1.8	289	1	S25286	riboosomal protein
509	6	1.8	289	2	T41305	hypothetical prote
510	6	1.8	291	2	F98202	sugar kinase [impo
511	6	1.8	293	2	S04649	PTS system, mann
512	6	1.8	293	2	T09171	uracil phosphoribo
513	6	1.8	293	2	T09170	hypothetical prote
514	6	1.8	293	2	A83623	probable drdp-rham
515	6	1.8	295	2	E84336	UDP-N-acetylenolp
516	6	1.8	295	2	AC0214	chromosome initiat
517	6	1.8	296	2	T45930	replication initia
518	6	1.8	296	2	T00559	replication initia
519	6	1.8	296	2	A36966	FLA17.4 [imported
520	6	1.8	297	2	A70347	hypothetical prote
521	6	1.8	297	2	AF0874	probable integral
522	6	1.8	297	2	S22098	osteoinductive fac
523	6	1.8	297	2	F85947	hypothetical prote
524	6	1.8	297	2	B91102	serine O-acetyltra
525	6	1.8	297	2	C96524	probable membrane
526	6	1.8	297	2	F70572	hypothetical prote
527	6	1.8	298	2	T36900	proteinase IV homo
528	6	1.8	298	2	B35272	spermidine synthas
529	6	1.8	298	2	T20841	hypothetical prote
530	6	1.8	299	2	T04669	chromosome initiat
531	6	1.8	299	2	AB0609	conserved hypotet
532	6	1.8	299	2	T20953	probable DNA-direc
533	6	1.8	300	2	A84420	ferriochrome-bindin
534	6	1.8	301	2	D90224	hypothetical prote
535	6	1.8	301	2	T37031	
536	6	1.8	302	2	AE0112	
537	6	1.8	302	2	H87476	
538	6	1.8	303	2	T30737	
539	6	1.8	303	2	AI0411	
540	6	1.8	303	2	S23440	

541	6	1.8	304	2	C81530	614	6	1.8	338	2	AP3617	oligopeptide trans
542	6	1.8	304	2	A86614	615	6	1.8	338	2	T49998	hypothetical prote
543	6	1.8	304	2	E72010	616	6	1.8	339	2	S08981	malate dehydrogena
544	6	1.8	304	2	T40316	617	6	1.8	339	2	S73840	ribonucleotide red
545	6	1.8	304	2	T34271	618	6	1.8	340	2	C64225	ribonucleotide red
546	6	1.8	305	2	UN0647	619	6	1.8	340	2	B96661	unknown protein, 8
547	6	1.8	305	2	AF2843	620	6	1.8	340	2	T22010	hypothetical prote
548	6	1.8	305	2	G97620	621	6	1.8	341	2	S55627	hypothetical prote
549	6	1.8	305	2	D88656	622	6	1.8	341	2	C90579	hypothetical prote
550	6	1.8	305	2	C84189	623	6	1.8	342	2	S53663	hydrogenase-relate
551	6	1.8	305	2	T35344	624	6	1.8	342	2	E90772	periplasmic protei
552	6	1.8	306	2	F83348	625	6	1.8	342	2	A85635	part of regulatio
553	6	1.8	306	2	S77062	626	6	1.8	342	2	H64840	lort protein precu
554	6	1.8	307	2	B75120	627	6	1.8	343	2	A84335	chloromucronate cyc
555	6	1.8	307	2	E71011	628	6	1.8	343	2	AC3403	general L-amino ac
556	6	1.8	307	2	C81862	629	6	1.8	344	2	E84376	Na+/Ca2+-exchangin
557	6	1.8	307	2	D81082	630	6	1.8	344	2	T34981	probable integral
558	6	1.8	308	1	CRH06	631	6	1.8	345	2	S28140	gas vesicle protei
559	6	1.8	308	2	AG3317	632	6	1.8	345	2	A98251	hypothetical prote
560	6	1.8	309	2	H75113	633	6	1.8	345	2	AB3035	conserved hypotet
561	6	1.8	309	2	H89832	634	6	1.8	347	2	T11338	NADH2 dehydrogenas
562	6	1.8	310	2	T40802	635	6	1.8	347	2	T11481	NADH2 dehydrogenas
563	6	1.8	311	2	S39661	636	6	1.8	347	2	JC5788	tsec-1 protein (A
564	6	1.8	311	2	D98045	637	6	1.8	347	2	B75610	probable 3-hydroxy
565	6	1.8	311	2	E95178	638	6	1.8	348	2	JC8007	N-myc downstream-x
566	6	1.8	311	2	AH3197	639	6	1.8	349	2	H95421	probable ABC trans
567	6	1.8	312	2	GH4058	640	6	1.8	350	2	B82777	conserved hypotet
568	6	1.8	312	2	H89884	641	6	1.8	350	2	JC7188	REIC protein - hum
569	6	1.8	313	2	T09670	642	6	1.8	351	2	S25480	heat shock transcr
570	6	1.8	313	2	AB3186	643	6	1.8	351	2	UQ2186	spindle body prote
571	6	1.8	313	2	H84169	644	6	1.8	352	2	S24559	Wnt-2 protein - fr
572	6	1.8	315	2	T37901	645	6	1.8	352	2	T08209	matrix protein - H
573	6	1.8	315	2	JC5836	646	6	1.8	352	2	T49432	Ribonuclease III r
574	6	1.8	317	2	E82362	647	6	1.8	353	1	A45052	L-iditol 2-dehydro
575	6	1.8	317	2	B83039	648	6	1.8	353	2	A87643	hypothetical prote
576	6	1.8	317	2	D89961	649	6	1.8	354	2	C71368	probable UDP-N-ace
577	6	1.8	317	2	T21046	650	6	1.8	354	2	A90012	hypothetical prote
578	6	1.8	317	2	A95282	651	6	1.8	354	2	B85647	hypothetical prote
579	6	1.8	319	2	S44746	652	6	1.8	354	2	B47065	phosphate stravat
580	6	1.8	323	2	A50324	653	6	1.8	354	2	T22274	ATP-binding pho re
581	6	1.8	324	2	A69648	654	6	1.8	354	2	S22181	hypothetical prote
582	6	1.8	324	2	B96606	655	6	1.8	355	1	T03785	gamma-L-microglobu
583	6	1.8	326	2	PRMVA	656	6	1.8	355	2	C70249	L-lactate dehydrog
584	6	1.8	327	2	G70402	657	6	1.8	356	2	G70249	hypothetical prote
585	6	1.8	328	2	A70871	658	6	1.8	356	2	S58529	alpha-complex prot
586	6	1.8	328	2	B84545	659	6	1.8	356	2	JQ2352	glycoprotein I - t
587	6	1.8	328	2	D69452	660	6	1.8	357	2	AD3491	hypothetical membr
588	6	1.8	328	2	C69358	661	6	1.8	358	2	D89823	hypothetical prote
589	6	1.8	328	2	D72566	662	6	1.8	359	2	H95892	probable oxidoredu
590	6	1.8	328	2	S57128	663	6	1.8	359	2	D83385	hypothetical prote
591	6	1.8	329	2	T10203	664	6	1.8	359	2	G86290	hypothetical prote
592	6	1.8	329	2	H71192	665	6	1.8	359	2	T26813	hypothetical prote
593	6	1.8	330	2	C71096	666	6	1.8	359	2	AH3465	oxidoreductase (BC
594	6	1.8	330	2	D95958	667	6	1.8	360	2	T27694	hypothetical prote
595	6	1.8	330	4	PS6079	668	6	1.8	360	2	T51870	hypothetical prote
596	6	1.8	331	2	D83480	669	6	1.8	360	2	B70863	hypothetical prote
597	6	1.8	331	2	T32168	670	6	1.8	361	2	S57182	probable polygalac
598	6	1.8	331	2	T32445	671	6	1.8	361	2	T31815	hypothetical prote
599	6	1.8	332	1	MMBP16	672	6	1.8	362	2	S29968	coat protein VPI -
600	6	1.8	332	1	MMBP26	673	6	1.8	362	2	S78515	single-stranded nu
601	6	1.8	332	2	AT1319	674	6	1.8	363	2	AC0244	conserved hypotet
602	6	1.8	332	2	AT1691	675	6	1.8	364	2	F96603	hypothetical prote
603	6	1.8	332	2	T33503	676	6	1.8	365	2	J00879	N55 protein - hepa
604	6	1.8	332	2	H82064	677	6	1.8	365	2	S42471	hnRNP protein B2 -
605	6	1.8	333	2	B86567	678	6	1.8	365	2	AT2940	acetyltransferase
606	6	1.8	333	2	G72058	679	6	1.8	366	2	E87457	conserved hypotet
607	6	1.8	334	2	D83750	680	6	1.8	366	2	A55525	carboxy-cis, cis-mu
608	6	1.8	334	2	S44299	681	6	1.8	366	2	T31933	hypothetical prote
609	6	1.8	334	2	T27658	682	6	1.8	367	2	B72644	probable transket
610	6	1.8	335	2	T25498	683	6	1.8	368	2	S71190	heat shock protein
611	6	1.8	336	2	B49683	684	6	1.8	368	2	AH2694	MFS permease [impo
612	6	1.8	337	2	E83961	685	6	1.8	370	2	A60089	transforming prote
613	6	1.8	337	2	B88957	686	6	1.8	370	2	S29139	aggrecan - pig (fr

687	6	1.8	370	2	G90248	conserved hypochet	760	6	1.8	402	2	A83398	probable MFS trans
688	6	1.8	371	2	A90044	hypothetical prote	761	6	1.8	404	2	F71718	alanine racemase (
689	6	1.8	371	2	A53908	brevican precursor	762	6	1.8	404	2	G75152	hypothetical prote
690	6	1.8	371	2	JC5498	G protein-coupled	763	6	1.8	404	2	H71193	hypothetical prote
691	6	1.8	372	1	G84358	N2,N2-dimethylguan	764	6	1.8	405	2	T10260	patacin-like prote
692	6	1.8	372	1	QOBE88	glycoprotein I pre	765	6	1.8	405	2	T16002	hypothetical prote
693	6	1.8	372	2	P00138	dhak-type molecula	766	6	1.8	405	2	T02649	hypothetical prote
694	6	1.8	372	2	B84856	hypothetical prote	767	6	1.8	406	2	T42926	hypothetical prote
695	6	1.8	372	2	A98342	rasp protein (AF14	768	6	1.8	407	2	T34535	hypothetical prote
696	6	1.8	374	2	A40756	hypothetical prote	769	6	1.8	407	2	T08732	hypothetical prote
697	6	1.8	375	2	AH0209	probable sugar ABC	770	6	1.8	407	2	AC2721	MFS permease [lipo
698	6	1.8	375	2	A12041	hypothetical prote	771	6	1.8	407	2	G97502	probable mfs trans
699	6	1.8	376	2	AG1410	cell division prot	772	6	1.8	408	2	D83191	conserved hypochet
700	6	1.8	376	2	G83280	hypothetical prote	773	6	1.8	409	1	JS0759	membrane dipeptid
701	6	1.8	376	2	JC6535	multidrugitcin-cha	774	6	1.8	409	2	S68247	adenosine A2a rece
702	6	1.8	376	2	B71981	DNA transformation	775	6	1.8	409	2	I48095	A2 adenosine recep
703	6	1.8	377	2	S21302	succinate dehydrog	776	6	1.8	409	2	F64396	hypothetical prote
704	6	1.8	377	2	S63671	26S proteinase cha	777	6	1.8	410	2	A71481	probable poly A po
705	6	1.8	377	2	F71520	hypothetical prote	778	6	1.8	411	2	E96665	protein P22C12.16
706	6	1.8	377	2	C69758	amino acid transpo	779	6	1.8	412	2	A48978	adenosine receptor
707	6	1.8	377	2	T24186	hypothetical prote	780	6	1.8	412	2	D30341	G protein-coupled
708	6	1.8	378	2	I46268	brevican precursor	781	6	1.8	412	2	S72579	hypothetical prote
709	6	1.8	378	2	H71307	probable spore coa	782	6	1.8	413	2	C89780	probable permease
710	6	1.8	378	2	A99263	transpore membrane	783	6	1.8	413	2	AC1045	conserved hypochet
711	6	1.8	380	2	H70144	ATP-binding protei	784	6	1.8	413	2	AF2728	hypothetical prote
712	6	1.8	384	2	T33762	hypothetical prote	785	6	1.8	413	2	G97509	hypothetical prote
713	6	1.8	384	2	I40867	hypothetical prote	786	6	1.8	414	2	A24872	hypothetical prote
714	6	1.8	384	2	I49528	hypothetical prote	787	6	1.8	414	2	T03996	hypothetical prote
715	6	1.8	385	2	D95350	probable transmemb	788	6	1.8	415	2	T29296	hypothetical prote
716	6	1.8	385	2	T35516	hypothetical prote	789	6	1.8	415	2	S12357	interleukin-5 rece
717	6	1.8	386	2	A42688	serotonin receptor	790	6	1.8	415	2	G64510	hypothetical prote
718	6	1.8	386	2	S18637	serotonin receptor	791	6	1.8	415	2	T09213	mRNA-binding prote
719	6	1.8	386	2	H84522	hypothetical prote	792	6	1.8	416	2	H69436	5-enolpyruvylshiki
720	6	1.8	386	2	T18890	hypothetical prote	793	6	1.8	416	2	T14554	calliculin - bee
721	6	1.8	387	2	F82998	probable iron-cont	794	6	1.8	416	2	T01159	hypothetical prote
722	6	1.8	387	2	T43140	probable heavy met	795	6	1.8	416	2	AF1127	rod shape-determin
723	6	1.8	387	2	T38252	probable zinc/cadm	796	6	1.8	417	1	MMBRHA	53K immediate-earl
724	6	1.8	387	2	A49498	dyetrophin-associ	797	6	1.8	419	2	G75252	probable brbK prot
725	6	1.8	387	2	A54746	adhalin precursor	798	6	1.8	419	2	E70489	processing protein
726	6	1.8	387	2	I48201	adhalin - golden h	799	6	1.8	420	2	H84890	hypothetical prote
727	6	1.8	387	2	JC5556	adhalin - mouse	800	6	1.8	420	2	F83494	hypothetical prote
728	6	1.8	389	2	S68422	serotonin receptor	801	6	1.8	421	2	F83400	hypothetical prote
729	6	1.8	390	1	QOBE77	glycoprotein I pre	802	6	1.8	422	1	A60503	sperm-binding glyc
730	6	1.8	390	2	UN0268	serotonin receptor	803	6	1.8	422	1	A69853	hexuronate transpo
731	6	1.8	390	2	S58126	serotonin receptor	804	6	1.8	422	1	AD2941	hypothetical prote
732	6	1.8	391	2	AH0052	Hm17 protein [lipo	805	6	1.8	424	1	S12793	modulation protein
733	6	1.8	391	2	S18666	KTN17 protein - mo	806	6	1.8	424	2	D71192	hypothetical prote
734	6	1.8	392	2	H84232	anion permease [im	807	6	1.8	424	2	E86367	protein P26R24.22
735	6	1.8	392	2	H97335	Na+ ABC transpote	808	6	1.8	424	2	G75579	branched-chain ami
736	6	1.8	393	2	UQ0461	genome polypotein	809	6	1.8	424	2	S43560	coiled coil protei
737	6	1.8	395	2	S70637	tubulin beta chain	810	6	1.8	425	2	T39967	probable proline-t
738	6	1.8	395	2	D69779	antibiotic resista	811	6	1.8	425	2	A70394	hypothetical prote
739	6	1.8	396	1	G64313	protein-export mem	812	6	1.8	425	2	D75164	hypothetical prote
740	6	1.8	396	2	JC2313	probable nitrite h	813	6	1.8	426	1	SAVLC	large surface anti
741	6	1.8	396	2	H86675	hypothetical prote	814	6	1.8	427	1	F97476	probable integral
742	6	1.8	396	2	H84383	porphobilinogen de	815	6	1.8	428	1	SAVUS	large surface anti
743	6	1.8	396	2	B82320	membrane-bound lyl	816	6	1.8	428	2	A83005	conserved hypochet
744	6	1.8	397	2	C81851	acetylornithine tr	817	6	1.8	428	2	AF1984	hypothetical prote
745	6	1.8	398	2	H81090	acetylornithine am	818	6	1.8	430	2	G75408	probable transpor
746	6	1.8	398	2	S16721	coenzyme F420 hydr	819	6	1.8	431	1	SAVL59	large surface anti
747	6	1.8	398	2	F70695	hypothetical prote	820	6	1.8	431	1	SAVL7	large surface anti
748	6	1.8	398	2	T02161	hypothetical prote	821	6	1.8	431	1	SAVL2	large surface anti
749	6	1.8	398	2	H75043	mg2+ transport pro	822	6	1.8	431	1	SAVLW8	large surface anti
750	6	1.8	398	2	AF0049	probable membrane	823	6	1.8	431	2	T50573	probable O-antigen
751	6	1.8	399	2	F83882	L-arabinose utiliz	824	6	1.8	431	2	B97277	probable integral
752	6	1.8	399	2	D84062	S-adenosylmethioni	825	6	1.8	431	2	B81124	conserved hypochet
753	6	1.8	399	2	T21649	hypothetical prote	826	6	1.8	431	2	E81900	hypothetical prote
754	6	1.8	400	2	B64071	lysosine-specific	827	6	1.8	432	2	G71683	NADH2 dehydrogen
755	6	1.8	400	2	AG7535	ispd/ispf bifuncti	828	6	1.8	432	2	B70110	hypothetical prote
756	6	1.8	400	2	AC2754	ISPD/ISPF bifuncti	829	6	1.8	432	2	T35263	probable carboxype
757	6	1.8	400	2	T35334	probable membrane	830	6	1.8	432	2	AI0351	peptidase B [limpor
758	6	1.8	401	2	AI2255	two-component sens	831	6	1.8	433	2	AI0536	probable membrane
759	6	1.8	401	2	B69501	sugar transporter	832	6	1.8	433	2	H97846	hypothetical prote

833	6	1.8	434	2	D81743	906	6	1.8	469	2	G69267	conserved hypotet
834	6	1.8	434	2	AG2349	907	6	1.8	470	1	A25685	hypothetical prote
835	6	1.8	435	2	G75363	908	6	1.8	470	2	T39796	negative sexual co
836	6	1.8	437	2	G34468	909	6	1.8	471	2	T43803	cytochrome-c oxida
837	6	1.8	437	2	G72570	910	6	1.8	471	2	B64099	undecaprenyl-phosp
838	6	1.8	437	2	H70918	911	6	1.8	473	1	F2LV44	photosystem II chl
839	6	1.8	438	2	T31889	912	6	1.8	473	2	G72205	hypothetical prote
840	6	1.8	440	2	G97620	913	6	1.8	473	2	B72457	probable phenylala
841	6	1.8	441	2	D95390	914	6	1.8	473	2	T04225	hypothetical prote
842	6	1.8	442	2	C45561	915	6	1.8	474	2	B83587	two-component sens
843	6	1.8	442	2	D97382	916	6	1.8	474	2	B83719	multidrug resistanc
844	6	1.8	442	2	AC2600	917	6	1.8	476	2	JC4646	bone morphogenetic
845	6	1.8	443	2	H83589	918	6	1.8	476	2	H95313	NeaA host specific
846	6	1.8	443	2	G90388	919	6	1.8	476	2	S71360	neoa protein - Rhi
847	6	1.8	444	1	F64138	920	6	1.8	476	2	T29054	probable transmemb
848	6	1.8	444	2	B82283	921	6	1.8	476	2	T23728	hypothetical prote
849	6	1.8	444	2	F98341	922	6	1.8	477	2	T47819	hypothetical prote
850	6	1.8	445	2	T31898	923	6	1.8	478	2	T38014	hypothetical zinc
851	6	1.8	446	2	T10103	924	6	1.8	480	2	D45561	merozoite surface
852	6	1.8	446	2	D64376	925	6	1.8	480	2	T36822	probable transcrip
853	6	1.8	446	2	T49149	926	6	1.8	481	2	H69275	signal-transducing
854	6	1.8	447	1	AJBCRS	927	6	1.8	482	1	JN0506	argininosuccinate
855	6	1.8	447	2	B81003	928	6	1.8	482	2	H82352	probable PTS syte
856	6	1.8	447	2	F82025	929	6	1.8	482	2	G75483	probable leucyl am
857	6	1.8	447	2	G85980	930	6	1.8	482	2	T49079	serine-type carbox
858	6	1.8	447	2	D91135	931	6	1.8	482	2	F71969	hypothetical prote
859	6	1.8	449	1	B43698	932	6	1.8	483	2	G75392	glycosyl hydrolase
860	6	1.8	449	2	AB0889	933	6	1.8	483	2	T10552	hypothetical prote
861	6	1.8	449	2	D85962	934	6	1.8	485	2	A11696	weakly probable su
862	6	1.8	449	2	H65089	935	6	1.8	486	2	H82377	ABC transporter. A
863	6	1.8	449	2	AS2597	936	6	1.8	487	1	AJSMRC	argininosuccinate
864	6	1.8	449	2	F97379	937	6	1.8	487	2	AF2652	MTS permease (limp
865	6	1.8	449	2	E71172	938	6	1.8	488	2	S27652	probable aldehyde
866	6	1.8	450	2	AC1791	939	6	1.8	488	2	B69415	group II decarboxy
867	6	1.8	450	2	AD1415	940	6	1.8	488	2	D64108	glucuronate transpor
868	6	1.8	451	2	G73433	941	6	1.8	489	2	D27657	hypothetical prote
869	6	1.8	451	2	T06090	942	6	1.8	490	2	I52410	cytochrome P450 1I
870	6	1.8	452	2	AB3222	943	6	1.8	490	2	A36122	cytochrome P450 2C
871	6	1.8	453	2	AG0326	944	6	1.8	490	2	T49016	hypothetical prote
872	6	1.8	453	2	S31313	945	6	1.8	490	2	T28382	ORF MSV221 hypoco
873	6	1.8	453	2	B88040	946	6	1.8	492	2	S71245	glucose-6-phosphat
874	6	1.8	453	2	T10239	947	6	1.8	492	2	AE3033	L-xyulose kinase
875	6	1.8	453	2	AD1556	948	6	1.8	492	2	D75619	codytic acid synth
876	6	1.8	453	2	AF1198	949	6	1.8	492	2	T44202	hypothetical prote
877	6	1.8	454	2	JC7231	950	6	1.8	492	2	T44015	hypothetical prote
878	6	1.8	454	2	F90602	951	6	1.8	493	2	S36931	chitinase (BC 3.2.
879	6	1.8	454	2	A84148	952	6	1.8	495	2	T20038	hypothetical prote
880	6	1.8	455	2	AE0191	953	6	1.8	497	2	AD0152	probable bacteriop
881	6	1.8	455	2	A70461	954	6	1.8	498	2	B69276	hypothetical prote
882	6	1.8	456	2	C86624	955	6	1.8	501	2	T44298	sodium/proline sym
883	6	1.8	456	2	H72000	956	6	1.8	502	2	AB3203	Tn3 family transpo
884	6	1.8	458	2	B90623	957	6	1.8	503	2	T51782	hypothetical prote
885	6	1.8	458	2	S75114	958	6	1.8	503	2	A49429	interleukin-1 beta
886	6	1.8	459	2	T37704	959	6	1.8	504	2	JC5287	SHP substrate-1 pr
887	6	1.8	459	2	T43538	960	6	1.8	505	2	AB2843	hydroxylase [import
888	6	1.8	459	2	B69580	961	6	1.8	505	2	AE3168	hypothetical prote
889	6	1.8	460	2	JL0145	962	6	1.8	507	2	G72418	sugar ABC transpor
890	6	1.8	460	2	A84281	963	6	1.8	508	1	S62599	UTP-glucose-1-phos
891	6	1.8	461	1	G64537	964	6	1.8	508	1	UX0277	UTP-glucose-1-phos
892	6	1.8	461	2	I64080	965	6	1.8	508	2	B81083	cardiolipin synthe
893	6	1.8	462	1	A37986	966	6	1.8	509	2	JC5288	SHP substrate-1 pr
894	6	1.8	462	2	T26401	967	6	1.8	509	2	A96749	unknown protein T1
895	6	1.8	462	2	A86459	968	6	1.8	510	2	A71816	hypothetical prote
896	6	1.8	462	2	AH1017	969	6	1.8	510	2	A64706	lipase-like protei
897	6	1.8	463	2	JC7372	970	6	1.8	511	2	T22835	hypothetical prote
898	6	1.8	464	2	H83006	971	6	1.8	511	2	G98252	cryptic D-xyulose
899	6	1.8	466	1	KFNU7	972	6	1.8	511	2	A40110	nicotinic acetylch
900	6	1.8	467	2	T45475	973	6	1.8	513	2	T01413	probable histone d
901	6	1.8	468	2	C90599	974	6	1.8	513	2	JC5289	SHP substrate-1 pr
902	6	1.8	468	2	A13241	975	6	1.8	513	2	T31596	hypothetical prote
903	6	1.8	468	2	T41294	976	6	1.8	513	2	A82432	sodium/solute sym
904	6	1.8	469	2	AC0902	977	6	1.8	513	2	B71683	NADH2 dehydrogenas
905	6	1.8	469	2	S73404	978	6	1.8	514	2	S52771	beta-glucosidase (

979	6	1.8	514	2	TJ5371	1052	6	1.8	559	2	T15282	hypothetical prote
980	6	1.8	514	2	B86164	1053	6	1.8	560	2	T02404	probable beta-gluc
981	6	1.8	515	2	P96700	1054	6	1.8	560	2	S46724	hexose transport p
982	6	1.8	516	2	S06443	1055	6	1.8	561	2	T31965	hypothetical prote
983	6	1.8	517	2	AF1976	1056	6	1.8	563	2	T51348	RNA helicase RH25
984	6	1.8	518	1	B46619	1057	6	1.8	566	2	S42257	lamin - Caenorhad
985	6	1.8	518	1	S43845	1058	6	1.8	566	2	T20380	hypothetical prote
986	6	1.8	519	1	T51367	1059	6	1.8	566	2	A83081	type 4 fibribrial p
987	6	1.8	520	2	H84663	1060	6	1.8	566	2	A35384	pl1B protein - pse
988	6	1.8	521	2	B64862	1061	6	1.8	567	2	A48895	myasthenic syndrom
989	6	1.8	521	2	B71717	1062	6	1.8	567	2	C69611	ABC transporter re
990	6	1.8	522	2	B82034	1063	6	1.8	568	2	S70873	tapB protein - Aer
991	6	1.8	522	2	T26163	1064	6	1.8	568	2	F71614	chromatinic RING f
992	6	1.8	524	2	S44982	1065	6	1.8	571	2	G89123	protein K07C11.4 l
993	6	1.8	525	2	B81859	1066	6	1.8	575	2	B84798	probable peptide/a
994	6	1.8	525	2	T25900	1067	6	1.8	576	1	ACFP42	nicotinic acetylch
995	6	1.8	526	2	T13687	1068	6	1.8	577	2	A72283	maltose ABC transp
996	6	1.8	527	1	OBXY1	1069	6	1.8	578	2	S47961	glucosyltransferas
997	6	1.8	527	1	A31908	1070	6	1.8	578	2	AG0119	probable OmpA-fam
998	6	1.8	527	2	S05290	1071	6	1.8	578	2	AC0179	probable exported
999	6	1.8	527	2	I84483	1072	6	1.8	579	2	A97099	ABC-type multidrug
1000	6	1.8	527	2	I49133	1073	6	1.8	579	2	A27650	phosphate response
1001	6	1.8	528	2	B97474	1074	6	1.8	580	2	B82450	PTS system, fructo
1002	6	1.8	528	2	T933919	1075	6	1.8	581	2	H95214	ABC transporter. A
1003	6	1.8	528	2	A10359	1076	6	1.8	583	2	C90327	n-methylhydantoina
1004	6	1.8	530	1	B48529	1077	6	1.8	583	2	T04531	nine-cis-epoxycaro
1005	6	1.8	530	1	B89044	1078	6	1.8	585	2	H83729	adenine deaminase
1006	6	1.8	531	2	D86862	1079	6	1.8	585	2	A27763	succinate dehydrog
1007	6	1.8	532	2	A75368	1080	6	1.8	586	2	T20816	hypothetical prote
1008	6	1.8	532	2	T49824	1081	6	1.8	587	2	B85429	hypothetical prote
1009	6	1.8	533	2	A12694	1082	6	1.8	587	2	JH0464	DM-GRASP precursor
1010	6	1.8	533	2	F75124	1083	6	1.8	587	2	A84078	two-component sens
1011	6	1.8	534	2	T19951	1084	6	1.8	588	2	H89885	succinate dehydrog
1012	6	1.8	535	2	B95952	1085	6	1.8	588	2	JH0506	adhesion molecule
1013	6	1.8	536	1	POWMD	1086	6	1.8	588	2	A45254	surface glycoprote
1014	6	1.8	537	2	T19764	1087	6	1.8	590	2	A47194	taurine and beta-a
1015	6	1.8	537	2	G85021	1088	6	1.8	590	2	A26638	homeotic protein D
1016	6	1.8	537	2	A82454	1089	6	1.8	591	2	A69291	transmembrane olig
1017	6	1.8	538	2	S60645	1090	6	1.8	591	2	B87361	flagellar hook pro
1018	6	1.8	538	2	G83653	1091	6	1.8	594	2	G98078	hypothetical prote
1019	6	1.8	538	2	T51560	1092	6	1.8	595	2	T05087	hypothetical prote
1020	6	1.8	540	2	H88086	1093	6	1.8	597	2	A32440	RNA-directed RNA p
1021	6	1.8	540	2	G95222	1094	6	1.8	598	2	T2610	hypothetical prote
1022	6	1.8	542	2	JN0661	1095	6	1.8	599	2	F87682	trkA family protei
1023	6	1.8	542	2	S32106	1096	6	1.8	599	2	T42328	hypothetical prote
1024	6	1.8	542	2	B86674	1097	6	1.8	601	2	S47896	probable molybdopt
1025	6	1.8	543	2	F72071	1098	6	1.8	601	2	S56144	SH3 domain binding
1026	6	1.8	543	2	C86551	1099	6	1.8	603	2	A70770	hypothetical glyci
1027	6	1.8	543	2	T20964	1100	6	1.8	603	2	A84451	probable AAA-type
1028	6	1.8	543	2	T32973	1101	6	1.8	603	2	H72276	phosphoribosylform
1029	6	1.8	544	2	C86405	1102	6	1.8	603	2	T00379	KIRA0640 protein -
1030	6	1.8	545	2	T05510	1103	6	1.8	605	1	A48665	methylinamonyl-CoA
1031	6	1.8	545	2	T47952	1104	6	1.8	605	1	T15291	sphingomyelin phos
1032	6	1.8	545	2	T02005	1105	6	1.8	609	2	T28736	hypothetical prote
1033	6	1.8	545	2	D69679	1106	6	1.8	613	2	T51938	inositol-1',4',5-eri
1034	6	1.8	546	2	P96562	1107	6	1.8	613	2	T16885	hypothetical prote
1035	6	1.8	546	2	F87343	1108	6	1.8	613	2	F89801	conserved hypothet
1036	6	1.8	546	2	F84900	1109	6	1.8	617	2	T52499	ferredoxin oxidore
1037	6	1.8	548	2	JC4073	1110	6	1.8	618	2	H70552	probable PPR prote
1038	6	1.8	548	2	T04058	1111	6	1.8	619	2	S29839	taurine transport
1039	6	1.8	550	2	T10564	1112	6	1.8	620	2	F83976	cytochrome-c oxida
1040	6	1.8	551	2	A80031	1113	6	1.8	620	2	G01426	taurine transporte
1041	6	1.8	551	2	JC7562	1114	6	1.8	620	2	S46487	taurine transporte
1042	6	1.8	551	2	S51941	1115	6	1.8	621	2	T45936	transporter-like p
1043	6	1.8	552	2	B82633	1116	6	1.8	621	1	D69295	endopeptidase Ia b
1044	6	1.8	552	2	T04653	1117	6	1.8	621	2	I57939	taurine transporte
1045	6	1.8	553	2	F86397	1118	6	1.8	622	2	B69609	cytochrome-c oxida
1046	6	1.8	556	2	JC5636	1119	6	1.8	622	2	E81981	probable lipopolys
1047	6	1.8	557	1	S23435	1120	6	1.8	622	2	AB1090	bacteriophage mino
1048	6	1.8	557	2	S43231	1121	6	1.8	622	2	A11453	bacteriophage mino
1049	6	1.8	557	2	T07116	1122	6	1.8	623	2	T48859	disease resistance
1050	6	1.8	559	2	AB1153	1123	6	1.8	623	2	T06674	hypothetical prote
1051	6	1.8	559	2	AC1512	1124	6	1.8	623	2	B81037	lipopolysaccharide

1125	6	1.8	624	2	T49366	myocyte-specific e
1126	6	1.8	625	2	D45335	cytochrome-c oxida
1127	6	1.8	626	2	C72035	succinate dehydrog
1128	6	1.8	626	2	C86589	succinate dehydrog
1129	6	1.8	627	2	T11125	NADH2 dehydrogenas
1130	6	1.8	630	2	S49959	probable membrane
1131	6	1.8	632	2	T45471	dnak-c-type molecula
1132	6	1.8	634	2	C81652	ATP-dependent helic
1133	6	1.8	634	2	D71493	probable DNA helic
1134	6	1.8	635	2	G86589	hypothetical prote
1135	6	1.8	635	2	H81793	hypothetical prote
1136	6	1.8	635	2	G72035	regulatory protein
1137	6	1.8	636	2	A48872	dnak-c-type molecula
1138	6	1.8	636	2	S63131	probable membrane
1139	6	1.8	637	2	B69627	cell-division prot
1140	6	1.8	639	2	T50148	probable ser/thr p
1141	6	1.8	640	1	HKHW7A	dnak-c-type molecula
1142	6	1.8	640	2	G37394	dnak-c-type molecula
1143	6	1.8	640	2	T21394	hypothetical prote
1144	6	1.8	640	2	A87606	excinuclease ABC,
1145	6	1.8	641	2	S63645	NADH2 dehydrogenas
1146	6	1.8	641	2	T07668	starch synthase (B
1147	6	1.8	642	2	T28866	hypothetical prote
1148	6	1.8	643	2	G64412	hypothetical prote
1149	6	1.8	643	2	H83635	conserved hypotnet
1150	6	1.8	643	2	B75055	hypothetical prote
1151	6	1.8	644	1	H69204	endopeptidase Ia h
1152	6	1.8	644	2	S67431	dnak-c-type molecula
1153	6	1.8	645	2	T05251	probable disease r
1154	6	1.8	646	2	T51937	probable inositol-1-
1155	6	1.8	648	2	A54892	Na+-dependent nucl
1156	6	1.8	649	2	S42488	dnak-c-type molecula
1157	6	1.8	653	2	B82872	transketolase I UU
1158	6	1.8	653	2	B87698	transketolase I [I
1159	6	1.8	653	2	S52727	dnak-c-type molecula
1160	6	1.8	653	2	S11448	hypothetical trans
1161	6	1.8	653	2	AG1190	hypothetical prote
1162	6	1.8	654	2	S27004	dnak-c-type molecula
1163	6	1.8	654	2	AH2445	hypothetical prote
1164	6	1.8	654	2	T32623	hypothetical prote
1165	6	1.8	655	2	A46270	Na and Cl dependen
1166	6	1.8	655	2	G75582	cell division prot
1167	6	1.8	655	2	UC7850	disintegrin and me
1168	6	1.8	656	2	C71361	probable long-chain
1169	6	1.8	657	2	S77543	short-chain alchoh
1170	6	1.8	660	2	S71949	metalloproteinas
1171	6	1.8	661	2	A25398	dnak-c-type molecula
1172	6	1.8	661	2	S50734	WH3 protein - yea
1173	6	1.8	662	2	T48128	probable reverse t
1174	6	1.8	664	2	B86714	hypothetical prote
1175	6	1.8	664	2	C71106	hypothetical prote
1176	6	1.8	665	2	AF0815	transketolase (BC
1177	6	1.8	667	1	A48660	transketolase (BC
1178	6	1.8	667	1	G91044	transketolase 2 is
1179	6	1.8	667	2	B85889	transketolase 2 is
1180	6	1.8	669	2	I38029	matrix metalloprot
1181	6	1.8	669	2	S76474	hypothetical prote
1182	6	1.8	672	2	AC0422	hypothetical prote
1183	6	1.8	674	2	S46092	probable membrane
1184	6	1.8	676	2	D95249	transcription regu
1185	6	1.8	676	2	A98114	conserved hypotnet
1186	6	1.8	677	2	S65573	phosphate-specific
1187	6	1.8	677	2	UC7303	pectate lyase (BC
1188	6	1.8	682	2	UC7385	multi-specific orga
1189	6	1.8	682	2	UC0420	beta-1,3-glucanas
1190	6	1.8	683	2	T12127	NADH2 dehydrogenas
1191	6	1.8	684	2	F70810	hypothetical prote
1192	6	1.8	686	2	B96526	unknown protein [i
1193	6	1.8	687	2	T02459	hypothetical prote
1194	6	1.8	687	2	S43587	F2F3.2 protein (c
1195	6	1.8	687	2	B84945	glycine-tRNA ligas
1196	6	1.8	690	2	A71520	hypothetical prote
1197	6	1.8	692	2	T12587	NADH2 dehydrogenas
1198	6	1.8	694	2	A82697	penicillin binding
1199	6	1.8	694	2	H95012	hypothetical prote
1200	6	1.8	696	2	B81677	conserved hypotnet
1201	6	1.8	698	2	AB3576	fusaric acid resis
1202	6	1.8	702	2	T13708	NADH2 dehydrogenas
1203	6	1.8	702	2	C97984	hypothetical prote
1204	6	1.8	703	1	C48562	coat protein - San
1205	6	1.8	704	2	T50303	hypothetical prote
1206	6	1.8	704	2	T31227	tran protein homol
1207	6	1.8	705	2	B75371	ABC transporter, A
1208	6	1.8	707	1	COORJ5	phosphotransferase
1209	6	1.8	709	2	G97337	topoisomerase B [i
1210	6	1.8	710	1	S70965	serine/threonine-s
1211	6	1.8	710	2	T39820	hypothetical prote
1212	6	1.8	712	2	T47243	amino-acid N-acetyl
1213	6	1.8	712	2	A48156	translacion regula
1214	6	1.8	713	2	B38992	cadherin 13 precu
1215	6	1.8	715	2	S73821	DNA helicase II -
1216	6	1.8	719	2	T47782	hypothetical prote
1217	6	1.8	720	2	T02734	hypothetical prote
1218	6	1.8	721	2	B83820	hypothetical prote
1219	6	1.8	723	2	JC7795	epithelial calcium
1220	6	1.8	724	2	H86427	unknown protein [i
1221	6	1.8	725	2	JC7531	calcium transport
1222	6	1.8	727	2	F82634	tail-specific prot
1223	6	1.8	727	2	JC7796	epithelial calcium
1224	6	1.8	728	1	T50719	C-Delta-1 - chicke
1225	6	1.8	735	1	PC4225	replication licens
1226	6	1.8	737	2	S47857	basic protein, cyt
1227	6	1.8	739	2	G96740	hypothetical prote
1228	6	1.8	740	1	DENTM5	NADH2 dehydrogenas
1229	6	1.8	740	2	S61568	probable membrane
1230	6	1.8	742	2	AH2166	hypothetical prote
1231	6	1.8	746	2	A84800	hypothetical prote
1232	6	1.8	751	2	S65469	DNA topoisomerase
1233	6	1.8	753	2	T28787	hypothetical prote
1234	6	1.8	753	2	A86756	probable p12 prote
1235	6	1.8	754	2	A85043	probable IRR recep
1236	6	1.8	755	2	T20950	hypothetical prote
1237	6	1.8	759	2	T16368	hypothetical prote
1238	6	1.8	761	2	B82167	5-methyltetrahydro
1239	6	1.8	761	2	AB1848	hypothetical prote
1240	6	1.8	761	2	H65083	glycolate oxidase
1241	6	1.8	762	2	G96999	hydrogenase matura
1242	6	1.8	764	2	A49448	irregular chiasm C
1243	6	1.8	766	2	A40258	RAS GTPase-activat
1244	6	1.8	767	1	COZPCD	cdc10 start contro
1245	6	1.8	770	2	S77523	hypothetical prote
1246	6	1.8	772	2	JC4636	transcription elon
1247	6	1.8	774	2	T03919	hypothetical prote
1248	6	1.8	775	2	S69515	replication initia
1249	6	1.8	777	2	T00208	transposase-like p
1250	6	1.8	777	2	AP2410	serine/threonine k
1251	6	1.8	779	1	S61571	suppressor protein
1252	6	1.8	779	2	E97778	endopeptidase Ia (
1253	6	1.8	782	2	A61625	tenascin-like prot
1254	6	1.8	782	2	JC5467	cellulase (BC 3.2.
1255	6	1.8	783	1	A71704	endopeptidase Ia (
1256	6	1.8	786	2	G85073	probable myosin-li
1257	6	1.8	786	2	T18469	hypothetical prote
1258	6	1.8	787	2	H70374	NADH2 dehydrogenas
1259	6	1.8	787	2	T41974	replication origin
1260	6	1.8	788	2	S48191	probable ubiquinol
1261	6	1.8	788	2	AE3153	NADP-dependent ald
1262	6	1.8	790	2	S71278	DNA ligase (ATP) (
1263	6	1.8	795	2	T34673	probable SecDF pro
1264	6	1.8	797	2	T21487	hypothetical prote
1265	6	1.8	798	2	D86459	probable disease r
1266	6	1.8	798	2	F98134	hypothetical prote
1267	6	1.8	800	2	A29003	cellulase (BC 3.2.
1268	6	1.8	801	1	MXMR5	RNA 5 protein - ri
1269	6	1.8	801	2	S50660	hypothetical prote
1270	6	1.8	802	2	T05596	probable potassium

1271	6	1.8	804	2	G64780	1344	6	1.8	949	2	E75352	glycine cleavage s
1272	6	1.8	804	2	A85549	1345	6	1.8	949	2	T03030	hypothetical prote
1273	6	1.8	804	2	G90638	1346	6	1.8	949	2	T44577	hypothetical prote
1274	6	1.8	807	2	T19836	1347	6	1.8	950	2	T25088	hypothetical prote
1275	6	1.8	809	2	T16645	1348	6	1.8	954	2	S46105	glucan 1,4-alpha-g
1276	6	1.8	812	2	T19446	1349	6	1.8	958	2	S47179	hypothetical prote
1277	6	1.8	822	2	TJ0611	1350	6	1.8	960	1	A39651	disc-large tumor
1278	6	1.8	823	2	AP3351	1351	6	1.8	961	2	T03467	NADH dehydrogenase
1279	6	1.8	824	2	UC7352	1352	6	1.8	962	2	AG2444	hypothetical prote
1280	6	1.8	827	2	S75622	1353	6	1.8	970	2	B84846	probable zinc prot
1281	6	1.8	828	2	S34695	1354	6	1.8	970	2	A13605	potassium efflux s
1282	6	1.8	834	2	S66258	1355	6	1.8	970	2	S63059	hypothetical prote
1283	6	1.8	835	2	S54152	1356	6	1.8	971	2	S54595	probable membrane
1284	6	1.8	843	2	H82352	1357	6	1.8	973	2	B86547	polymorphic outer
1285	6	1.8	845	2	T52518	1358	6	1.8	973	2	F72076	polymorphic outer
1286	6	1.8	848	2	C70203	1359	6	1.8	973	2	T41272	hypothetical prote
1287	6	1.8	849	2	T38728	1360	6	1.8	973	2	T21069	hypothetical prote
1288	6	1.8	850	2	G70332	1361	6	1.8	978	1	RGBY13	regulatory protein
1289	6	1.8	852	2	S25359	1362	6	1.8	985	2	DJBE11	DNA-directed DNA p
1290	6	1.8	855	2	A34810	1363	6	1.8	985	2	T51672	receptor tyrosine
1291	6	1.8	855	2	T19405	1364	6	1.8	995	2	C81593	polymorphic membra
1292	6	1.8	856	2	S46750	1365	6	1.8	1003	2	A39521	glycine dehydrogen
1293	6	1.8	858	2	T47223	1366	6	1.8	1003	2	D71490	probable exodeoxyr
1294	6	1.8	862	2	A05028	1367	6	1.8	1004	2	D86381	hypothetical prote
1295	6	1.8	863	1	S64720	1368	6	1.8	1012	2	S62435	probable glycine d
1296	6	1.8	863	2	D88216	1369	6	1.8	1017	2	T40253	hypothetical prote
1297	6	1.8	864	2	A43954	1370	6	1.8	1018	2	T22318	hypothetical prote
1298	6	1.8	868	2	T02635	1371	6	1.8	1018	2	A89696	protein T21H8.1 [i
1299	6	1.8	869	2	S35792	1372	6	1.8	1026	2	D96786	protein P10A5.15 [
1300	6	1.8	870	2	T39731	1373	6	1.8	1037	2	T31097	chitin synthase (E
1301	6	1.8	874	2	H83533	1374	6	1.8	1041	2	T31097	hypothetical prote
1302	6	1.8	874	2	J00883	1375	6	1.8	1042	2	T16169	hypothetical prote
1303	6	1.8	874	2	E75278	1376	6	1.8	1045	2	F90365	hypothetical prote
1304	6	1.8	880	2	AD1953	1377	6	1.8	1049	2	A27079	fibronectin recept
1305	6	1.8	881	2	T49279	1378	6	1.8	1054	2	T01556	Ca2+-transporting
1306	6	1.8	881	2	T31739	1379	6	1.8	1056	1	GNTJG3	HIV-1 retropepsin
1307	6	1.8	883	2	S57653	1380	6	1.8	1061	2	T18085	DNA topoisomerase
1308	6	1.8	883	2	S49126	1381	6	1.8	1068	2	A40265	retinoblastoma-a88
1309	6	1.8	883	2	T37208	1382	6	1.8	1077	2	T38900	probable alpha-man
1310	6	1.8	887	2	B84954	1383	6	1.8	1078	2	T18352	protein P120 - Myc
1311	6	1.8	887	2	G88484	1384	6	1.8	1085	2	F96712	hypothetical prote
1312	6	1.8	888	2	A54280	1385	6	1.8	1085	2	JC2227	probable helicase
1313	6	1.8	889	2	TC7083	1386	6	1.8	1088	2	T30330	gelsofin-related p
1314	6	1.8	890	2	T21000	1387	6	1.8	1088	2	E86312	FLA6.9 protein -
1315	6	1.8	891	2	T40137	1388	6	1.8	1089	2	S48244	NMD2 protein - yea
1316	6	1.8	898	2	S65474	1389	6	1.8	1089	2	T21582	hypothetical prote
1317	6	1.8	899	2	T38153	1390	6	1.8	1099	2	A55405	adenylate cyclase
1318	6	1.8	899	2	S49634	1391	6	1.8	1099	2	A59300	myosin-II - mouse
1319	6	1.8	902	1	S54495	1392	6	1.8	1100	1	DBBYD1	RAD1 protein - yea
1320	6	1.8	902	2	D83467	1393	6	1.8	1113	2	D86142	hypothetical prote
1321	6	1.8	903	2	T00358	1394	6	1.8	1114	2	T28139	RNA-directed RNA p
1322	6	1.8	906	2	AD3267	1395	6	1.8	1123	2	T30819	PK4 protein kinase
1323	6	1.8	906	2	T48898	1396	6	1.8	1127	1	E71156	endopeptidase La h
1324	6	1.8	907	2	S54353	1397	6	1.8	1136	2	T48184	hypothetical prote
1325	6	1.8	908	2	S19098	1398	6	1.8	1144	2	A81983	probable DNA-direc
1326	6	1.8	908	2	T48899	1399	6	1.8	1148	2	T27408	hypothetical prote
1327	6	1.8	912	2	T00009	1400	6	1.8	1148	2	AD0198	transcription-repa
1328	6	1.8	912	2	A54423	1401	6	1.8	1155	2	AC2426	adenylate cyclase
1329	6	1.8	922	2	D75615	1402	6	1.8	1173	2	T25893	hypothetical prote
1330	6	1.8	923	1	MMBY7C	1403	6	1.8	1174	2	A39927	RNA-directed RNA p
1331	6	1.8	923	2	A53054	1404	6	1.8	1190	2	S21977	Pm5 protein - huma
1332	6	1.8	928	1	VGBBERG	1405	6	1.8	1194	2	T03818	apoptotic proteina
1333	6	1.8	928	2	T38419	1406	6	1.8	1198	2	T34340	dynamin heavy chain
1334	6	1.8	932	1	VGBBRC	1407	6	1.8	1201	2	F86386	hypothetical prote
1335	6	1.8	933	2	TJ0618	1408	6	1.8	1205	2	T27053	hypothetical prote
1336	6	1.8	935	2	S53608	1409	6	1.8	1208	2	S69015	AXL1 protein - yea
1337	6	1.8	937	2	C97168	1410	6	1.8	1212	2	C82834	DNA polymerase III
1338	6	1.8	940	2	D89723	1411	6	1.8	1221	2	T25005	hypothetical prote
1339	6	1.8	940	2	T31575	1412	6	1.8	1225	2	A36607	E2 glycoprotein -
1340	6	1.8	943	2	B48474	1413	6	1.8	1227	2	T48028	hypothetical prote
1341	6	1.8	945	2	T19943	1414	6	1.8	1245	2	G86404	probable P-glycopr
1342	6	1.8	945	2	T21998	1415	6	1.8	1247	2	A33812	interphotoreceptor
1343	6	1.8	948	2	A56602	1416	6	1.8	1272	2	C90593	hypothetical prote
									1283	2	T13799	neurexin IV - fru1

1417	6	1.8	1285	2	S70582	botulinum neurotoxin
1418	6	1.8	1286	1	RIBOP	interphotoreceptor
1419	6	1.8	1289	2	I84505	calcium-dependent
1420	6	1.8	1291	2	H71143	probable ribonucleo-
1421	6	1.8	1297	2	G525714	son-of-seventless-2
1422	6	1.8	1302	2	A41249	multiplying resistan
1423	6	1.8	1304	2	T14073	dynamin lb heavy ch
1424	6	1.8	1305	2	T18548	flax rust resistanc
1425	6	1.8	1307	2	T17453	ERG-associated pro
1426	6	1.8	1311	2	C84528	hypothetical prote
1427	6	1.8	1327	2	T14594	guanidine nucleoti
1428	6	1.8	1333	2	T37488	Ras guanine nucleo
1429	6	1.8	1335	2	S07245	xanthine dehydrog
1430	6	1.8	1336	2	G25716	Ras guanine nucleo
1431	6	1.8	1336	2	T17479	hypothetical prote
1432	6	1.8	1339	2	T17841	hypothetical prote
1433	6	1.8	1388	2	A57655	cim (timeless) pro
1434	6	1.8	1400	2	T22644	hypothetical prote
1435	6	1.8	1405	2	T04426	hypothetical prote
1436	6	1.8	1416	2	T70823	hypothetical prote
1437	6	1.8	1423	1	G27941	serum albumin - se
1438	6	1.8	1426	2	A29580	hypothetical prote
1439	6	1.8	1436	2	F68904	conserved hypothet
1440	6	1.8	1436	2	A46496	antigen WC1.i prec
1441	6	1.8	1445	2	T10728	probable gag/pol p
1442	6	1.8	1449	2	B81963	iga-specific serini
1443	6	1.8	1459	2	D71551	hypothetical prote
1444	6	1.8	1457	2	DB1019	adhesion and penet
1445	6	1.8	1460	2	T00095	hypothetical prote
1446	6	1.8	1462	1	S32437	pol polypeptid -
1447	6	1.8	1468	1	G30818	hypothetical prote
1448	6	1.8	1475	2	AD1173	hypothetical prote
1449	6	1.8	1475	2	AE1530	hypothetical prote
1450	6	1.8	1488	2	T02856	probable membrane
1451	6	1.8	1509	2	B89985	hypothetical prote
1452	6	1.8	1512	2	T14883	hypothetical prote
1453	6	1.8	1513	2	G45768	mitotic spindle pr
1454	6	1.8	1534	2	S59604	DNA (cytosolin-5)-
1455	6	1.8	1549	1	A40691	trichoglyalin - she
1456	6	1.8	1557	2	G68419	probable reverse t
1457	6	1.8	1557	2	T09074	sensaphorin recept
1458	6	1.8	1612	2	T30805	ductil protein - mo
1459	6	1.8	1643	2	T05647	hypothetical prote
1460	6	1.8	1651	2	T14160	transmembrane rece
1461	6	1.8	1655	2	G47446	nucleoporin Mp18
1462	6	1.8	1657	2	T25421	hypothetical prote
1463	6	1.8	1670	2	G71551	DNA-directed DNA p
1464	6	1.8	1682	1	C70588	probable mbur prot
1465	6	1.8	1707	2	G77910	hypothetical prote
1466	6	1.8	1712	2	A28261	masking protein pr
1467	6	1.8	1737	2	T00209	MEGF protein - hu
1468	6	1.8	1737	2	T17101	probable voltage-re
1469	6	1.8	1740	2	T33215	ribonucleotide red
1470	6	1.8	1756	2	T02559	hypothetical prote
1471	6	1.8	1769	2	G53378	probable membrane
1472	6	1.8	1780	2	T12772	hypothetical prote
1473	6	1.8	1785	2	T23255	hypothetical prote
1474	6	1.8	1787	2	G97232	hypothetical protee
1475	6	1.8	1794	2	T38459	hypothetical diver
1476	6	1.8	1806	1	CGRHUR	collagen alpha I(X)
1477	6	1.8	1806	1	T23298	hypothetical prote
1478	6	1.8	1882	1	GNVYTR	genome polyprotein
1479	6	1.8	1891	2	T43262	calcium channel al
1480	6	1.8	1893	1	AA0262	transcription init
1481	6	1.8	1898	1	A45973	trichoglyalin - hum
1482	6	1.8	1911</			

1490	6	1.8	2104	2	D91286	hypothetical prote
1491	6	1.8	2104	2	H86137	hypothetical prote
1492	6	1.8	2105	2	T18958	hypothetical prote
1493	6	1.8	2124	2	A28452	probable serine-ty
1494	6	1.8	2126	2	E70522	probable polypeptid
1495	6	1.8	2132	1	A55182	aggrean precursor
1496	6	1.8	2150	2	S13553	hypothetical prote
1497	6	1.8	2154	2	F83068	hypothetical prote
1498	6	1.8	2165	1	RNNZ42	genome polypeptain
1499	6	1.8	2167	2	AP1489	cell wall-associat
1500	6	1.8	2228	2	B97942	beta-galactosidase

ALIGNMENTS

RESULT 1
H72621
hypochemical protein APE1433 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H72621
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hakiwara, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, AeropyrumReference number: A72450; MUID:99310339; PMID:1038266
A:Accession: H72621
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-156 <KAM>
A:Cross-references: UNIPROT:Q9YC18; UNIPARC:UPI00005DF4B; DDBJ:AP000061; NID:G5104821;
A:Experimental source: strain K1
A:Genetics:
A:Gene: APE1433

Query Match	2.7%	Score 9;	DB 2;	Length 156;
Best Match	100.0%	Score 10;	DB 2;	Length 156;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LTGSAASGP 25

Db 105 LTGSASGP 113

RESULT 2

microtubule-associated protein MAP1B - mouse

C;Species: Mus musculus (house mouse)

R;Noble, M.; Lewis, S.A.; Cowan, N.J.

A;Title: The microtubule binding domain of microtubule-associated protein MAP1B contains

A;Accession: S07549

A;Residues: 1-2464 <NOB>

R; Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.

A; Title: Binding of heat-shock protein 70 (hsp70) to tubulin

A;Accession: S44387

A;Molecule type: protein

A;Cross-references: UNIPARC:UPI0000173D97

C/Keywords: microtubule binding; phosphoprotein; tandem repeat

F; 589-592, 639-642, 649-652, 655-658, 660-663, 668-671, 674-677, 679-682, 683-686, 687-690, 691-69

R-K-E/D-X)
F;1861-2064/Region: 17-residue repeats
F;91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site: pH
F;147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (cd
F;1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 2.7%; Score 9; DB 1; Length 2466;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AASGPVKEL 29
DB 812 AASGPVKEL 820

RESULT 3
S76681
hypothetical protein - *Synechocystis* sp. (strain PCC 6803)
C;Species: *Synechocystis* sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76681
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3; 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
8.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76681
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <KAN>
A;Cross-references: UNIPROT:Q55866; UNIPARC:UPI00000C0F86; EMBL:D64004; GB:AB001339; NID
C;Superfamily: cyanelle *Cyanophora paradoxa* hypothetical protein ycc36

Query Match 2.4%; Score 8; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 LLTSLFVL 243
DB 85 LLTSLFVL 92

RESULT 4
A82159
hypothetical protein VC1772 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
C;Species: *Vibrio cholerae*
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A82159
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406; 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82159
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <HEI>
A;Cross-references: UNIPROT:Q9KR71; UNIPARC:UPI00000C030DC; GB:AE004254; GB:AE003852; NID
C;Genetics:
A;Gene: VC1772
A;Map position: 1

Query Match 2.4%; Score 8; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 EKKRVDIC 268
|||||

DB 134 EKKRVDIC 141

RESULT 5
S18733
glutenin high molecular weight chain 1B9 precursor - wheat
C;Species: *Triticum aestivum* (common wheat)
C;Date: 08-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
R;Halford, N.G.; Forde, J.; Anderson, O.D.; Greene, F.C.; Shewry, P.R.
Theor. Appl. Genet. 75; 117-126, 1987
A;Title: The nucleotide and deduced amino acid sequences of an HMW glutenin subunit gene
A and 1D.
A;Reference number: S18733
A;Accession: S18733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-705 <HML>
A;Cross-references: UNIPROT:Q03871; UNIPARC:UPI00000A6F03; EMBL:X61026; NID:g22089; PIDN
C;Superfamily: glutenin

Query Match 2.4%; Score 8; DB 2; Length 705;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 YSSSLQOP 115
DB 496 YSSSLQOP 503

RESULT 6
S38673
desmoglein 2 - human
N;Alternate names: desmoglein HDGC
C;Species: *Homo sapiens* (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S38673; B38672
R;Zimbelmann, R.
submitted to the EMBL Data Library, September 1993
A;Reference number: S38673
A;Accession: S38673
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <ZIM>
A;Cross-references: UNIPROT:Q14126; UNIPARC:UPI000004CAAB; EMBL:Z26317; NID:g416177; PIDN
R;Koch, P.J.; Goldschmidt, M.D.; Waleh, M.J.; Zimbelmann, R.; Franke, W.W.
Eur. J. Cell Biol. 55; 200-208, 1991
A;Title: Complete amino acid sequence of the epidermal desmoglein precursor polypeptide
A;Reference number: A38672; MUID:92037656; PMID:1935985
A;Accession: B38672
A;Molecule type: mRNA
A;Residues: 777-117 <KOC>
A;Cross-references: UNIPARC:UPI0000177AF; GB:S64273
C;Genetics:
A;Gene: GDB:DSG2
A;Cross-references: GDB:128808; OMIM:125671
A;Map position: 18q12.1-18q12.2
C;Superfamily: cadherin; cadherin repeat homology
C;Keywords: calcium binding; cell adhesion; duplication; glycoprotein; membrane protein
F;51-158/Domain: cadherin repeat homology <CR1>
F;161-271/Domain: cadherin repeat homology <CR2>

Query Match 2.4%; Score 8; DB 2; Length 1117;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 LLTVPILL 238
DB 624 LLTVPILL 631

RESULT 7
T29918

hypothetical protein ZC449.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T29918
R:Latreille, P.; Gattung, S.
A:Description: The sequence of *C. elegans* cosmid ZC449.
A:Reference number: Z20708
A/Accession: T29918
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-105 <LAT>
A/Cross-references: UNIPROT:Q23329, UNIPARC:UPI000007E7AD, EMBL:U41510, PIDD:AAA82633.1,
C:Superfamily: *Caenorhabditis elegans* hypothetical protein ZC449.4

Query Match 2.1%; Score 7; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 MVLLCL 232
DB 63 MVLLCL 69

RESULT 8
E71866
hypothetical protein jhp0956 - *Helicobacter pylori* (strain J99)
C:Species: *Helicobacter pylori*
A/Variety: strain J99
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C/Accession: E71866
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.J.; Gibson, R.; Wexberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A/Reference number: A71800; MUID:99120557; PMID:9923682
A/Accession: E71866
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-161 <ARN>
A/Cross-references: UNIPROT:Q9ZKH9, UNIPARC:UPI00000D72A4, GB:AE001525, GB:AE001439, NID
C/Genetics:
A:Experimental source: strain J99
A:Gene: jhp0956
C:Superfamily: *Helicobacter pylori* hypothetical protein jhp0956

Query Match 2.1%; Score 7; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 PLTSLF 241
DB 102 PLTSLF 108

RESULT 9
AE1817
hypothetical protein all0085 [imported] - *Nostoc* sp. (strain PCC 7120)
C:Species: *Nostoc* sp. PCC 7120
A/Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AE1817
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriguchi,
Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
A/Reference number: AE1807; MUID:21595285; PMID:11759840
A/Accession: AE1817
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-170 <KUR>
A/Cross-references: UNIPROT:Q9ZOK6, UNIPARC:UPI00000CC017, GB:BA000019, PIDD:BA877609.1;
A:Experimental source: strain PCC 7120
C/Genetics:
A:Gene: all0085

Query Match 2.1%; Score 7; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLLCLL 233
DB 14 VLLCLL 20

RESULT 10
F97283
ribosomal protein L6 [imported] - *Clostridium acetobutylicum*
C:Species: *Clostridium acetobutylicum*
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: F97283
R:Nolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clo*
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: F97283
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-179 <KUR>
A/Cross-references: UNIPROT:Q97EBJ, UNIPARC:UPI00000CA72A, GB:AE001437, PIDD:AAK81057.1;
A:Experimental source: *Clostridium acetobutylicum* ATCC824
C/Genetics:
A:Gene: CAC3118
C:Superfamily: ribosomal protein L6/L9

Query Match 2.1%; Score 7; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KELVGSV 33
DB 139 KELVGSV 145

RESULT 11
F83305
hypothetical protein PA2724 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: F83305
R:Stover, C.K.; Pham, X.Q.; Ervin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathoc
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: F83305
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-179 <STD>
A/Cross-references: UNIPROT:Q91088, UNIPARC:UPI00000C57D0, GB:AE004700, GB:AE004091, NID
C/Genetics:
A:Gene: PA2724

Query Match 2.1%; Score 7; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 RVDPFDG 86
DB 42 RVDPFDG 48

RESULT 12

F97499

hypothetical protein AGR_C_2123 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 31-Dec-2004

C/Accession: F97499

R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: F97499

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-182 <KUR>

A/Cross-references: UNIPROT:Q8UG92; UNIPARC:UPI00000D1A64; GB:AE007869; P1DN:AAK6951.1;

A/Gene: AGR_C_2123

A/Map position: circular chromosome

C/Superfamily: Bacillus subtilis hypothetical protein yung

Query Match

Best Local Similarity 2.1%; Score 7; DB 2; Length 182;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 LLSTFLV 243

DB 34 LLSTFLV 40

RESULT 13

I40220

hypothetical protein 2 - Bacillus licheniformis (fragment)

C/Species: Bacillus licheniformis

C/Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Jul-2004

C/Accession: I40220

R/Harry, B.J.; Partridge, S.R.; Weiss, A.S.; Wake, R.G.

Gene 147, 85-89, 1994

A/Title: Conservation of the 168 divB gene in Bacillus subtilis W23 and B. licheniformi

A/Reference number: I40220; MUID:94374713; PMID:8088553

A/Accession: I40220

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-184 <RES>

A/Cross-references: UNIPROT:Q45305; UNIPARC:UPI000012P92D; EMBL:U01958; NID:g404008; P1D

C/Superfamily: UDP-N-acetylmuramate dehydrogenase

Query Match

Best Local Similarity 2.1%; Score 7; DB 2; Length 184;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GSVGAV 37

DB 9 GSVGAV 15

RESULT 14

H70416

hypothetical protein aq_1348 - Aquifex aeolicus

C/Species: Aquifex aeolicus

C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C/Accession: H70416

R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy

V. Nature 392, 353-358, 1998

A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A/Reference number: A70300; MUID:98196666; PMID:9537320

A/Accession: H70416

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-189 <ACF>

A/Cross-references: UNIPROT:O67363; UNIPARC:UPI00000565CC; GB:AE00736; NID:g2983763; P1D
A/Experimental source: strain VF5
C/Genetics:
A/Gene: aq_1348
C/Superfamily: Aquifex aeolicus hypothetical protein aq_1348

Query Match

Best Local Similarity 2.1%; Score 7; DB 2; Length 189;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 GLFLMFL 250

DB 142 GLFLMFL 148

RESULT 15

T45543

hypothetical protein 2 [imported] - Klebsiella pneumoniae transposon Tn5711

C/Species: Klebsiella pneumoniae

C/Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004

C/Accession: T45543

R/Albigier, B.; Hubert, J.C.; Lett, M.C.

submitted to the EMBL Data Library, October 1998

A/Description: Composite transposons Tn5708 and Tn5709 are based on a Tn3-like element Tr

A/Reference number: Z23003

A/Accession: T45543

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-199 <ALB>

A/Cross-references: UNIPROT:O87756; UNIPARC:UPI0000BA6E5; EMBL:AJ011907; P1DN:CAA09858.1

A/Experimental source: strain KIITA

C/Genetics:

A/Mobile element: transposon Tn5711

C/Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain hom

Query Match

Best Local Similarity 2.1%; Score 7; DB 2; Length 199;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 LLSTFLV 242

DB 132 LLSTFLV 138

Search completed: December 16, 2005, 11:53:49
Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 11:46:50 ; Search time 231 Seconds
(without alignments)
1023.169 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 335
Sequence: 1 MAGSPCTCLTLYITIMQITGS.....PMSLITMPDTPRLPAYENV1 335

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1500 summaries

Database : UniProt_05.80:*

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	335	100.0	335	1	SLAF7_HUMAN
2	156	2.7	333	1	SLAF7_MOUSE
3	9	2.7	572	1	Q5NSI_CRYNE
4	9	2.7	2464	1	MAP1B_MOUSE
5	9	2.7	83	2	Q884T6_PSESM
6	9	2.4	129	2	Q81VU0_HUMAN
7	8	2.4	136	2	Q54WZ7_DICDI
8	8	2.4	139	2	Q5VYV9_NOCFA
9	8	2.4	155	2	Q6ERB1_ORISA
10	8	2.4	173	2	Q55866_SYNY3
11	8	2.4	202	2	Q7V2B6_PROMP
12	8	2.4	211	2	Q9S488_PROS9
13	8	2.4	230	2	Q5V1D5_HALMA
14	8	2.4	240	2	Q5V4S6_HALMA
15	8	2.4	279	2	Q7MJC1_VIBRV
16	8	2.4	284	2	Q6LP53_PHOTO
17	8	2.4	286	2	Q9KR71_VIBCH
18	8	2.4	317	2	Q9TPE7_MONDO
19	8	2.4	328	2	Q9BDP0_AOTTR
20	8	2.4	343	2	Q6MDM3_BDBRA
21	8	2.4	346	2	Q4R6C4_MACFA
22	8	2.4	347	2	Q9TPE7_MONDO
23	8	2.4	348	2	Q7USC6_RHOBA
24	8	2.4	360	1	HEPLN3_HUMAN
25	8	2.4	362	2	Q9TPE7_MONDO
26	8	2.4	364	2	Q5WSU5_MONDO
27	8	2.4	364	2	Q5WSU5_MONDO
28	8	2.4	364	2	Q5WSU5_MONDO
29	8	2.4	412	2	Q6FRV6_BRAJA
30	8	2.4	421	2	Q6FRV7_ACTIAD
31	8	2.4	439	2	Q6SHV3_BACLD

32	8	2.4	467	2	Q8D7P9_VIBVU
33	8	2.4	469	2	Q7MERO_VIBVY
34	8	2.4	533	1	INT_CHLRE
35	8	2.4	551	2	Q5P4J3_AZOSE
36	8	2.4	653	2	Q58D55_BOVIN
37	8	2.4	669	1	BGAL_FELCA
38	8	2.4	671	2	Q829F0_STRAM
39	8	2.4	705	2	Q03871_WHEAT
40	8	2.4	720	2	Q84TG6_TRTTU
41	8	2.4	720	2	Q941J6_WHEAT
42	8	2.4	801	2	Q4SDX7_TETNG
43	8	2.4	808	2	Q4T2D9_TETNG
44	8	2.4	868	2	Q9VH63_PROME
45	8	2.4	1053	2	Q81A08_PLAF7
46	8	2.4	1117	1	DSG2_HUMAN
47	8	2.4	1118	8	Q4KTU6_HUMAN
48	8	2.4	1122	1	DSG2_MOUSE
49	8	2.4	1235	2	Q9S4Z8_HUMAN
50	8	2.1	31	2	Q4QTH0_LEIMA
51	8	2.1	64	2	Q4Y596_PLACH
52	8	2.1	66	2	Q9QWE3_MURRI
53	8	2.1	69	2	Q64WJ2_BACPR
54	8	2.1	71	2	Q6MNM5_BDEBA
55	8	2.1	72	2	Q5D864_PREEN
56	8	2.1	75	1	MTRE_METKA
57	8	2.1	75	2	Q4WE52_ASPPV
58	8	2.1	76	2	Q233Z9_CAEEL
59	8	2.1	82	2	Q4JBF2_SULAC
60	8	2.1	82	2	Q6Z5Z6_ORYSA
61	8	2.1	83	2	Q4ZOK3_PSEST
62	8	2.1	90	2	Q9GK67_RABIT
63	8	2.1	91	2	Q4H6A4_9DEIO
64	8	2.1	93	2	Q4P200_USTMA
65	8	2.1	93	2	Q5BRQ7_SCHJA
66	8	2.1	96	2	Q83R08_COXBU
67	8	2.1	97	1	CCL8_MOUSE
68	8	2.1	97	2	Q64DH5_YARCH
69	8	2.1	97	2	Q9TTS6_BOVIN
70	8	2.1	97	2	Q5SR19_MOUSE
71	8	2.1	97	2	Q9Z318_CAVPO
72	8	2.1	98	1	CCL13_HUMAN
73	8	2.1	98	2	Q6ICQ6_HUMAN
74	8	2.1	99	2	Q4Q4G7_LEIMA
75	8	2.1	101	1	PHS_STRAM
76	8	2.1	104	2	Q4JIR8_AZOVI
77	8	2.1	115	2	Q8KX15_SYNP2
78	8	2.1	117	2	Q8HXK4_MACFA
79	8	2.1	120	2	Q9VNS7_DROME
80	8	2.1	122	2	Q6NMX3_DROME
81	8	2.1	124	2	Q9BNJ9_MYTRI
82	8	2.1	126	2	Q9BB60_MACFA
83	8	2.1	132	2	Q5RIZ6_BRARE
84	8	2.1	132	2	Q6GQ49_XENLA
85	8	2.1	135	2	Q5UXU6_HALMA
86	8	2.1	145	2	Q8GWH4_ARATH
87	8	2.1	145	2	Q5D863_CALJA
88	8	2.1	145	2	Q8TY49_METKA
89	8	2.1	146	2	Q4TRO6_GSPRN
90	8	2.1	149	2	Q5NXL6_AZOSE
91	8	2.1	150	2	Q9RFN9_MYCFE
92	8	2.1	153	2	Q9XK65_KLEBO
93	8	2.1	156	2	Q9EMQ1_AMEPV
94	8	2.1	159	2	Q6PEY1_HUMAN
95	8	2.1	159	2	Q8BRC2_MOUSE
96	8	2.1	159	2	Q9DON8_MOUSE
97	8	2.1	160	2	Q5S867_DICDI
98	8	2.1	160	2	Q7TUK7_PROWM
99	8	2.1	161	2	Q4HUB0_GIBZE
100	8	2.1	161	2	Q9ZKH9_HILPJ
101	8	2.1	162	2	Q67LKL_SYMTN
102	8	2.1	162	2	Q98P38_RHILQ
103	8	2.1	165	2	Q7YXD5_GLORO
104	8	2.1	165	2	Q98J36_RHILQ

Q8D7P9_VIBVU	Q8D7P9_VIBVU
Q7MERO_VIBVY	Q7MERO_VIBVY
INT_CHLRE	INT_CHLRE
Q5P4J3_AZOSE	Q5P4J3_AZOSE
Q58D55_BOVIN	Q58D55_BOVIN
BGAL_FELCA	BGAL_FELCA
Q829F0_STRAM	Q829F0_STRAM
Q03871_WHEAT	Q03871_WHEAT
Q84TG6_TRTTU	Q84TG6_TRTTU
Q941J6_WHEAT	Q941J6_WHEAT
Q4SDX7_TETNG	Q4SDX7_TETNG
Q4T2D9_TETNG	Q4T2D9_TETNG
Q9VH63_PROME	Q9VH63_PROME
Q81A08_PLAF7	Q81A08_PLAF7
DSG2_HUMAN	DSG2_HUMAN
Q4KTU6_HUMAN	Q4KTU6_HUMAN
DSG2_MOUSE	DSG2_MOUSE
Q9S4Z8_HUMAN	Q9S4Z8_HUMAN
Q4QTH0_LEIMA	Q4QTH0_LEIMA
Q4Y596_PLACH	Q4Y596_PLACH
Q9QWE3_MURRI	Q9QWE3_MURRI
Q64WJ2_BACPR	Q64WJ2_BACPR
Q6MNM5_BDEBA	Q6MNM5_BDEBA
Q5D864_PREEN	Q5D864_PREEN
MTRE_METKA	MTRE_METKA
Q4WE52_ASPPV	Q4WE52_ASPPV
Q233Z9_CAEEL	Q233Z9_CAEEL
Q4JBF2_SULAC	Q4JBF2_SULAC
Q6Z5Z6_ORYSA	Q6Z5Z6_ORYSA
Q4ZOK3_PSEST	Q4ZOK3_PSEST
Q9GK67_RABIT	Q9GK67_RABIT
Q4H6A4_9DEIO	Q4H6A4_9DEIO
Q4P200_USTMA	Q4P200_USTMA
Q5BRQ7_SCHJA	Q5BRQ7_SCHJA
Q83R08_COXBU	Q83R08_COXBU
CCL8_MOUSE	CCL8_MOUSE
Q64DH5_YARCH	Q64DH5_YARCH
Q9TTS6_BOVIN	Q9TTS6_BOVIN
Q5SR19_MOUSE	Q5SR19_MOUSE
Q9Z318_CAVPO	Q9Z318_CAVPO
CCL13_HUMAN	CCL13_HUMAN
Q6ICQ6_HUMAN	Q6ICQ6_HUMAN
Q4Q4G7_LEIMA	Q4Q4G7_LEIMA
PHS_STRAM	PHS_STRAM
Q4JIR8_AZOVI	Q4JIR8_AZOVI
Q8KX15_SYNP2	Q8KX15_SYNP2
Q8HXK4_MACFA	Q8HXK4_MACFA
Q9VNS7_DROME	Q9VNS7_DROME
Q6NMX3_DROME	Q6NMX3_DROME
Q9BNJ9_MYTRI	Q9BNJ9_MYTRI
Q9BB60_MACFA	Q9BB60_MACFA
Q5RIZ6_BRARE	Q5RIZ6_BRARE
Q6GQ49_XENLA	Q6GQ49_XENLA
Q5UXU6_HALMA	Q5UXU6_HALMA
Q8GWH4_ARATH	Q8GWH4_ARATH
Q5D863_CALJA	Q5D863_CALJA
Q8TY49_METKA	Q8TY49_METKA
Q4TRO6_GSPRN	Q4TRO6_GSPRN
Q5NXL6_AZOSE	Q5NXL6_AZOSE
Q9RFN9_MYCFE	Q9RFN9_MYCFE
Q9XK65_KLEBO	Q9XK65_KLEBO
Q9EMQ1_AMEPV	Q9EMQ1_AMEPV
Q6PEY1_HUMAN	Q6PEY1_HUMAN
Q8BRC2_MOUSE	Q8BRC2_MOUSE
Q9DON8_MOUSE	Q9DON8_MOUSE
Q5S867_DICDI	Q5S867_DICDI
Q7TUK7_PROWM	Q7TUK7_PROWM
Q4HUB0_GIBZE	Q4HUB0_GIBZE
Q9ZKH9_HILPJ	Q9ZKH9_HILPJ
Q67LKL_SYMTN	Q67LKL_SYMTN
Q98P38_RHILQ	Q98P38_RHILQ
Q7YXD5_GLORO	Q7YXD5_GLORO
Q98J36_RHILQ	Q98J36_RHILQ

105	7	2.1	167	2	046295_CLOPE	046295_clostridium	178	7	2.1	215	2	0701S1_ANOGA	0701S1_anopheles g
106	7	2.1	167	2	08XPC3_CLOPE	08XPC3_clostridium	179	7	2.1	215	2	06UT14_9CAUD	06UT14_bacterioph
107	7	2.1	169	2	094S06_ZENNE	094S06_zenopsis ne	180	7	2.1	215	2	08W6N4_9CAUD	08W6N4_bacterioph
108	7	2.1	170	2	06ZSF8_HUMAN	06ZSF8_homo sapien	181	7	2.1	215	2	09FG66_ARATH	09FG66_arabidopsis
109	7	2.1	170	2	08Z0K6_ANASP	08Z0K6_anabaena sp	182	7	2.1	216	2	072M18_LEPIC	072M18_leptospira
110	7	2.1	171	2	085DH2_9TELE	085DH2_corydoras r	183	7	2.1	216	2	08E254_LEPIN	08E254_leptospira
111	7	2.1	173	2	06D693_ERWCT	06D693_erwinia car	184	7	2.1	217	2	04HT04_9DEIO	04HT04_deinococcus
112	7	2.1	173	2	094YR3_9TELE	094YR3_erythrulia j	185	7	2.1	217	2	0566V2_BRARE	0566V2_baccharidantio
113	7	2.1	173	2	06T233_AMICA	06T233_ama calva	186	7	2.1	220	2	094BC4_ARATH	094BC4_arabidopsis
114	7	2.1	173	2	08H0L0_AMICA	08H0L0_ama calva	187	7	2.1	220	2	04L9S9_STAUT	04L9S9_staphylococ
115	7	2.1	173	2	071EL4_EUDEI	071EL4_eudromia el	188	7	2.1	221	2	09RRZ0_DEIRA	09RRZ0_deinococcus
116	7	2.1	174	2	0870Y3_NEUCR	0870Y3_neurospora	189	7	2.1	221	2	07TF12_RHMC6	07TF12_rhensu cyto
117	7	2.1	174	2	08H162_SYNMA	08H162_synthbranchus	190	7	2.1	224	2	08W6X2_9CAUD	08W6X2_cyanophage
118	7	2.1	175	1	NU6M_UR0TA	07Y8d2_urotrichus	191	7	2.1	224	2	093NK7_YEREN	093NK7_yersinia en
119	7	2.1	175	2	07Y8B4_MOGMO	07Y8B4_mogera wogu	192	7	2.1	224	2	09KKH2_YEREN	09KKH2_yersinia en
120	7	2.1	175	2	09MJAS_TALEU	09MJAS_talpa europ	193	7	2.1	224	2	062DW8_BURMA	062DW8_burkholderi
121	7	2.1	175	2	05P663_AZOSE	05P663_azarcus sp	194	7	2.1	224	2	063JD1_BURPS	063JD1_burkholderi
122	7	2.1	175	2	04RYN1_TETNG	04RYN1_tetradodon n	195	7	2.1	225	2	061UK2_DROME	061UK2_drosophila
123	7	2.1	177	1	RL18A_SPOFR	084qd7_epidoptera	196	7	2.1	225	2	068BQ4_ORYSA	068BQ4_oryza sativ
124	7	2.1	177	1	06F445_PLUXY	06F445_plutella xy	197	7	2.1	225	2	04LIS0_9BURK	04LIS0_burkholderi
125	7	2.1	179	2	0910B8_PSEAB	0910B8_pseudomonas	198	7	2.1	226	2	05VON8_ORYSA	05VON8_oryza sativ
126	7	2.1	179	2	097EJ3_CIOAB	097EJ3_clostridium	199	7	2.1	226	2	04NAV5_9MICC	04NAV5_arthrobacte
127	7	2.1	182	2	07CZV8_AGR75	07CZV8_agrobacteri	200	7	2.1	226	2	05XAB3_STRP6	05XAB3_streptococc
128	7	2.1	182	2	08Y365_RALSO	08Y365_ralstonia s	201	7	2.1	226	2	0601H5_MYCHY	0601H5_mycoplasm
129	7	2.1	183	2	057UZ6_9TRYP	057UZ6_trypanosoma	202	7	2.1	226	2	099YAB_9STRPY	099YAB_streptococc
130	7	2.1	183	2	08UH31_CHICK	08UH31_gallus gall	203	7	2.1	226	2	08NZL3_STRP8	08NZL3_streptococ
131	7	2.1	184	1	MURB_BACLI	045305_bacillus ii	204	7	2.1	226	2	08K607_STRP3	08K607_streptococ
132	7	2.1	185	2	07ZH77_9HIV1	07ZH77_human immun	205	7	2.1	228	1	UTP11_ARATH	UTP11_arath
133	7	2.1	185	2	07ZH80_9HIV1	07ZH80_human immun	206	7	2.1	229	2	054E70_DICD1	054E70_dicystosceli
134	7	2.1	186	2	080UC0_MOUSE	080UC0_mus musculu	207	7	2.1	233	2	082DQ3_STRAW	082DQ3_streptomyce
135	7	2.1	187	2	09EUY8_SALRY	09EUY8_salmonella	208	7	2.1	233	2	063A70_BACCZ	063A70_bacillus ce
136	7	2.1	187	2	07DAN4_SALRY	07DAN4_salmonella	209	7	2.1	235	2	06ST68_9GOBI	06ST68_gymnogobius
137	7	2.1	187	1	05J4A2_SALCH	05J4A2_salmonella	210	7	2.1	235	2	06STG5_9GOBI	06STG5_gymnogobius
138	7	2.1	189	1	Y1348_AQUAE	067363_aquilex aeo	211	7	2.1	235	2	06JT09_9GOBI	06JT09_gymnogobius
139	7	2.1	189	2	04LIU2_9ENTR	04LIU2_salmonella	212	7	2.1	235	2	06JU02_9GOBI	06JU02_gymnogobius
140	7	2.1	189	2	07ZH66_9HIV1	07ZH66_human immun	213	7	2.1	235	2	06JU01_9GOBI	06JU01_gymnogobius
141	7	2.1	189	2	07ZH70_9HIV1	07ZH70_human immun	214	7	2.1	235	2	06U000_9GOBI	06U000_gymnogobius
142	7	2.1	189	2	07ZH75_9HIV1	07ZH75_human immun	215	7	2.1	235	2	06J1Z8_9GOBI	06J1Z8_gymnogobius
143	7	2.1	190	2	07ZH67_9HIV1	07ZH67_human immun	216	7	2.1	235	2	06J1Z6_9GOBI	06J1Z6_gymnogobius
144	7	2.1	190	2	07ZH68_9HIV1	07ZH68_human immun	217	7	2.1	235	2	06J1Z3_9GOBI	06J1Z3_gymnogobius
145	7	2.1	190	2	07ZH71_9HIV1	07ZH71_human immun	218	7	2.1	235	2	06JU07_9GOBI	06JU07_gymnogobius
146	7	2.1	190	2	07ZH72_9HIV1	07ZH72_human immun	219	7	2.1	235	2	06JU05_9GOBI	06JU05_gymnogobius
147	7	2.1	190	2	07ZH73_9HIV1	07ZH73_human immun	220	7	2.1	235	2	06JU03_9GOBI	06JU03_gymnogobius
148	7	2.1	190	2	07ZH74_9HIV1	07ZH74_human immun	221	7	2.1	235	2	06S9Z6_9GOBI	06S9Z6_gymnogobius
149	7	2.1	191	2	09J4B8_9BETA	09J4B8_baboon cyto	222	7	2.1	235	2	06STH2_9GOBI	06STH2_gymnogobius
150	7	2.1	191	2	08U0S5_PYRFU	08U0S5_pyrococcus	223	7	2.1	235	2	06J1Z4_9GOBI	06J1Z4_gymnogobius
151	7	2.1	195	2	07ZH48_9HIV1	07ZH48_human immun	224	7	2.1	235	2	06STG6_9GOBI	06STG6_gymnogobius
152	7	2.1	195	2	07ZHS1_9HIV1	07ZHS1_human immun	225	7	2.1	235	2	05GYP5_XANOR	05GYP5_xanthomonas
153	7	2.1	195	2	07ZHS2_9HIV1	07ZHS2_human immun	226	7	2.1	236	2	07PMX3_ANOGA	07PMX3_anopheles g
154	7	2.1	195	2	07ZHS3_9HIV1	07ZHS3_human immun	227	7	2.1	238	2	06IOH9_BACAN	06IOH9_bacillus an
155	7	2.1	195	2	07ZHS7_9HIV1	07ZHS7_human immun	228	7	2.1	238	2	P97032_BACSV	P97032_bacillus su
156	7	2.1	195	2	07ZHS8_9HIV1	07ZHS8_human immun	229	7	2.1	238	2	09PPZ8_UREPA	09PPZ8_ureaplaasma
157	7	2.1	195	2	07ZHE1_9HIV1	07ZHE1_human immun	230	7	2.1	239	1	YTML_BACSU	YTML_bacillus su
158	7	2.1	196	2	09AG89_DDEBA	09AG89_belliovibri	231	7	2.1	239	2	09LSE6_ARATH	09LSE6_arabidopsis
159	7	2.1	199	2	087756_KLEBN	087756_klebsiella	232	7	2.1	241	2	04J5B6_SULAC	04J5B6_sulfolobus
160	7	2.1	199	2	074JH7_LACCO	074JH7_lactobacilli	233	7	2.1	243	2	06K7K8_ORYSA	06K7K8_oryza sativ
161	7	2.1	204	2	066087_9ALPH	066087_canine hepr	234	7	2.1	244	2	04JW49_CORJK	04JW49_corynebacte
162	7	2.1	205	2	05Y3C1_9HIV1	05Y3C1_human immun	235	7	2.1	244	2	035892_9CHON	035892_squatinella ne
163	7	2.1	208	2	04LIJH8_9BURK	04LIJH8_burkholderi	236	7	2.1	246	2	04WC42_ASPTU	04WC42_aspergillus
164	7	2.1	210	1	MATA1_CANAL	09W23_candida alb	237	7	2.1	246	2	08L655_ORYSA	08L655_oryza sativ
165	7	2.1	211	2	05K273_GUTTA	05K273_gulliardia	238	7	2.1	246	2	08E7M3_STRAS	08E7M3_streptococ
166	7	2.1	212	2	04RVC0_TETNG	04RVC0_tetradodon n	239	7	2.1	246	2	08G7M3_BIFLO	08G7M3_bifidobacte
167	7	2.1	212	2	08LWK7_9GOBI	08LWK7_gymnogobius	240	7	2.1	246	2	08E263_STRAS	08E263_streptococ
168	7	2.1	212	2	08LWU1_9GOBI	08LWU1_gymnogobius	241	7	2.1	248	2	0886J4_PSEEM	0886J4_pseudomonas
169	7	2.1	212	2	08LWK8_9GOBI	08LWK8_gymnogobius	242	7	2.1	255	2	04K601_PSEEM	04K601_pseudomonas
170	7	2.1	212	2	08LWU0_9GOBI	08LWU0_gymnogobius	243	7	2.1	258	2	05RBG0_PONRY	05RBG0_pongo pygma
171	7	2.1	212	2	08LWU2_9GOBI	08LWU2_gymnogobius	244	7	2.1	262	2	05T1P5_HUMAN	05T1P5_homo sapien
172	7	2.1	212	2	08LWK9_9GOBI	08LWK9_gymnogobius	245	7	2.1	266	1	FLIP_CANCR	FLIP_caulobacter
173	7	2.1	212	2	08LWK6_9GOBI	08LWK6_gymnogobius	246	7	2.1	266	2	08A871_BACTN	08A871_bacteroides
174	7	2.1	212	2	08LVD2_9GOBI	08LVD2_gymnogobius	247	7	2.1	267	2	067N79_SYMTN	067N79_symblabacte
175	7	2.1	212	2	08LVD0_9GOBI	08LVD0_gymnogobius	248	7	2.1	274	2	05J3Z6_PYRKO	05J3Z6_pyrococcus
176	7	2.1	212	2	08LVD1_9GOBI	08LVD1_gymnogobius	249	7	2.1	274	2	09HRP3_HALSA	09HRP3_halo bacteri
177	7	2.1	212	2	08LUT5_9GOBI	08LUT5_gymnogobius	250	7	2.1	274	2	09L2E8_STRCO	09L2E8_streptomyce

251	7	2.1	279	2	Q73ZR3_MYCPA	Q73zr3 mycobacteri	324	7	2.1	344	2	Q8VJG4_SMPV	Q8vjg4 sheepox vi
252	7	2.1	282	2	Q7ORC6_GIALA	Q7orc6 giardia lam	325	7	2.1	345	1	Q116I1_HEASP	Q7vub6 helicobact
253	7	2.1	284	2	Q4SPD6_TETNG	Q4spdc tetradon n	326	7	2.1	345	2	Q4X1I7_ASFPV	Q4x1i7 aspergillus
254	7	2.1	286	2	Q7OIJ0_AMOGA	Q7oiJO amopheles g	327	7	2.1	346	2	Q5LM00_SILPO	Q5lm00 silicibacte
255	7	2.1	287	2	Q7MJ57_VIBVY	Q7mj57 vibrio vuln	328	7	2.1	347	2	Q5OUK3_ENTHI	Q5ouk3 entamoeba h
256	7	2.1	290	2	Q986W0_RHIL0	Q986w0 rhizobium 1	329	7	2.1	347	2	Q8LMB8_GIACA	Q8lwb8 glaucidium
257	7	2.1	292	2	Q6FE32_ACIA0	Q6fe32 actinetobact	330	7	2.1	347	2	Q8HIV9_BUBBS	Q8hiv9 bubo aescala
258	7	2.1	291	2	Q6FP77_ALCEB	Q6up77 alcaligenes	331	7	2.1	347	2	Q8HIV8_BUBBB	Q8hiv8 bubo bubo (
259	7	2.1	292	2	Q6UP77_ALCEB	Q6up77 alcaligenes	332	7	2.1	347	2	Q8HIV7_BUBBB	Q8hiv7 bubo bubo (
260	7	2.1	293	1	CEXQ_GUTTH	Q78450 quillardia	333	7	2.1	347	2	Q8HIV6_BUBBB	Q8hiv6 bubo bubo (
261	7	2.1	296	2	Q5L5A3_CHIAB	Q5l5a3 chlamydophi	334	7	2.1	347	2	Q8HIE5_OTUAT	Q8hie5 otus arctica
262	7	2.1	296	2	Q728V0_DBSVH	Q728v0 desulfovibr	335	7	2.1	347	2	Q8HC11_BUBB	Q8hc11 bubo bubo (
263	7	2.1	300	1	MURB_ENTPA	Q830p3 enterococcu	336	7	2.1	347	2	Q8HCG3_BUBBB	Q8hcg3 bubo bubo (
264	7	2.1	300	1	MURB_STRAS	P55464 streptococc	337	7	2.1	347	2	Q8HRS5_BUBBB	Q8hrs5 bubo bubo (
265	7	2.1	300	1	MURB1_BACAN	P55465 streptococc	338	7	2.1	347	2	Q8HAS5_BUBBB	Q8has5 bubo bubo (
266	7	2.1	301	1	MURB1_BACCR	Q81wd1 bacillus an	339	7	2.1	347	2	Q8LM43_BUBVI	Q8lm43 bubo virgini
267	7	2.1	301	1	MURB1_BACCH	Q81964 bacillus ce	340	7	2.1	348	2	Q9HPV6_HAUSA	Q9hpv6 halobacteri
268	7	2.1	301	1	MURB1_BACHD	Q939c4 bacillus ha	341	7	2.1	348	2	Q6XR59_GBACT	Q6xr59 uncultured
269	7	2.1	301	2	Q8TES8_HUMAN	Q8tes8 homo sapien	342	7	2.1	349	2	Q5WKI4_BACSK	Q5wk14 bacillus cl
270	7	2.1	301	2	Q93FJ1_9ENTR	Q93fj1 citrobacter	343	7	2.1	349	2	Q98N17_RHIL0	Q98n17 rhizobium 1
271	7	2.1	301	2	Q50573_BACPF	Q50573 bacillus ps	344	7	2.1	351	2	Q87AJ8_XYLEPT	Q87aj8 xylella fas
272	7	2.1	301	2	Q4MT93_BACCE	Q4mt93 bacillus th	345	7	2.1	351	2	Q9PF30_XYLEPA	Q9pf30 xylella fas
273	7	2.1	301	2	Q6H805_BACHX	Q6h8e5 bacillus th	346	7	2.1	353	2	Q4IXD4_XANCP	Q4uxd4 xanthomonas
274	7	2.1	301	2	Q732F9_BACCI	Q732f9 bacillus ce	347	7	2.1	353	2	Q8P6S6_XANCP	Q8p6s6 xanthomonas
275	7	2.1	301	2	Q74K66_LACCO	Q74k66 lactobacill	348	7	2.1	355	2	Q70CV9_9SOLA	Q70cv9 nicotiana s
276	7	2.1	301	2	Q636B7_BACCC	Q636b7 bacillus ce	349	7	2.1	355	2	Q70CW2_9SOLA	Q70cw2 nicotiana s
277	7	2.1	302	2	Q5R019_IDILO	Q5r019 idiomarina	350	7	2.1	356	1	COX2_BACSV	Q4ke6 pseudomonas
278	7	2.1	303	1	MURB_BACSU	Q9rue6 deinozococ	351	7	2.1	356	2	Q4KE36_PSEBS	Q4ke36 pseudomonas
279	7	2.1	303	2	Q5QN31_ORYSA	P18579 bacillus nu	352	7	2.1	356	2	Q6FAZ7_ACIAD	Q6faz7 acinetobact
280	7	2.1	303	2	Q65UJ9_BACLD	Q5qmj3 oryza sativ	353	7	2.1	356	2	Q9TBF0_BUBVI	Q9tbf0 bubo virgini
281	7	2.1	304	2	Q89E11_BRAJA	Q65jx9 bacillus 11	354	7	2.1	357	2	Q7SDH7_ASHCO	Q7sdh7 ashbya goss
282	7	2.1	305	1	MURB_CIOAB	Q89e11 bradyrhizob	355	7	2.1	357	2	Q5BJW9_RAT	Q5bjw9 ratulus norv
283	7	2.1	306	2	Q82BN1_STRAW	Q97lp4 clostridium	356	7	2.1	360	2	Q8VIF0_RAT	Q8vif0 ratulus norv
284	7	2.1	307	2	Q4L4G3_STRAU	Q82bn1 streptococc	357	7	2.1	362	1	ASPG2_YEAST	P1163 saccharomyc
285	7	2.1	308	2	Q5NW79_AZOSB	Q4l4g3 streptococc	358	7	2.1	362	2	Q9VRF5_DROME	Q9vrf5 drosophila
286	7	2.1	309	2	Q8DJ14_SYNEL	Q5nw79 azoarcus sp	359	7	2.1	367	1	GLNA_CABEL	P3447 caenorhabdi
287	7	2.1	309	2	Q91T37_LSDV	Q8dj14 synecchococc	360	7	2.1	367	2	Q6DSV7_CABER	Q6dsv7 caenorhabdi
288	7	2.1	311	1	Q5MDX4_BACSK	Q91t37 lumby skin	361	7	2.1	367	2	Q88QG3_PSEBK	Q88qg3 pseudomonas
289	7	2.1	312	1	Q6FAH0_RAT	Q5mdx4 bacillus cl	362	7	2.1	368	2	Q6SDP5_BACLD	Q6sdp5 bacillus 11
290	7	2.1	312	1	Q88H04_PSEPK	P02650 rectus norv	363	7	2.1	369	2	Q9XVU2_CABEL	Q9xvu2 caenorhabdi
291	7	2.1	315	1	MURB_STRPN	Q6pah0 rectus norv	364	7	2.1	370	2	Q4TKZ3_9SPRN	Q4tkz3 9spn
292	7	2.1	316	1	MURB_STRPN	Q88h04 pseudomonas	365	7	2.1	374	2	Q6MDU7_PARUV	Q6mdu7 parachlamyd
293	7	2.1	316	1	Q5JGSA_PYRKO	P55467 streptococc	366	7	2.1	375	2	Q4LRM0_9BUDK	Q4lrm0 burkholderi
294	7	2.1	317	2	Q86915_SPROX	Q5jgsa pyrococcus	367	7	2.1	378	2	Q859J4_9CAUD	Q859j4 staphylococ
295	7	2.1	317	2	Q86915_SPROX	Q5jgs4 pyrococcus	368	7	2.1	378	2	Q859L5_STEALD	Q859l5 staphylococ
296	7	2.1	319	2	Q4WR24_BUBBB	Q86915 sheepox vi	369	7	2.1	378	2	Q85DZ8_9TELE	Q85dz8 eigemannia
297	7	2.1	320	2	Q4WR24_BUBBB	Q5wr24 bubo bubo k	370	7	2.1	379	2	Q4RMT0_TETNG	Q4rmt0 tetradodon n
298	7	2.1	322	2	Q7M968_WOLISU	Q4wr24 aepergillus	371	7	2.1	380	1	Q9XKJ7_HIMSI	Q9xkj7 himantusa s
299	7	2.1	323	2	Q8LK49_LEUGL	Q7m968 wolucella s	372	7	2.1	381	1	CYB_ISUPA	P34871 isurus pauc
300	7	2.1	323	2	Q73RJ5_TREDE	Q8lk49 leucaena gl	373	7	2.1	381	1	CYB_SCYCA	Q79413 scyllorhinu
301	7	2.1	325	2	Q5FUV7_LACAC	Q73rj5 treponema d	374	7	2.1	381	1	CYCH_RHIME	P45400 rhizobium m
302	7	2.1	325	2	Q98B70_RHIL0	Q5fjv7 lactobacill	375	7	2.1	381	2	Q8PL48_XANNC	Q8pl48 xanthomonas
303	7	2.1	328	2	Q8JU20_LSDV	Q98b70 rhizobium 1	376	7	2.1	382	2	Q79571_9CHON	Q79571 musculus ma
304	7	2.1	329	2	Q986Z1_RHIL0	Q8ju20 lumby skin	377	7	2.1	382	2	Q4IZG7_AZOVY	Q4izg7 azotobacter
305	7	2.1	331	2	Q54H04_DICDI	Q986z1 rhizobium 1	378	7	2.1	383	2	Q4IILD_GIBZE	Q4ilid gibberella
306	7	2.1	331	2	Q19173_CABER	Q54h04 dictyosteli	379	7	2.1	383	2	Q4IYV1_AZOVY	Q4iyv1 azotobacter
307	7	2.1	331	2	Q7NEU0_GLOVI	Q19173 caenorhabdi	380	7	2.1	386	2	Q6AYH0_RAT	Q6ayh0 ratulus norv
308	7	2.1	332	2	Q86UT8_HUMAN	Q7nel0 gloeobacter	381	7	2.1	388	2	Q8VYU8_9ACTO	Q8vyu8 9actro
309	7	2.1	333	1	Y2204_WOLISU	Q8eub8 homo sapien	382	7	2.1	390	2	Q5LRR8_SILPO	Q5lrr8 silicibacte
310	7	2.1	333	2	Q4N0U6_9DELT	Q7mj14 wolinnella s	383	7	2.1	392	2	Q8KIN8_THRSM	Q8kin8 thryonomyx
311	7	2.1	334	2	Q56D13_TPIWO	Q4n0u6 anaeromyxob	384	7	2.1	392	2	Q8KIO8_9HYST	Q8ki08 petromys ty
312	7	2.1	334	2	Q4QV85_9TELE	Q56d13 triticum mo	385	7	2.1	393	2	Q6AAV1_PROAC	Q6aav1 propionibac
313	7	2.1	336	2	Q4QV85_9TELE	Q4qv85 prochloridus	386	7	2.1	394	2	Q8KNC8_MICRC	Q8knc8 micromonos
314	7	2.1	336	2	Q7XVK0_ORYSA	Q4qv85 acetorhyn	387	7	2.1	394	2	Q8VIE8_RAT	Q8vie8 ratulus norv
315	7	2.1	337	2	Q7O286_ANOGA	Q7xvk0 oryza sativ	388	7	2.1	395	2	Q8VIE8_RAT	Q8vie8 ratulus norv
316	7	2.1	339	2	Q7O286_ANOGA	Q7o286 anopheles g	389	7	2.1	399	2	Q8N772_HUMAN	Q8n772 homo sapien
317	7	2.1	341	2	Q8A703_BACTN	Q7o286 anopheles g	390	7	2.1	400	2	Q6LEB3_YEAST	Q6leb3 saccharomyc
318	7	2.1	341	2	Q73IK1_WOLPM	Q73ik1 bacteroides	391	7	2.1	401	2	Q63M80_BURPS	Q63m80 burkholderi
319	7	2.1	341	2	Q8JTX8_LSDV	Q73ik1 wolbachia p	392	7	2.1	401	2	Q62D43_BURMA	Q62d43 burkholderi
320	7	2.1	341	2	Q91MZ1_LSDV	Q8jtx8 lumby skin	393	7	2.1	404	2	Q82IHS_STRAW	Q82ihs streptomyce
321	7	2.1	343	2	Q61HB4_CABER	Q91mz1 lumby skin	394	7	2.1	406	2	Q9AUD8_ORYSA	Q9aud8 oryza sativ
322	7	2.1	343	2	Q6NM87_ARATH	Q61hb4 caenorhabdi	395	7	2.1	408	2	Q4JOZ5_AZOVY	Q4joz5 azotobacter
323	7	2.1	343	2	Q8R0W2_MOUSE	Q6nm87 arabidopsis	396	7	2.1	410	2	Q9PLM2_CHLNU	Q9plm2 chlamydia m

397	7	2.1	411	2	Q9NP81_LEIMA	Q9NF81_leishmania	470	7	2.1	480	2	Q7CZV1_AGRFS	Q7CZV1_agrobacteri
398	7	2.1	413	2	Q9LYC2_ARATH	Q9LYC2_arabidopsis	471	7	2.1	486	2	Q7SIF4_ORYSA	Q7SIF4_oryza sativ
399	7	2.1	415	2	Q4ZE47_GCAUD	Q4ZE47_bacterioph	472	7	2.1	487	2	Q9VZ97_DROME	Q9VZ97_drosophila
400	7	2.1	415	2	Q6A6B9_PROAC	Q6A6B9_propionibac	473	7	2.1	487	2	Q6Y154_9ASTR	Q6Y154_lactuca sal
401	7	2.1	418	1	MTR_HABFIN	P44614_haemophilus	474	7	2.1	490	2	Q4KCP0_PSEFS	Q4KCP0_pseudomonas
402	7	2.1	418	2	Q4ONQ4_HABFS	Q4QND4_haemophilus	475	7	2.1	492	2	Q4HN36_CAMLA	Q4HN36_campylobact
403	7	2.1	419	2	Q55XU1_CRYNE	Q55XU1_cryptococcu	476	7	2.1	492	2	Q9A4P0_CAUCR	Q9A4P0_caulobacter
404	7	2.1	419	2	Q5KM51_CRYNE	Q5KM51_cryptococcu	477	7	2.1	493	2	Q9A4F0_ORYSA	Q9A4F0_oryza sativ
405	7	2.1	419	2	Q89M64_BRATA	Q89M64_bradyrhizob	478	7	2.1	493	2	Q4V912_BRARE	Q4V912_b Bradydiano
406	7	2.1	427	2	Q83410_ENTFA	Q83410_enterococcu	479	7	2.1	495	2	Q75AL8_ASHGO	Q75AL8_ashbya goss
407	7	2.1	428	2	Q52DX6_MAGGR	Q52DX6_magnaporthe	480	7	2.1	496	2	Q96119_DROME	Q96119_drosophila
408	7	2.1	428	2	Q4UDM6_RICPE	Q4UDM6_rickettsia	481	7	2.1	496	2	Q9VX74_DROME	Q9VX74_drosophila
409	7	2.1	428	2	Q8Z716_SALT1	Q8Z716_salmonella	482	7	2.1	500	2	Q91KGI_MESCR	Q91KGI_mesembryant
410	7	2.1	428	2	Q8ZPG6_SALTY	Q8ZPG6_salmonella	483	7	2.1	501	2	Q9BUD5_HUMAN	Q9BUD5_homo sapien
411	7	2.1	429	2	Q5BRT7_EMENT	Q5BRT7_aspergillus	484	7	2.1	501	2	Q92X18_RHIME	Q92X18_rhizobium m
412	7	2.1	430	2	Q88NK6_PSEPK	Q88NK6_pseudomonas	485	7	2.1	504	2	Q951K5_MACPA	Q951K5_mactanomonas
413	7	2.1	431	2	Q4RTIS_TETNG	Q4RTIS_tetradomonas	486	7	2.1	504	2	Q5GZL9_XANOR	Q5GZL9_xanthomonas
414	7	2.1	433	1	YBL4_YEAST	P38211_saccharomyc	487	7	2.1	505	2	Q8IM14_DROME	Q8IM14_drosophila
415	7	2.1	433	2	Q84HT4_STRMA	Q84HT4 Streptomyces	488	7	2.1	505	2	Q8U664_CHICK	Q8U664_gallus gall
416	7	2.1	434	2	Q7NVT0_CHRVO	Q7NVT0_chromobacte	489	7	2.1	506	2	Q4SIC8_TETNG	Q4SIC8_tetradodon n
417	7	2.1	437	2	Q4WPT7_ASPFU	Q4WPT7_aspergillus	490	7	2.1	507	2	AL7A1_MALDO	Q9ZP7_malus domes
418	7	2.1	438	2	Q65RA8_MANSM	Q65RA8_mannheimia	491	7	2.1	507	2	Q8VIF1_RAT	Q8VIF1_rattus norv
419	7	2.1	439	2	Q8AAJ1_BACTN	Q8AAJ1_bacteroides	492	7	2.1	508	1	PD12_ARATH	Q9SR3_arabidopsis
420	7	2.1	442	2	Q8H0O9_THRIT	Q8H0O9_thripes imag	493	7	2.1	509	2	Q8IOQ3_DROME	Q8IOQ3_drosophila
421	7	2.1	443	2	Q9V6N4_DROME	Q9V6N4_drosophila	494	7	2.1	509	2	Q4HA39_9DETO	Q4HA39_deinococcus
422	7	2.1	443	2	Q8UG85_AGRFS	Q8UG85_agrobacteri	495	7	2.1	513	2	Q9HMS7_HALSA	Q9HMS7_halobacteri
423	7	2.1	445	2	Q4Q482_LEIMA	Q4Q482_leishmania	496	7	2.1	513	2	Q5LTA7_SILPO	Q5LTA7_silicibacte
424	7	2.1	445	2	P97001_STRPN	P97001_streptococc	497	7	2.1	513	2	Q8K052_MOUSE	Q8K052_mus musculu
425	7	2.1	448	1	GNTF_BACLI	P46832_bacillus li	498	7	2.1	514	2	Q872D0_NEUCR	Q872D0_neurospora
426	7	2.1	448	2	Q4S5T3_BACST	Q4S5T3_bacillus su	499	7	2.1	515	1	SIR2_CANAL	SIR2_candida alb
427	7	2.1	448	2	Q4MUX8_BACCE	Q4MUX8_bacillus ce	500	7	2.1	516	2	Q5UKJ1_ORYSA	Q5UKJ1_oryza sativ
428	7	2.1	448	2	Q6HPK7_BACHK	Q6HPK7_bacillus th	501	7	2.1	517	2	Q4WFK6_ASPFU	Q4WFK6_aspergillus
429	7	2.1	448	2	Q81VN2_BACAN	Q81VN2_bacillus an	502	7	2.1	517	2	Q8KY45_STRCU	Q8KY45_streptomyces
430	7	2.1	448	2	Q63H39_BACCC	Q63H39_bacillus ac	503	7	2.1	518	2	Q7Y0Y8_ORYSA	Q7Y0Y8_oryza sativ
431	7	2.1	448	2	Q65CW3_BACLD	Q65CW3_bacillus li	504	7	2.1	518	2	Q6DG87_BRARE	Q6DG87_bradycydanio
432	7	2.1	450	2	Q75AOT7_ASHGO	Q75AOT7_ashbya goss	505	7	2.1	522	2	Q8NP67_CORGL	Q8NP67_corynebacte
433	7	2.1	451	2	Q67NE1_SYMTA	Q67NE1_erythrobacte	506	7	2.1	524	2	Q6OSY5_CABER	Q6OSY5_caenorhabdi
434	7	2.1	452	2	Q7YF45_9BIVA	Q7YF45_venenuplis	507	7	2.1	524	2	Q86385_9RHAB	Q86385_rabies viru
435	7	2.1	452	2	Q7YF47_9BIVA	Q7YF47_venenuplis	508	7	2.1	524	2	Q86393_9RHAB	Q86393_rabies viru
436	7	2.1	452	2	Q7YF50_9BIVA	Q7YF50_venenuplis	509	7	2.1	524	2	Q86404_9RHAB	Q86404_rabies viru
437	7	2.1	452	2	Q7YF51_9BIVA	Q7YF51_venenuplis	510	7	2.1	524	2	Q9DDK1_9RHAB	Q9DDK1_rabies viru
438	7	2.1	452	2	Q7YF52_9BIVA	Q7YF52_venenuplis	511	7	2.1	524	2	Q6DPL0_XENLA	Q6DPL0_xenopus lae
439	7	2.1	452	2	Q8WF40_9BIVA	Q8WF40_venenuplis	512	7	2.1	525	2	Q4ZYF1_PSEBY	Q4ZYF1_pseudomonas
440	7	2.1	453	2	Q756A3_ASHGO	Q756A3_ashbya goss	513	7	2.1	525	2	Q5P8K4_AZOSE	Q5P8K4_azoarcus sp
441	7	2.1	453	2	Q61P95_CABER	Q61P95_caenorhabdi	514	7	2.1	526	2	Q6M477_CORGL	Q6M477_corynebacte
442	7	2.1	454	2	Q9U3P6_CABEL	Q9U3P6_caenorhabdi	515	7	2.1	527	2	Q65XTH_ORYSA	Q65XTH_oryza sativ
443	7	2.1	458	2	Q26297_METTH	Q26297_methanobact	516	7	2.1	528	2	Q4ZZX6_PSEBY	Q4ZZX6_pseudomonas
444	7	2.1	459	2	Q4S6I5_METNG	Q4S6I5_tetradodon n	517	7	2.1	530	2	Q691M5_ORYSA	Q691M5_oryza sativ
445	7	2.1	460	2	Q5VP94_ORYSA	Q5VP94_oryza sativ	518	7	2.1	532	1	LGPI_MOUSE	Q99J23_mus musculu
446	7	2.1	460	2	Q803K4_BRARE	Q803K4_bradycydanio	519	7	2.1	532	2	Q6FRE9_CANCA	Q6FRE9_candida gla
447	7	2.1	462	2	Q70JW8_BACAN	Q70JW8_bacillus an	520	7	2.1	532	2	Q9VCQ0_DROME	Q9VCQ0_drosophila
448	7	2.1	463	2	Q34474_BACSV	Q34474_bacillus su	521	7	2.1	532	2	Q94CQ5_ORYSA	Q94CQ5_oryza sativ
449	7	2.1	464	2	Q722X6_LISMF	Q722X6_listeria mo	522	7	2.1	534	2	Q73EG1_BACCI	Q73EG1_bacillus ce
450	7	2.1	464	2	Q836T7_ENTPA	Q836T7_enterococcu	523	7	2.1	537	1	Q4KXN9_PSEFS	Q4KXN9_pseudomonas
451	7	2.1	464	2	Q819F4_LISMO	Q819F4_listeria in	524	7	2.1	539	1	RIPK2_MOUSE	P58801_mus musculu
452	7	2.1	464	2	Q92E77_LISIN	Q92E77_listeria in	525	7	2.1	539	2	Q991L2_MOUSE	Q991L2_mus musculu
453	7	2.1	465	2	Q4ZYM6_PSEBY	Q4ZYM6_pseudomonas	526	7	2.1	539	2	Q547H1_MOUSE	Q547H1_mus musculu
454	7	2.1	467	2	Q97U81_SULSO	Q97U81_sulfolobus	527	7	2.1	540	1	RIPK2_HUMAN	Q43333_h receptor-
455	7	2.1	468	2	Q5PAM0_ANAMM	Q5PAM0_anaplasma m	528	7	2.1	540	2	Q88BX4_PSEEM	Q88BX4_pseudomonas
456	7	2.1	469	1	NUZM_YAKLI	Q9D6C8_yarrowia li	529	7	2.1	541	2	Q9WU61_RAT	Q9WU61_rattus norv
457	7	2.1	469	2	Q4MUD4_BACCE	Q4MUD4_bacillus ce	530	7	2.1	541	2	Q6H0U5_RAT	Q6H0U5_rattus norv
458	7	2.1	469	2	Q6HKH3_BACHK	Q6HKH3_bacillus th	531	7	2.1	546	2	Q5B860_EMENT	Q5B860_aspergillus
459	7	2.1	469	2	Q81F82_BACCR	Q81F82_bacillus ce	532	7	2.1	549	2	Q4SNZ3_TETNG	Q4SNZ3_tetradodon n
460	7	2.1	469	2	Q73AD4_BACCI	Q73AD4_bacillus ac	533	7	2.1	550	2	Q6FX45_CANCA	Q6FX45_candida gla
461	7	2.1	469	2	Q81NB5_BACAN	Q81NB5_bacillus an	534	7	2.1	550	2	Q4KXU3_HUMAN	Q4KXU3_homo sapien
462	7	2.1	469	2	Q639G8_BACCC	Q639G8_bacillus ce	535	7	2.1	551	2	Q96S66_HUMAN	Q96S66_homo sapien
463	7	2.1	469	2	Q63D32_BACCC	Q63D32_bacillus ce	536	7	2.1	551	2	Q7R3Y0_GITALA	Q7R3Y0_giardia lam
464	7	2.1	470	2	Q9N4U9_CABEL	Q9N4U9_caenorhabdi	537	7	2.1	556	2	Q6P9H7_HUMAN	Q6P9H7_homo sapien
465	7	2.1	470	2	Q50510_XENTR	Q50510_xenopus tro	538	7	2.1	558	2	Q6AXD5_MOUSE	Q6AXD5_mus musculu
466	7	2.1	472	2	Q4UIF3_TTHEAN	Q4UIF3_theileria a	539	7	2.1	558	2	Q6YNN4_LACHI	Q6YNN4_lactobacillu
467	7	2.1	474	2	Q41AW9_GIBZE	Q41AW9_gibberella	540	7	2.1	572	2	Q8UBH4_AGRFS	Q8UBH4_agrobacteri
468	7	2.1	475	2	Q9M3D9_ARATH	Q9M3D9_arabidopsis	541	7	2.1	574	2	Q6FKX3_CANCA	Q6FKX3_candida gla
469	7	2.1	477	2	Q4WAQ5_ASPFU	Q4WAQ5_aspergillus	542	7	2.1	577	2	Q8KAB6_CHLTE	Q8KAB6_chlorobium

543	7	2.1	577	2	08K338_CHLRE	08K338_chlorobium	616	7	2.1	742	2	04H347_CIOIN	04H347_ciona_intes
544	7	2.1	578	2	06PV2_MOUSE	06PV2_mus_musculu	617	7	2.1	750	2	05A2H1_CANAL	05A2H1_candida_alb
545	7	2.1	579	2	08T7M1_PHYPO	08T7M1_physarum_po	618	7	2.1	757	2	06TFT7_ERWAM	06TFT7_erwinia_amy
546	7	2.1	582	2	08PRA6_XANAC	08PRA6_xanthomonas	619	7	2.1	759	2	05INS3_MAGGR	05INS3_magnaporthe
547	7	2.1	585	2	ENV_MPMV	P07575 simian maso	620	7	2.1	765	2	Q20479_CAEEL	Q20479_caenorhabdi
548	7	2.1	586	2	Q77TG6_MPMV	Q77YG6 simian maso	621	7	2.1	769	2	Q4PHM4_USTMA	Q4PHM4_ustilago_ma
549	7	2.1	587	1	ENV_SRV1	P04027 simian retr	622	7	2.1	775	2	Q5VSJ9_ORYSA	Q5VSJ9_oryza_sativ
550	7	2.1	588	2	001465_CAEEL	P01465 caenorhabdi	623	7	2.1	777	2	06PKS8_HUMAN	06PKS8_homo_sapien
551	7	2.1	591	1	CALX_MOUSE	P35565 ratu musculu	624	7	2.1	786	2	Q6BGH4_PARTE	Q6BGH4_parmectum
552	7	2.1	591	1	CALX_MOUSE	P35565 ratu musculu	625	7	2.1	789	2	Q6FUT6_CANGA	Q6FUT6_candida_gla
553	7	2.1	591	2	05SUC3_MOUSE	Q5SUC3 mus musculu	626	7	2.1	790	2	Q6B129_DEBBA	Q6B129_debaryomyce
554	7	2.1	591	2	08K3H8_CRIGR	08K3H8_cricetulus	627	7	2.1	791	2	Q5MT99_BACSA	Q5MT99_bacillus_cl
555	7	2.1	593	2	064JP8_GAMPH	Q64JP8 scolecocorp	628	7	2.1	797	2	Q9UTK6_SCHPO	Q9UTK6_schizosacch
556	7	2.1	597	2	054X44_DICDI	Q54X44 dictyosteli	629	7	2.1	799	1	Q4GZD9_9TRYP	Q4GZD9_lypdonema_p
557	7	2.1	600	2	08FPD5_CORER	Q8FPD5 corynebacte	630	7	2.1	801	2	Q9LWV8_ORYSA	Q9LWV8_oryza_sativ
558	7	2.1	602	2	086VJ9_HUMAN	Q86VJ9 homo sapien	631	7	2.1	803	2	Q8S808_ORYSA	Q8S808_oryza_sativ
559	7	2.1	604	1	PGH2_CAYPO	P70682 cavia porce	632	7	2.1	814	2	Q6NUT7_BRARE	Q6NUT7_brachydanio
560	7	2.1	605	1	PCOA_ECOLI	Q47452 escherichia	633	7	2.1	814	2	Q6NUT7_BRARE	Q6NUT7_brachydanio
561	7	2.1	605	2	Q71M97_KLEBP	Q71M97 klebsiella	634	7	2.1	815	2	Q72K11_THRT2	Q72K11_thermus_the
562	7	2.1	605	2	Q6MXP4_SBRMA	Q6MXP4 serratia ma	635	7	2.1	818	2	Q5SK21_THRT8	Q5SK21_thermus_the
563	7	2.1	607	2	Q6USP5_KLEBP	Q6USP5 klebsiella	636	7	2.1	819	2	Q70B30_ANOGA	Q70B30_anopheles_g
564	7	2.1	613	2	Q5IKC8_MAGGR	Q5IKC8 magnaporthe	637	7	2.1	835	2	Q4WKX7_ASFPF	Q4WKX7_aspergillus
565	7	2.1	613	2	Q98C87_RHILLO	Q98C87 rhizodium_1	638	7	2.1	842	2	Q4T648_TERNNG	Q4T648_tetradon n
566	7	2.1	615	2	Q5N0S8_SYNP6	Q5N0S8 synechococc	639	7	2.1	845	2	Q5BRG8_EMENI	Q5BRG8_emerit
567	7	2.1	616	2	Q4R7A7_MACFA	Q4R7A7 macaca fasc	640	7	2.1	847	2	Q5SKP7_CANPA	Q5SKP7_canis_famil
568	7	2.1	617	2	Q8VDQ7_MOUSE	Q8VDQ7 mus musculu	641	7	2.1	855	2	Q54R00_DICDI	Q54R00_dictyosteli
569	7	2.1	619	2	Q51PM8_MAGGR	Q51PM8 magnaporthe	642	7	2.1	856	2	Q5RE45_PONPY	Q5RE45_pongo_pygma
570	7	2.1	619	2	Q4PP05_USTMA	Q4PP05_ustilago_ma	643	7	2.1	870	1	GP155_HUMAN	Q723F1_homo_sapien
571	7	2.1	619	2	Q9VUK5_DROME	Q9VUK5 drosophila	644	7	2.1	870	2	Q4G0V6_HUMAN	Q4G0V6_homo_sapien
572	7	2.1	622	2	Q5A120_CANAL	Q5A120 candida alb	645	7	2.1	872	1	GP155_FONPY	Q5X9A7_pongo_pygma
573	7	2.1	623	2	Q6T448_LEIMA	Q6T448 leishmania	646	7	2.1	873	2	Q5AXH0_EMENI	Q5AXH0_aspergillus
574	7	2.1	624	2	Q9BNC2_9MYRI	Q9BNC2 abscission mag	647	7	2.1	878	2	Q9USU3_SCHPO	Q9USU3_schizosacch
575	7	2.1	624	2	Q4SRN5_TERNNG	Q4SRN5 tetradon n	648	7	2.1	890	2	Q5VUB5_HUMAN	Q5VUB5_homo_sapien
576	7	2.1	624	2	Q4UC10_THEAN	Q4UC10 theileria a	649	7	2.1	890	2	Q5RBD3_PONPY	Q5RBD3_pongo_pygma
577	7	2.1	634	2	Q9YCH6_ABRER	Q9YCH6 aeropyrum p	650	7	2.1	892	2	Q9Y438_HUMAN	Q9Y438_homo_sapien
578	7	2.1	643	2	Q7UV17_RHOBA	Q7UV17 rhodospirell	651	7	2.1	900	2	Q6AX42_XENLA	Q6AX42_xenopus_lae
579	7	2.1	646	2	Q9KMZ5_VIBCH	Q9KMZ5 vibrio chol	652	7	2.1	912	2	Q61KTY_CABER	Q61KTY_caenorhabdi
580	7	2.1	648	2	Q55RR9_CRYNE	Q55RR9 cryptococcu	653	7	2.1	914	1	PBPA_BACSV	P39793_bacillus_su
581	7	2.1	648	2	Q5KSE1_CRYNE	Q5KSE1 cryptococcu	654	7	2.1	929	1	Q5PYG6_SALPA	Q5PYG6_salmonella
582	7	2.1	650	1	LIRB1_HUMAN	Q5H16 h leukocyte	655	7	2.1	941	2	Q73Z06_MYCPA	Q73Z06_mycobacteri
583	7	2.1	650	2	Q8NAB4_HUMAN	Q8NAB4 homo sapien	656	7	2.1	941	2	Q5H722_FUGRU	Q5H722_fugu_rubrip
584	7	2.1	650	2	Q4V729_XENLA	Q4V729 xenopus lae	657	7	2.1	943	1	UVRA_STRPN	P63384_streptococc
585	7	2.1	656	2	Q9Y114_DROME	Q9Y114 drosophila	658	7	2.1	946	2	Q44825_CAEEL	Q44825_caenorhabdi
586	7	2.1	660	2	Q8ZNM7_SALTY	Q8ZNM7 salmonella	659	7	2.1	946	2	Q827G6_STRAM	Q827G6_streptomyce
587	7	2.1	675	1	HPBA_XANAC	Q8PH20 xanthomonas	660	7	2.1	946	2	Q9B1A3_CAEEL	Q9B1A3_caenorhabdi
588	7	2.1	675	1	HPBA_XANAC	Q8PH20 xanthomonas	661	7	2.1	947	2	Q9B1A3_CAEEL	Q9B1A3_caenorhabdi
589	7	2.1	675	2	Q4UYB5_XANCP	Q4UYB5 xanthomonas	662	7	2.1	951	2	Q7Z268_HELAM	Q7Z268_helicoverpa
590	7	2.1	679	2	Q6C335_YARLI	Q6C335 yarrowia li	663	7	2.1	951	2	Q86Q16_HELAM	Q86Q16_helicoverpa
591	7	2.1	694	2	Q4MOR4_ASFPF	Q4MOR4 aspergillus	664	7	2.1	951	2	Q8MUT5_HELAM	Q8MUT5_helicoverpa
592	7	2.1	694	2	Q7UNZ3_RHOBA	Q7UNZ3 rhodospirell	665	7	2.1	951	2	Q8MUT5_HELAM	Q8MUT5_helicoverpa
593	7	2.1	695	2	Q7S5Z3_NEUCR	Q7S5Z3 neurospora	666	7	2.1	953	2	Q5NOD4_SYNP6	Q5NOD4_synechococc
594	7	2.1	695	2	Q55XL5_CRYNE	Q55XL5 cryptococcu	667	7	2.1	954	1	GCSP_AGRTS	Q82F66_agrobacteri
595	7	2.1	695	2	Q5KMC0_CRYNE	Q5KMC0 cryptococcu	668	7	2.1	954	1	GCSP_RHIME	Q92G11_rhizobium_m
596	7	2.1	695	2	Q32508_LYCCR	Q32508 lycium cest	669	7	2.1	954	1	GCSP_SYNEL	Q8D133_synechococc
597	7	2.1	695	2	Q32700_NOLSP	Q32700 nolana spat	670	7	2.1	954	1	GCSP_VIBPA	Q87J05_vibrio_para
598	7	2.1	695	2	Q33168_BSOLA	Q33168 salpiglossi	671	7	2.1	954	1	GCSP_VIBPV	Q87J97_vibrio_vuln
599	7	2.1	696	2	Q17479_HYACE	Q17479 hyalophora	672	7	2.1	954	2	GCSP_VIBVY	Q7me99_vibrio_vuln
600	7	2.1	700	2	Q4R6H5_MACFA	Q4R6H5 macaca fasc	673	7	2.1	954	2	Q4KA16_PSEB5	Q4KA16_pseudomonas
601	7	2.1	701	2	Q6J2B2_PSEYM	Q6J2B2 pseudomonas	674	7	2.1	955	2	Q5DZM3_VIBF1	Q5DZM3_vibrio_fisc
602	7	2.1	708	2	Q8ZXU4_PYPAR	Q8ZXU4 pyrobaculum	675	7	2.1	956	1	GCSP_ECO57	Q8XD33_escherichia
603	7	2.1	711	2	Q6LWFS_LACP1	Q6LWFS lactobacill	676	7	2.1	956	1	GCSP_ECOL6	Q8F6E7_escherichia
604	7	2.1	715	2	Q8WMS5_9TROC	Q8WMS5 okpopleura	677	7	2.1	956	1	GCSP_ECOLI	P33195_escherichia
605	7	2.1	716	2	Q87CY5_XYLPF	Q87CY5 xylophila fas	678	7	2.1	956	1	GCSP_SALTY	Q82K30_salmonella
606	7	2.1	717	2	Q9VLC6_DROME	Q9VLC6 drosophila	679	7	2.1	956	1	GCSP_SALTY	Q8ZMT6_salmonella
607	7	2.1	719	2	Q5YTH1_NOCFA	Q5YTH1 nocardia fa	680	7	2.1	957	1	GCSP2_PSEBP	Q83G42_salmonella
608	7	2.1	719	2	Q7Q858_ANOGA	Q7Q858 anopheles g	681	7	2.1	957	1	GCSP2_PSEBP	Q83G42_salmonella
609	7	2.1	724	2	Q4RMA0_TERNNG	Q4RMA0 tetradon n	682	7	2.1	958	1	Q6D974_BRWCT	Q6D974_erwinia_car
610	7	2.1	726	2	Q8GFR4_CITFR	Q8GFR4 citrobacter	683	7	2.1	958	1	GCSP2_PSEAR	Q9HKT7_pseudomonas
611	7	2.1	728	2	Q81EM1_PLAF7	Q81EM1 plasmodium	684	7	2.1	958	1	GCSP_PHOIL	Q7N139_phocorhabdu
612	7	2.1	730	2	Q9B698_EXAAL	Q9B698 eracium affi	685	7	2.1	958	2	GCSP_YERPR	Q8Z118_yersinia_pe
613	7	2.1	730	2	Q6PFN2_BRARE	Q6PFN2 brachydanio	686	7	2.1	958	2	Q6MPZ6_BDBBA	Q6MPZ6_bdellovibri
614	7	2.1	730	2	Q80ZD0_BRARE	Q80ZD0 brachydanio	687	7	2.1	959	1	GCSP_STNFX	Q7N335_synechococc
615	7	2.1	732	1	ACPH_HUMAN	P13798 homo sapien	688	7	2.1	959	2	Q666R7_YERPS	Q666R7_yersinia_ps

689	7	2.1	963	1	TRES_THETH	066458	thermus the	762	7	2.1	1398	2	06E2N4_BRARE	06e2r4	brachydanio
690	7	2.1	963	2	Q8BX19_MOUSE	Q8bx19	mus musculus	763	7	2.1	1415	2	08A9R6_BACTN	08a9r6	bacteroides
691	7	2.1	964	1	GCSP_ROMA	Q7v9k4	prochloroco	764	7	2.1	1422	2	Q95KU4_CANFA	095ku4	cane famli
692	7	2.1	965	2	Q7WU15_THETH	Q7wu15	thermus the	765	7	2.1	1447	2	Q4WPJ3_ASPEU	04wpj3	aspeggillius
693	7	2.1	965	2	Q9RA59_THETH	Q9ras9	thermus cal	766	7	2.1	1471	2	Q41399_GIBZE	041399	gibberella
694	7	2.1	965	2	Q4FTK9_GGAMM	Q4ftk9	thermus the	767	7	2.1	1487	2	Q03626_RAT	003626	rattus norv
695	7	2.1	965	2	Q5SL15_THETH	Q5sl15	thermus the	768	7	2.1	1510	2	Q4S9X7_TETNG	04s9x7	tetradodon n
696	7	2.1	969	2	Q7WR47_BORER	Q7wr47	bordeletia	769	7	2.1	1543	2	Q7Z219_HUMAN	07z219	homo sapien
697	7	2.1	969	2	Q7U2J5_PROMP	Q7uzj5	prochloroco	770	7	2.1	1543	2	Q8W2W4_HUMAN	08w2w4	homo sapien
698	7	2.1	972	2	Q4VAK4_HUMAN	Q4vak4	homo sapien	771	7	2.1	1552	2	Q49370_ARATH	049370	arabidopsis
699	7	2.1	972	2	Q5NZ93_AZOSZ	Q5nz93	azotarcus sp	772	7	2.1	1560	2	Q88323_MOUSE	088323	mus musculus
700	7	2.1	975	1	GCSP_XANCP	Q8pbk7	xanthomonas	773	7	2.1	1560	2	Q925J9_MOUSE	0925j9	mus musculus
701	7	2.1	975	2	Q4URZ4_XANCP	Q4urz4	xanthomonas	774	7	2.1	1560	2	Q925K0_MOUSE	0925k0	mus musculus
702	7	2.1	975	2	Q4LZ94_SBURK	Q4lzz4	xanthomonas	775	7	2.1	1581	1	PPRE_HUMAN	PPRE	human
703	7	2.1	975	2	Q6ZFN1_BURMA	Q6zfn1	burkholderi	776	7	2.1	1581	2	Q5RES4_PONPY	05res4	pongo pygma
704	7	2.1	975	2	Q63PL2_BURPS	Q6zfn1	burkholderi	777	7	2.1	1585	2	Q8UBT4_AGRY5	08ubt4	agrobacteri
705	7	2.1	977	1	GCSP_XANAC	Q8p312	xanthomonas	778	7	2.1	1620	2	Q24984_GIALA	024984	giardia lam
706	7	2.1	977	2	Q8WRU7_9TRYP	Q8wrut	thermoplasma	779	7	2.1	1630	2	Q70XB2_GIALA	070xb2	giardia lam
707	7	2.1	979	1	PPRPN_BOVIN	P56722	bos taurus	780	7	2.1	1630	1	NHS_HUMAN	NHS	human
708	7	2.1	979	2	Q4PGJ9_USITMA	Q4pgj9	usellago ma	781	7	2.1	1704	2	Q4IZD0_GIBZE	04izd0	gibberella
709	7	2.1	982	1	GCSP_RALSO	Q8xue8	raistecnia s	782	7	2.1	1781	2	Q86KX8_DICD1	086kx8	dicyostelli
710	7	2.1	982	2	Q6CHEO_YARLI	Q6cheo	yarrovicia ii	783	7	2.1	1785	2	Q7YYR5_CRYPV	07yyr5	cryptospori
711	7	2.1	994	2	Q57K62_SALCH	Q57k62	salmonella	784	7	2.1	1821	2	Q7PSP2_AMOCA	07psp2	anopheles g
712	7	2.1	996	2	Q4UHT9_THEAN	Q4uht9	thelateria a	785	7	2.1	1868	2	Q6BNV2_DEBHA	06bnv2	debrayomyce
713	7	2.1	1002	1	SYIM_YEAST	P48526	saccharomyce	786	7	2.1	2025	2	Q4Q534_LEIMA	04q534	leishmania
714	7	2.1	1009	2	Q7SE77_NEUCR	Q7sey7	neurospora	787	7	2.1	2055	2	Q7XSV2_ARATH	07xsv2	arabidopsis
715	7	2.1	1009	2	Q5GWX0_XANOR	Q5gwax0	xanthomonas	788	7	2.1	2061	2	Q91TV5_ARATH	091tv5	arabidopsis
716	7	2.1	1012	2	Q8PD1_HUMAN	Q75665	homo sapien	789	7	2.1	2087	2	Q8MX12_LEIMA	08mx12	leishmania
717	7	2.1	1019	2	Q8BJQ7_MOUSE	Q8bjq7	mus musculus	790	7	2.1	2301	2	Q5LI96_GEOGA	05li96	geobacillus
718	7	2.1	1020	1	GCSP_HITMAN	P23378	homo sapien	791	7	2.1	2378	2	Q5OXT0_ENTHI	05oxt0	entamoeba h
719	7	2.1	1025	1	GCSP_MOUSE	Q91w43	mus musculus	792	7	2.1	2623	2	Q6WR10_HUMAN	06wr10	homo sapien
720	7	2.1	1031	2	Q5IZM7_FELCA	Q5izm7	felis silve	793	7	2.1	2747	2	Q9LB00_AERSA	09lb00	aeromonas s
721	7	2.1	1032	1	Q8HZ52_FELCA	Q8hz52	felis silve	794	7	2.1	2787	1	TELI_YEAST	TELI	yeast
722	7	2.1	1032	1	MET18_YEAST	P40469	saccharomyce	795	7	2.1	2961	2	Q7P389_FUSNV	07p389	fusobacteri
723	7	2.1	1036	2	Q5VYQ3_HUMAN	Q5vyq3	homo sapien	796	7	2.1	3322	2	Q6BEO3_CAEEL	06beo3	caenorhabdi
724	7	2.1	1057	2	Q7SAD5_NEUCR	Q7sad5	neurospora	797	7	2.1	3405	2	Q6BRO5_CAEEL	06bro5	caenorhabdi
725	7	2.1	1057	2	Q8MRS3_DROME	Q8mr3	drosophila	798	7	2.1	3436	2	Q86NPF_CAEEL	086nfp	caenorhabdi
726	7	2.1	1057	2	Q86YU6_DICD1	Q86yue6	dicyostelli	799	7	2.1	3436	2	Q86NPF_CAEEL	086nfp	caenorhabdi
727	7	2.1	1062	2	Q5SFC4_STRB1	Q5sfc4	streptomyce	800	7	2.1	3436	2	Q18290_CAEEL	018290	caenorhabdi
728	7	2.1	1067	2	Q6CSG8_KLULA	Q6csg8	kluyveromyce	801	7	2.1	3522	2	Q86NF7_CAEEL	086nf7	caenorhabdi
729	7	2.1	1070	2	Q9SVJ6_ARATH	Q9svj6	arabidopsis	802	7	2.1	3821	2	Q7NUJ3_CHRYO	07nuj3	chrysothabate
730	7	2.1	1084	2	Q5IKZ9_MAGGR	Q5ikz9	magnaporthe	803	7	2.1	4091	2	Q96Z04_PLAF7	096z04	plasmodium
731	7	2.1	1085	1	IFH1_YEAST	P39520	saccharomyce	804	7	2.1	4340	2	Q30764_9ACTO	030764	9actomyce
732	7	2.1	1100	2	Q7SG89_NEUCR	Q7sg89	neurospora	805	7	2.1	4410	2	Q6EUT7_CAEEL	06eut7	caenorhabdi
733	7	2.1	1101	2	Q59H95_HUMAN	Q59h95	homo sapien	806	7	2.1	4545	2	Q61291_MOUSE	061291	mus musculus
734	7	2.1	1128	2	Q9DFU8_XENLA	Q9dfu8	xenopus lae	807	7	2.1	4862	2	Q5R127_BRARE	05r127	brachydanio
735	7	2.1	1134	2	Q6ZPY0_MOUSE	Q6zpy0	mus musculus	808	7	2.1	4944	2	Q7K7B6_CAEEL	07k7b6	caenorhabdi
736	7	2.1	1142	2	Q4QSK4_LEIMA	Q4qsk4	leishmania	809	7	2.1	4955	2	Q867D9_CAEEL	0867d9	caenorhabdi
737	7	2.1	1142	2	Q7SZV2_XENLA	Q7szv2	xenopus lae	810	7	2.1	5359	2	Q5VXR4_SACER	05vxr4	saccharopol
738	7	2.1	1161	2	Q7KQV5_DROME	Q7kqv5	drosophila	811	7	2.1	6145	2	Q93H84_STRAM	093h84	streptomyce
739	7	2.1	1185	2	Q5BJ30_MOUSE	Q5bj30	mus musculus	812	7	2.1	6239	2	Q9S0R7_STEAM	09s0r7	steptomyce
740	7	2.1	1186	2	Q4PI08_USITMA	Q4pi08	usellago ma	813	7	2.1	8402	2	Q4R8R9_TETNG	04r8r9	tetradodon n
741	7	2.1	1201	1	PER3_HUMAN	P56645	homo sapien	814	7	1.8	21	2	Q9UMU6_HUMAN	09umu6	homo sapien
742	7	2.1	1210	2	Q5H8X5_HUMAN	Q5h8x5	homo sapien	815	7	1.8	22	2	Q9T2R5_SOLTV	09t2r5	solanum tub
743	7	2.1	1244	1	PER1_RAT	Q8ch15	rattus norv	816	7	1.8	25	2	Q6U282_HUMAN	06u282	homo sapien
744	7	2.1	1254	2	Q4QAP3_LEIMA	Q4qap3	leishmania	817	7	1.8	26	2	Q9QVZ8_9MURI	09qvz8	mus sp. b c
745	7	2.1	1269	1	FLI1_HUMAN	Q13045	homo sapien	818	7	1.8	29	2	Q88224_MOUSE	088224	mus musculus
746	7	2.1	1269	2	Q5RA49_PONPY	Q5ra49	pongo pygma	819	7	1.8	30	2	Q34897_9MEYA	034897	lasiorhinus
747	7	2.1	1271	2	Q8CHRI_MOUSE	Q8chri	mus musculus	820	7	1.8	32	2	Q4YM48_PLABE	04ym48	plasmodium
748	7	2.1	1271	2	Q17517_CAEEL	Q17517	caenorhabdi	821	7	1.8	35	2	Q6QNA6_HUMAN	06qna6	homo sapien
749	7	2.1	1281	2	Q7RFM4_PLAYO	Q7rfm4	plasmodium	822	7	1.8	35	2	Q8M1N3_9DYTI	08m1n3	limbodesus
750	7	2.1	1285	2	Q8K3T3_SPAJD	Q8k3t3	spalax juda	823	7	1.8	36	2	Q25409_HELPY	025409	helpyobate
751	7	2.1	1290	1	PER1_HUMAN	Q15534	homo sapien	824	7	1.8	37	2	Q8FPD8_LEPIN	08fpd8	leptocystira
752	7	2.1	1291	1	PER1_MOUSE	Q35973	mus musculus	825	7	1.8	39	2	Q4Z7A6_PLABE	04z7a6	plasmodium
753	7	2.1	1291	2	Q5CWZ4_CRYPV	Q5cwz4	cryptospori	826	7	1.8	39	2	Q98RB8_MYCPU	098rb8	mycoplasma
754	7	2.1	1291	2	Q5NCG2_MOUSE	Q5ncg2	mus musculus	827	7	1.8	40	2	Q6XYV1_SPTUO	06xyv1	spiroplasma
755	7	2.1	1312	1	DPOL_PYRSD	Q51134	pyrococcus	828	7	1.8	41	2	Q5BKX2_SCHUA	05bkx2	schistosoma
756	7	2.1	1331	2	Q6A060_MOUSE	Q6a060	mus musculus	829	7	1.8	41	2	Q931M0_HELPY	0931m0	helicobacte
757	7	2.1	1345	2	Q54437_STAMA	Q54437	staphyloche	830	7	1.8	41	2	Q931M5_HELPY	0931m5	helicobacte
758	7	2.1	1345	2	Q51242_MAGGR	Q51242	magnaporthe	831	7	1.8	41	2	Q931M5_HELPY	0931m5	helicobacte
759	7	2.1	1365	2	Q76DY4_CYNPY	Q76dy4	cynops pyrr	832	7	1.8	42	2	Q5BVU2_SCHUA	05bvu2	schistosoma
760	7	2.1	1383	2	Q89232_SALPH	Q89232	canine hiep	833	7	1.8	43	2	Q82949_CHRYI	082949	chriatogoma
761	7	2.1	1398	2	Q6UV33_BRARE	Q6uv33	brachydanio	834	7	1.8	44	2	Q93U23_CHRYI	093u23	chromatium

835	6	1.8	46	2	093LS1_HELPY	0931st helicobacte	908	6	1.8	66	2	08NMN2_STAMM	08nmn2 staphylococ
836	6	1.8	46	2	093LS3_HELPY	0931st helicobacte	909	6	1.8	66	2	099U22_STAMM	099u22 staphylococ
837	6	1.8	46	2	093LS6_HELPY	0931st helicobacte	910	6	1.8	67	2	07Y8G4_9ETH	07y8g4 hemielectroc
838	6	1.8	46	2	093LT0_HELPY	0931st helicobacte	911	6	1.8	67	2	086132_9RNB	086132 vesicular s
839	6	1.8	46	2	093LT1_HELPY	0931st helicobacte	912	6	1.8	68	2	093LL6_NOSP	093ll6 nostoc punc
840	6	1.8	46	2	093LT2_HELPY	0931st helicobacte	913	6	1.8	68	2	08DX22_STRA5	08dx22 streptococ
841	6	1.8	46	2	093LUD_HELPY	0931st helicobacte	914	6	1.8	68	2	05QW8_IDILO	05qw8 idiomarina
842	6	1.8	46	2	093LUT_HELPY	0931st helicobacte	915	6	1.8	68	2	0710T1_JACJA	0710t1 jaculus jac
843	6	1.8	48	2	093LUT_HELPY	0931st helicobacte	916	6	1.8	68	2	098SP3_BRARB	098sp3 brachydanio
844	6	1.8	49	1	093LUT_HELPY	0931st helicobacte	917	6	1.8	70	1	GBG1_DROME	gbg1 drosophila
845	6	1.8	49	2	057C16_BRUB	057c16 bruceella su	918	6	1.8	70	2	054Y08_DROME	054y08 drosophila
846	6	1.8	49	2	08G004_BRUSU	08g004 bruceella su	919	6	1.8	72	2	08T1A1_DICD1	08t1a1 dictyosteli
847	6	1.8	50	2	0570K9_ARATH	0570k9 arabidopsis	920	6	1.8	72	2	0817F6_BACR	0817f6 bacillus ce
848	6	1.8	51	2	09UDD2_HUMAN	09udd2 homo sapien	921	6	1.8	72	2	09HYJ4_PSEAR	09hyj4 pseudomonas
849	6	1.8	51	2	05BZ15_SCHJA	05bz15 schistosoma	922	6	1.8	72	2	071BL6_GRETR	071bl6 simian retr
850	6	1.8	52	1	CD3E_BOVIN	CD3E bos taurus	923	6	1.8	73	2	09XVG6_CAEBL	09xvg6 caenorhabdi
851	6	1.8	52	2	05EJRO_CEPNE	05ejro cepaea nemo	924	6	1.8	73	2	003922_9CAUD	003922 bacterioph
852	6	1.8	52	2	05EJL3_CEPNE	05ejl3 cepaea nemo	925	6	1.8	73	2	085WY1_PINKO	085wy1 pinus korai
853	6	1.8	52	2	05EJL7_CEPNE	05ejl7 cepaea nemo	926	6	1.8	73	2	032310_BACTV	032310 bacillus th
854	6	1.8	52	2	05EJL8_CEPNE	05ejl8 cepaea nemo	927	6	1.8	74	2	06JCJ3_BORBU	06jcj3 borellia bu
855	6	1.8	52	2	05EJL9_CEPNE	05ejl9 cepaea nemo	928	6	1.8	74	2	05P284_AZOSE	05p284 azoarcus sp
856	6	1.8	52	2	05EJL9_CEPNE	05ejl9 cepaea nemo	929	6	1.8	74	2	097PB7_STRPN	097pb7 streptococ
857	6	1.8	52	2	05EJL9_CEPNE	05ejl9 cepaea nemo	930	6	1.8	75	2	05RJ63_HUMAN	05rj63 homo sapien
858	6	1.8	52	2	05EJL9_CEPNE	05ejl9 cepaea nemo	931	6	1.8	75	2	09TTQ1_HORSE	09ttq1 equus caball
859	6	1.8	52	2	05EJL9_CEPNE	05ejl9 cepaea nemo	932	6	1.8	75	2	0941C7_ARATH	0941c7 arabidopsis
860	6	1.8	52	2	05EJL9_CEPNE	05ejl9 cepaea nemo	933	6	1.8	75	2	0570K8_ARATH	0570k8 arabidopsis
861	6	1.8	52	2	05EJL9_CEPNE	05ejl9 cepaea nemo	934	6	1.8	75	2	04V213_BACCE	04v213 bacillus ce
862	6	1.8	52	2	05EJL9_CEPNE	05ejl9 cepaea nemo	935	6	1.8	75	2	0920Z5_RHIME	0920z5 rhizobium m
863	6	1.8	52	2	05EJL9_CEPNE	05ejl9 cepaea nemo	936	6	1.8	76	2	06BUG6_DEBHA	06bug6 debaryomyce
864	6	1.8	52	2	05EJL9_CEPNE	05ejl9 cepaea nemo	937	6	1.8	76	2	024505_DROSOP	024505 drosophila
865	6	1.8	52	2	05EJL9_CEPNE	05ejl9 cepaea nemo	938	6	1.8	76	2	0618M2_CAEBR	0618m2 caenorhabdi
866	6	1.8	52	2	05EJL9_CEPNE	05ejl9 cepaea nemo	939	6	1.8	76	2	04YX67_PLABE	04yx67 plasmodium
867	6	1.8	53	2	05BYS8_SCHJA	05bys8 schistosoma	940	6	1.8	77	2	05NVV9_9ARCH	05nvv9 uncultured
868	6	1.8	53	2	04XTL3_PLACH	04xtl3 plasmodium	941	6	1.8	77	2	08YP97_9ANAS	08yp97 anabena sp
869	6	1.8	53	2	064VV2_BACPR	064vv2 bacteroides	942	6	1.8	77	2	05RL04_MOUSE	05rl04 mus musculu
870	6	1.8	53	2	06N0X3_RHOPA	06n0x3 streptomyce	943	6	1.8	78	2	0800K6_METMA	0800k6 methanosarc
871	6	1.8	53	2	082EM7_STRAM	082em7 rhodospirille	944	6	1.8	78	2	05HYU8_HUMAN	05hyu8 homo sapien
872	6	1.8	53	2	08VA91_POVBK	08va91 polymaviru	945	6	1.8	78	2	07Y2F7_9CAUD	07y2f7 rhodococcha
873	6	1.8	54	2	0592S5_LYMST	0592s5 lymphaea sta	946	6	1.8	78	2	05DKS6_9NOCA	05dks6 rhodococcha
874	6	1.8	54	2	067J85_SYMTM	067j85 streptomyce	947	6	1.8	79	2	05TVF8_9NOCA	05tvf8 anopheles g
875	6	1.8	54	2	082AA3_STRAM	082aa3 streptomyce	948	6	1.8	79	2	06PFM8_ACTIAD	06pfm8 actinobact
876	6	1.8	56	2	0273B8_METTM	0273b8 methanobact	949	6	1.8	80	2	06XHG6_DROVA	06xhg6 drosophila
877	6	1.8	57	2	092X78_RHIME	092x78 rhizobium m	950	6	1.8	80	2	04YX8_PLABE	04yx8 plasmodium
878	6	1.8	57	2	05QUV3_IDILO	05quv3 idiomarina	951	6	1.8	81	2	06RH77_HUMAN	06rh77 homo sapien
879	6	1.8	58	2	05C7L1_SCHJA	05c7l1 schistosoma	952	6	1.8	81	2	07OPR5_GIALA	07opr5 giardia lam
880	6	1.8	58	2	0517S1_PSEFL	0517s1 pseudomonas	953	6	1.8	81	2	09TTQ2_HORSE	09ttq2 equus caball
881	6	1.8	58	2	04KG24_PSEFL	04kg24 pseudomonas	954	6	1.8	81	2	04HT87_CAMCO	04ht87 campylobact
882	6	1.8	59	2	05C5K2_SCHJA	05c5k2 schistosoma	955	6	1.8	81	2	05HYU5_CAMJR	05hyu5 campylobact
883	6	1.8	59	2	05QMO7_ORYSA	05qmo7 oryza sativ	956	6	1.8	81	2	06L739_PHOPR	06l739 photobacter
884	6	1.8	60	2	06BS48_ORYSA	06bs48 oryza sativ	957	6	1.8	81	2	04JUN1_9HEPC	04jun1 hepatitis c
885	6	1.8	60	2	057L03_SALCH	057l03 salmonella	958	6	1.8	81	2	04JUN3_9HEPC	04jun3 hepatitis c
886	6	1.8	60	2	04HGT2_CAMCO	04hgt2 campylobact	959	6	1.8	81	2	04JUN4_9HEPC	04jun4 hepatitis c
887	6	1.8	60	2	069131_9GAMA	069131 human herpe	960	6	1.8	81	2	04JUN5_9HEPC	04jun5 hepatitis c
888	6	1.8	61	2	004361_9GAMA	004361 human herpe	961	6	1.8	81	2	04JUN7_9HEPC	04jun7 hepatitis c
889	6	1.8	61	2	05NKB7_AZOSE	05nkb7 azoarcus sp	962	6	1.8	82	2	09PPD2_CAMBE	09ppd2 campylobact
890	6	1.8	61	2	0836K7_ENTPA	0836k7 enterococcu	963	6	1.8	82	2	07ZTF8_BRARB	07ztf8 brachydanio
891	6	1.8	61	2	037321_HABPV	037321 helicobact	964	6	1.8	83	1	PRRP_RAT	prpp rat
892	6	1.8	62	2	07PEX8_9NOGA	07pex8 anopheles g	965	6	1.8	83	2	0978H2_THYVO	0978h2 thelyodon
893	6	1.8	62	2	067S86_SYMTM	067s86 symbiobacte	966	6	1.8	83	2	05D866_9PRIM	05d866 gorilla gor
894	6	1.8	63	2	096374_MANSE	096374 manduca sex	967	6	1.8	83	2	05XIF6_BORGA	05xif6 borrelia ga
895	6	1.8	63	2	04XB71_PLACH	04xb71 plasmodium	968	6	1.8	83	2	05P2E9_AZOSE	05p2e9 azoarcus sp
896	6	1.8	63	2	0940T4_ARATH	0940t4 arabidopsis	969	6	1.8	83	2	070182_MOUSE	070182 mus musculu
897	6	1.8	63	2	0519S1_BACPN	0519s1 bacteroides	970	6	1.8	84	1	RL27_CHLTH	rl27 chlamydia
898	6	1.8	64	2	057F94_BRUB	057f94 bruceella ab	971	6	1.8	84	2	04H1E2_LEIMA	04h1e2 leishmania
899	6	1.8	64	2	08G2D6_BRUSU	08g2d6 bruceella su	972	6	1.8	84	2	06KIT0_ORYSA	06kit0 oryza sativ
900	6	1.8	65	2	05T7A4_9NOGA	05t7a4 anopheles g	973	6	1.8	84	2	05YD52_9NOSO	05yd52 nostoc sp.
901	6	1.8	65	2	05D867_9PRIM	05d867 gorilla gor	974	6	1.8	84	2	04NSE8_9DELT	04nse8 anatemyrob
902	6	1.8	65	2	06K7K9_ORYSA	06k7k9 oryza sativ	975	6	1.8	84	2	08Q540_9BETH	08q540 pongine her
903	6	1.8	66	2	06T5T5_HRLPY	06t5t5 helicobacte	976	6	1.8	85	2	09TIG8_PLAYO	09tig8 plasmodium
904	6	1.8	66	2	06G995_STRAS	06g995 staphylococ	977	6	1.8	85	2	09TUG8_SHEEP	09tug8 ovis aries
905	6	1.8	66	2	05HFV6_STAAC	05hfve staphylococ	978	6	1.8	85	2	04ZCB7_VIRU	04zcb7 bacterioph
906	6	1.8	66	2	07ASJ5_STAMN	07asj5 staphylococ	979	6	1.8	85	2	04NV04_9DELT	04nv04 anatemyrob
907	6	1.8	66	2	08K6N7_STRP3	08k6n7 streptococ	980	6	1.8	85	2	04M031_BACCE	04m031 bacillus ce

981	6	1.8	85	2	Q738K8_BACCI	Q738K8 bacillus ce	1054	6	1.8	96	1	VGE_BPG4	P03640 bacterioph
982	6	1.8	85	2	Q738K8_TETNG	Q738K8 tetrarodon n	1055	6	1.8	96	2	Q715B8_9ECMI	Q715B8 ophiophila
983	6	1.8	86	2	Q5D218_VYEST	Q5D218 halictis as	1056	6	1.8	96	2	Q8W6C5_BPG4	Q8W6C5 bacterioph
984	6	1.8	86	2	Q4TT97_CABEL	Q4TT97 caenorhabdi	1057	6	1.8	96	2	Q5GR72_WOLFR	Q5GR72 wolbachia s
985	6	1.8	86	2	Q84JY6_ARATH	Q84JY6 arabidopsis	1058	6	1.8	96	2	Q5B8B7_VIBF1	Q5B8B7 vibrio fisc
986	6	1.8	86	2	Q53845_SPICI	Q53845 spiroplasma	1059	6	1.8	96	2	Q8K1W6_9ENTR	Q8K1W6 buchiera ap
987	6	1.8	86	2	Q9EUC4_SRRMA	Q9EUC4 serratia ma	1060	6	1.8	96	2	Q8K1W8_9ENTR	Q8K1W8 buchiera ap
988	6	1.8	86	2	Q9EXM6_9ENTR	Q9EXM6 enterobacte	1061	6	1.8	96	2	Q4QNO6_HAE18	Q4QNO6 haemophilus
989	6	1.8	86	2	Q9EXM8_9ENTR	Q9EXM8 enterobacte	1062	6	1.8	96	2	Q83DL6_COXBU	Q83DL6 coxelia bu
990	6	1.8	86	2	Q8YU64_ANASP	Q8YU64 anabeena sp	1063	6	1.8	96	2	Q5QV73_IDILIO	Q5QV73 idiomarina
991	6	1.8	87	2	Q527N3_MAGSR	Q527N3 magnaporthe	1064	6	1.8	96	2	Q65LY8_BACLD	Q65LY8 bacillus li
992	6	1.8	87	2	Q79P19_BACGR	Q79P19 bacillus su	1065	6	1.8	97	1	CC17_M0USE	CC17 mus musculu
993	6	1.8	88	2	Q4X1Y5_PLACH	Q4X1Y5 plasmodium	1066	6	1.8	97	1	CH10_BUCBP	CH10_BUCBP
994	6	1.8	88	2	Q4TZ19_SFABA	Q4TZ19 vigna radia	1067	6	1.8	97	1	CH10_BUCBU	CH10_BUCBU
995	6	1.8	88	2	Q66189_ENTAS	Q66189 enterobacte	1068	6	1.8	97	1	CH10_BUCPP	CH10_BUCPP
996	6	1.8	88	2	Q66191_ENTIT	Q66191 enterobacte	1069	6	1.8	97	1	CH10_BUCPS	CH10_BUCPS
997	6	1.8	88	2	Q66193_ENTTG	Q66193 enterobacte	1070	6	1.8	97	1	CH10_BUCTC	CH10_BUCTC
998	6	1.8	88	2	Q66195_ENTME	Q66195 enterobacte	1071	6	1.8	97	1	CH10_BUCTS	CH10_BUCTS
999	6	1.8	88	2	Q66197_ENTTA	Q66197 enterobacte	1072	6	1.8	97	1	CH10_BUCTT	CH10_BUCTT
1000	6	1.8	88	2	Q66201_SRRU	Q66201 serratia ru	1073	6	1.8	97	1	CH10_EC057	CH10_EC057
1001	6	1.8	88	2	Q66203_SRRF1	Q66203 serratia fi	1074	6	1.8	97	1	CH10_EC016	CH10_EC016
1002	6	1.8	88	2	Q66205_SRRMA	Q66205 serratia ma	1075	6	1.8	97	1	CH10_EC01I	CH10_EC01I
1003	6	1.8	88	2	Q66207_KLEPN	Q66207 klebsiella	1076	6	1.8	97	1	CH10_ENTAB	CH10_ENTAB
1004	6	1.8	88	2	Q66209_KLEFX	Q66209 klebsiella	1077	6	1.8	97	1	CH10_ERMCT	CH10_ERMCT
1005	6	1.8	88	2	Q66211_KLEPL	Q66211 klebsiella	1078	6	1.8	97	1	CH10_SALTI	CH10_SALTI
1006	6	1.8	88	2	Q66213_KLEOR	Q66213 klebsiella	1079	6	1.8	97	1	CH10_SALFI	CH10_SALFI
1007	6	1.8	88	2	Q66217_PANAN	Q66217 pantoea ana	1080	6	1.8	97	1	CH10_SHIFL	CH10_SHIFL
1008	6	1.8	88	2	Q66219_ERWCA	Q66219 erwina car	1081	6	1.8	97	1	CH10_WIGBR	CH10_WIGBR
1009	6	1.8	88	2	Q66221_ERWAP	Q66221 erwina aph	1082	6	1.8	97	1	CH10_XANMA	CH10_XANMA
1010	6	1.8	88	2	Q31217_DESVU	Q31217 desulfovibr	1083	6	1.8	97	1	GATC2_C10AB	GATC2 cloab
1011	6	1.8	88	2	Q66199_ENTAG	Q66199 enterobacte	1084	6	1.8	97	2	Q6TUT1_ASCSU	Q6TUT1 ascisu
1012	6	1.8	88	2	Q66215_ENTAG	Q66215 enterobacte	1085	6	1.8	97	2	Q8MXM8_DICDI	Q8MXM8 dictyosteli
1013	6	1.8	88	2	Q72EL6_DESVH	Q72EL6 desulfovibr	1086	6	1.8	97	2	Q70XF1_DROAV	Q70XF1 dromaciops
1014	6	1.8	88	2	Q4T082_TETNG	Q4T082 tetrarodon n	1087	6	1.8	97	2	Q6ASV5_ORYSA	Q6ASV5 oryza sativ
1015	6	1.8	89	2	Q81ER1_PLAF7	Q81ER1 plasmadia	1088	6	1.8	97	2	Q9FAB9_9BACT	Q9FAB9 bacillus ma
1016	6	1.8	89	2	Q8L1J37_ORYSA	Q8L1J37 oryza sativ	1089	6	1.8	97	2	Q7BGB6_BCOLI	Q7BGB6 escherichia
1017	6	1.8	89	2	Q33687_BENTR	Q33687 primary end	1090	6	1.8	97	2	Q6LXK1_PHOFR	Q6LXK1 photobacter
1018	6	1.8	89	2	Q73NM2_TRENDE	Q73NM2 treponema d	1091	6	1.8	97	2	Q5FL63_SALPA	Q5FL63 salmonella
1019	6	1.8	89	2	Q8DJC6_SYNEL	Q8DJC6 synechococc	1092	6	1.8	97	2	Q7U349_CANBP	Q7U349 candidatus
1020	6	1.8	90	2	Q6ZD73_ORYSA	Q6ZD73 oryza sativ	1093	6	1.8	97	2	Q5SVU0_MOUSE	Q5SVU0 mus musculu
1021	6	1.8	90	2	Q6NFP3_CORDI	Q6NFP3 corynebacte	1094	6	1.8	97	2	Q4PIY1_9Z2ZZ	Q4PIY1 unidentified
1022	6	1.8	90	2	Q5LXZ4_SRR1T	Q5LXZ4 streptococc	1095	6	1.8	98	1	CC113_CANPA	CC113 canis famli
1023	6	1.8	91	2	Q86BD7_DROME	Q86BD7 dirosophila	1096	6	1.8	98	1	NU41M_BALMU	NU41M balenopter
1024	6	1.8	91	2	Q9N038_WACFA	Q9N038 macaca fasc	1097	6	1.8	98	1	NU41M_BALPH	NU41M balenopter
1025	6	1.8	91	2	Q56ZHO_ARATH	Q56ZHO arabidopsis	1098	6	1.8	98	1	NU41M_MUNFE	NU41M mungo
1026	6	1.8	92	1	Y1050_HAEIN	Y1050 haemophilus	1099	6	1.8	98	1	NU41M_MUNGO	NU41M mungo
1027	6	1.8	92	2	Q4QUN3_HAE18	Q4QUN3 haemophilus	1100	6	1.8	98	1	NU41M_MUNVU	NU41M mungo
1028	6	1.8	92	2	Q64U73_BACFR	Q64U73 bacteroides	1101	6	1.8	98	1	NU41M_RABIT	NU41M rabbit
1029	6	1.8	93	2	Q64BM1_PARCK	Q64BM1 uncultured	1102	6	1.8	98	1	PRRP_BOVIN	PRRP bovin
1030	6	1.8	93	2	Q9X7B6_MYCLE	Q9X7B6 mycobacteri	1103	6	1.8	98	1	PRRP_SHEEP	PRRP sheep
1031	6	1.8	93	2	Q6MJN7_BDEBA	Q6MJN7 bdellovibri	1104	6	1.8	98	2	Q556E0_DICDI	Q556E0 dictyosteli
1032	6	1.8	93	2	Q4SDK3_TETNG	Q4SDK3 tetrarodon n	1105	6	1.8	98	2	Q679A3_9CARN	Q679A3 oxtaria byro
1033	6	1.8	94	2	Q65SH8_MANSM	Q65SH8 manheimia	1106	6	1.8	98	2	Q69B62_BALAC	Q69B62 balaeonpter
1034	6	1.8	95	1	CH10_ALTHA	CH10 alteromonas	1107	6	1.8	98	2	Q69B65_BALBN	Q69B65 balaeonpter
1035	6	1.8	95	2	Q7RUJ9_NEUCR	Q7RUJ9 neurospora	1108	6	1.8	98	2	Q69B76_DELEA	Q69B76 delphinapte
1036	6	1.8	95	2	Q5SMZ7_ORYSA	Q5SMZ7 oryza sativ	1109	6	1.8	98	2	Q69B78_EUBAS	Q69B78 eubalaena a
1037	6	1.8	95	2	Q57B59_BRUAB	Q57B59 bruceella ab	1110	6	1.8	98	2	Q69B80_9CERY	Q69B80 eugalaena g
1038	6	1.8	95	2	Q9ALB6_9GAMM	Q9ALB6 pseudocalter	1111	6	1.8	98	2	Q69B84_MEGNO	Q69B84 megabactera n
1039	6	1.8	95	2	Q8FTN4_BRUSU	Q8FTN4 bruceella su	1112	6	1.8	98	2	Q69B86_ZIPCA	Q69B86 ziphius cav
1040	6	1.8	95	2	Q61EB1_ORYXA	Q61EB1 oryzias lat	1113	6	1.8	98	2	Q70RZ3_BALAC	Q70RZ3 balaeonpter
1041	6	1.8	96	1	CH101_VIBCH	CH101 vibrio chol	1114	6	1.8	98	2	Q70S06_ESCGI	Q70S06 eschrichti
1042	6	1.8	96	1	CH101_VIBPA	CH101 vibrio para	1115	6	1.8	98	2	Q70S32_BALMY	Q70S32 balaena mys
1043	6	1.8	96	1	CH101_VIBVU	CH101 vibrio vuln	1116	6	1.8	98	2	Q71VU7_MUNMU	Q71VU7 muntiacus m
1044	6	1.8	96	1	CH101_VIBVY	CH101 vibrio vuln	1117	6	1.8	98	2	Q71VU9_MUNMU	Q71VU9 muntiacus m
1045	6	1.8	96	1	CH10_ACTAC	CH10 actinobacil	1118	6	1.8	98	2	Q71VU0_MUNMU	Q71VU0 muntiacus m
1046	6	1.8	96	1	CH10_ACTPL	CH10 actinobacil	1119	6	1.8	98	2	Q71VU1_MUNMU	Q71VU1 muntiacus m
1047	6	1.8	96	1	CH10_BUCAI	CH10 buchnera ap	1120	6	1.8	98	2	Q71VU6_MUNKE	Q71VU6 buchnera r
1048	6	1.8	96	1	CH10_BUCAP	CH10 buchnera ap	1121	6	1.8	98	2	Q7Y6H3_9EUTH	Q7Y6H3 elephantiacu
1049	6	1.8	96	1	CH10_BUCWP	CH10 buchnera ap	1122	6	1.8	98	2	Q85RW9_MUNMU	Q85RW9 muntiacus m
1050	6	1.8	96	1	CH10_HAEIN	CH10 haemophilus	1123	6	1.8	98	2	Q81WPM4_TUPGB	Q81WPM4 tupapa glis
1051	6	1.8	96	1	CH10_PASMU	CH10 pastorella	1124	6	1.8	98	2	Q94YCS_PIPAB	Q94YCS pipistrellu
1052	6	1.8	96	1	CH10_PHOFR	CH10 photobacter	1125	6	1.8	98	2	Q9B1C5_MUNCR	Q9B1C5 muntiacus c
1053	6	1.8	96	1	CH10_SHRON	CH10 shewanella	1126	6	1.8	98	2	Q9B9Y1_MUNMU	Q9B9Y1 muntiacus m

1127	6	1.8	98	2	09G3R5_CHARTU	09G3R5_chalinojobu	1200	6	1.8	101	2	05C573_SCHUA	05C573_schistosoma
1128	6	1.8	98	2	09GA22_RUPGB	09GA22_tupaia glis	1201	6	1.8	101	2	08MKN8_DROME	08MKN8_drosophila
1129	6	1.8	98	2	0599C1_BALEN	0599C1_balaenopter	1202	6	1.8	101	2	09SK94_MACPA	09SK94_macaca fasc
1130	6	1.8	98	2	0598U3_3CAUD	0598U3_eubalaena j	1203	6	1.8	101	2	06YNE6_MOUSE	06YNE6_mus musculus
1131	6	1.8	98	2	06PVM3_9CAUD	06PVM3_pseudomnas	1204	6	1.8	101	2	04RXH1_TETNG	04RXH1_tetraodon n
1132	6	1.8	98	2	07X811_ORYSA	07X811_oryza sativ	1205	6	1.8	101	2	04SGR2_TETNG	04SGR2_tetraodon n
1133	6	1.8	98	2	04LYR4_9BURE	04LYR4_burkholderi	1206	6	1.8	102	1	CH101_VIBNA	083V9_vibrio harv
1134	6	1.8	98	2	09QEW0_9CORO	09QEW0_porcine res	1207	6	1.8	102	2	0608Y6_METCA	0608Y6_methylcoccc
1135	6	1.8	98	2	09QEW1_9CORO	09QEW1_porcine res	1208	6	1.8	102	2	09DFZ5_XENLA	09DFZ5_xenopus lae
1136	6	1.8	98	2	09QEW2_9CORO	09QEW2_porcine res	1209	6	1.8	102	2	04S175_TETNG	04S175_tetraodon n
1137	6	1.8	99	1	CCL2_HORSE	09T33 equus caball	1210	6	1.8	102	2	091931_9H1V2	091931_human immun
1138	6	1.8	99	1	CCL2_HUMAN	P1350 homo sapien	1211	6	1.8	102	2	09YVG5_9H1V2	09YVG5_human immun
1139	6	1.8	99	1	CCL2_MACPA	P61274 macaca fasc	1212	6	1.8	103	2	05A411_CANAL	05A411_candida alb
1140	6	1.8	99	1	CCL2_MACMU	P61275 macaca mula	1213	6	1.8	103	2	081PRL_DROME	081PRL_drosophila
1141	6	1.8	99	1	CCL2_PIG	P2831 sus scrofa	1214	6	1.8	103	2	09UIP6_CABEL	09UIP6_caenorhabdi
1142	6	1.8	99	1	CCL2_PONPY	05RA28 pongo pygma	1215	6	1.8	103	2	06H891_ORYSA	06H891_oryza sativ
1143	6	1.8	99	1	CCL7_HUMAN	P80098 homo sapien	1216	6	1.8	103	2	06BXT5_RICFY	06BXT5_rickettsia
1144	6	1.8	99	1	CCL8_BOVIN	009141 bos taurus	1217	6	1.8	103	2	08WMS9_BRLJA	08WMS9_bradrythzob
1145	6	1.8	99	1	CCL8_CANPA	068AY9 canis famli	1218	6	1.8	103	2	08XK86_CLOPE	08XK86_clostridium
1146	6	1.8	99	1	CCL8_HUMAN	P80075 homo sapien	1219	6	1.8	103	2	091930_9H1V2	091930_human immun
1147	6	1.8	99	1	CCL8_PIG	P4873 sus scrofa	1220	6	1.8	104	1	CCL12_MOUSE	062401 mus musculu
1148	6	1.8	99	1	MCPA_BOVIN	P48291 bos taurus	1221	6	1.8	104	2	0874J5_SCYSE	0874J5_scylla serr
1149	6	1.8	99	2	09C235_NEUCR	09C235_neutrosora	1222	6	1.8	104	2	04XWG0_PLACH	04XWG0_plaemodiu
1150	6	1.8	99	2	0569J6_HUMAN	Q569J6 homo sapien	1223	6	1.8	104	2	042028_ARATH	042028_arabidopsis
1151	6	1.8	99	2	P92624_DIOAS	P92624_diodora asp	1224	6	1.8	104	2	06EUE0_ORYSA	06EUE0_oryza sativ
1152	6	1.8	99	2	0516F8_CANPA	0516F8 canis famli	1225	6	1.8	104	2	05MAE9_BACSK	05MAE9_bacillus cl
1153	6	1.8	99	2	05K5U7_CANPA	05K5U7 canis famli	1226	6	1.8	104	2	09FPM5_STRCO	09FPM5_streptomyces
1154	6	1.8	99	2	06XVMS_MACNE	06XVMS macaca neme	1227	6	1.8	104	2	074B59_GEOSL	074B59_geobacter s
1155	6	1.8	99	2	0865F4_MACNE	0865F4 macaca neme	1228	6	1.8	104	2	05SVB4_MOUSE	05SVB4_mus musculu
1156	6	1.8	99	2	08MKC8_HORSE	08MKC8 equus cabal	1229	6	1.8	104	2	091929_9H1V2	091929_human immun
1157	6	1.8	99	2	08HYQ0_MACMU	08HYQ0 macaca mula	1230	6	1.8	104	2	091934_9H1V2	091934_human immun
1158	6	1.8	99	2	07IME7_MACMU	07IME7 macaca mula	1231	6	1.8	105	2	051IR1_MAGGR	051IR1_magnaporthe
1159	6	1.8	99	2	08GBV8_OSCAG	08GBV8 plantochtri	1232	6	1.8	105	2	060384_HUMAN	060384_homo sapien
1160	6	1.8	99	2	08GBV9_9CYAN	08GBV9 plantochtri	1233	6	1.8	105	2	070332_ANOGA	070332_anopheles g
1161	6	1.8	99	2	08GBW0_9CYAN	08GBW0 plantochtri	1234	6	1.8	105	2	05DAB6_SCHUA	05DAB6_schistosoma
1162	6	1.8	99	2	08GBW1_9CYAN	08GBW1 plantochtri	1235	6	1.8	105	2	05ZAI9_ORYSA	05ZAI9_oryza sativ
1163	6	1.8	99	2	08GBW2_9CYAN	08GBW2 plantochtri	1236	6	1.8	105	2	04RA95_TETNG	04RA95_tetraodon n
1164	6	1.8	99	2	08GBW3_OSCAG	08GBW3 plantochtri	1237	6	1.8	106	2	0847N9_ASTYP	0847N9_astet yellu
1165	6	1.8	99	2	08GBW4_OSCAG	08GBW4 plantochtri	1238	6	1.8	106	2	0921Z5_RICCN	0921Z5_rickettsia
1166	6	1.8	99	2	08GBW5_OSCAG	08GBW5 plantochtri	1239	6	1.8	106	2	091928_9H1V2	091928_human immun
1167	6	1.8	99	2	08GBZ0_NOSO	08GBZ0 nostoc sp.	1240	6	1.8	106	2	091932_9H1V2	091932_human immun
1168	6	1.8	99	2	08GF14_9NOST	08GF14 anabaena sp	1241	6	1.8	107	2	06CMN4_KLUDA	06CMN4_kluyveromyc
1169	6	1.8	99	2	08GF15_9NOST	08GF15 anabaena sp	1242	6	1.8	107	2	04ZC10_9CAUD	04ZC10_bacterioph
1170	6	1.8	99	2	08GF16_9NOST	08GF16 anabaena sp	1243	6	1.8	107	2	0516S1_BORBU	0516S1_borrelia bu
1171	6	1.8	99	2	08GF17_9NOST	08GF17 anabaena le	1244	6	1.8	107	2	05NMGO_ZYMOX	05NMGO_zygomonas m
1172	6	1.8	99	2	08GF18_9NOST	08GF18 anabaena ci	1245	6	1.8	107	2	08AJ53_PSEBX	08AJ53_pseudomonas
1173	6	1.8	99	2	08GFN4_ANAFU	08GFN4 anabaena fl	1246	6	1.8	107	2	06GCM5_STARK	06GCM5_staphylococ
1174	6	1.8	99	2	04TFE0_TETNG	04TFE0 tetraodon n	1247	6	1.8	107	2	08CAE6_MOUSE	08CAE6_mus musculu
1175	6	1.8	99	2	06L7Q5_9DELA	06L7Q5 human t-lym	1248	6	1.8	107	2	091TU9_TUHV1	091TU9_tupaliid her
1176	6	1.8	99	2	06L7V4_9DELA	06L7V4 human t-lym	1249	6	1.8	107	2	04PRT2_MNV	04PRT2_west nile v
1177	6	1.8	99	2	08UI16_9H1V1	08UI16 human immun	1250	6	1.8	107	2	04PRT3_MNV	04PRT3_west nile v
1178	6	1.8	99	2	09IXS2_9H1V1	09IXS2 human immun	1251	6	1.8	107	2	04PRT4_MNV	04PRT4_west nile v
1179	6	1.8	99	2	098X59_9H1V1	098X59 human immun	1252	6	1.8	107	2	04PRT5_MNV	04PRT5_west nile v
1180	6	1.8	100	1	CCL11_HORSE	09TC4 equus cabal	1253	6	1.8	107	2	04RFB6_TETNG	04RFB6_tetraodon n
1181	6	1.8	100	1	NWOK_ECOLI	P33606 escherichia	1254	6	1.8	107	2	091910_9H1V2	091910_human immun
1182	6	1.8	100	1	YICE_BACSU	031627 bacillus su	1255	6	1.8	107	2	091920_9H1V2	091920_human immun
1183	6	1.8	100	2	09POF3_HUMAN	Q9POF3 homo sapien	1256	6	1.8	107	2	091927_9H1V2	091927_human immun
1184	6	1.8	100	2	Q4N4M1_THERA	Q4N4M1 theileria p	1257	6	1.8	107	2	077WP8_9H1V2	077WP8_human immun
1185	6	1.8	100	2	08LNS1_ORYSA	08LNS1 oryza sativ	1258	6	1.8	107	2	077WP9_9H1V2	077WP9_human immun
1186	6	1.8	100	2	05EIK0_VIBFI	05EIK0 vibrio fisc	1259	6	1.8	107	2	09YIL5_9H1V2	09YIL5_human immun
1187	6	1.8	100	2	057M37_SALCH	057M37 salmonella	1260	6	1.8	107	2	09YVF6_9H1V2	09YVF6_human immun
1188	6	1.8	100	2	093IA4_STANU	093IA4 staphylococ	1261	6	1.8	107	2	09YVG7_9H1V2	09YVG7_human immun
1189	6	1.8	100	2	Q4DM11_RICPE	Q4DM11 rickettsia	1262	6	1.8	107	2	09YVH2_9H1V2	09YVH2_human immun
1190	6	1.8	100	2	Q7CQ53_SALTY	Q7CQ53 salmonella	1263	6	1.8	107	2	YCF54_FORPU	YCF54_forpuz
1191	6	1.8	100	2	Q7N2D6_PHOHL	Q7N2D6 photorhabdu	1264	6	1.8	108	1	07PC93_MALZE	07PC93_pozymyza pu
1192	6	1.8	100	2	08ZDL6_YERPE	08ZDL6 yerinia pe	1265	6	1.8	108	2	053NY6_ORYSA	053NY6_oryza sativ
1193	6	1.8	100	2	05PN65_SALPA	05PN65 salmonella	1266	6	1.8	108	2	044706_BORBU	044706_borrelia bu
1194	6	1.8	100	2	08XPA3_SALTI	08XPA3 salmonella	1267	6	1.8	108	2	045800_BACVU	045800_bacteroides
1195	6	1.8	100	2	0669A9_YERPS	0669A9 yerinia ps	1268	6	1.8	108	2	08KYR7_BACPR	08KYR7_bacteroides
1196	6	1.8	100	2	06D2S6_ERWCT	06D2S6 erwinia car	1269	6	1.8	108	2	04MOB4_9BURE	04MOB4_burkholderi
1197	6	1.8	101	1	CCL2_CANPA	P52203 canis famli	1270	6	1.8	109	2	058093_PYRIO	058093_pyrococcus
1198	6	1.8	101	1	YGV4_YEAST	P53089 saccharomyc	1271	6	1.8	109	2	0727Q8_HUMAN	0727Q8_homo sapien
1199	6	1.8	101	2	Q4P3P8_USTWA	Q4P3P8 utillago ma	1272	6	1.8	109	2		

1273	6	1.8	109	2	Q4YU6_PLABE	Q4YU6_plasmodium	1346	6	1.8	118	1	VATG1_PANTR	Q86246_pan troglod
1274	6	1.8	109	2	Q6R58_SBACT	Q6R58_uncultured	1347	6	1.8	118	1	VATG2_HUMAN	Q95670_homo sapien
1275	6	1.8	109	2	Q5YNZ6_NOCFA	Q5YNZ6_nocardia fa	1348	6	1.8	118	1	VATG2_MACMU	Q5TM38_macaca mla
1276	6	1.8	109	2	Q88CE9_PSEPK	Q88CE9_pseudomonas	1349	6	1.8	118	1	VATG2_MOUSE	Q9WT44_mus musculu
1277	6	1.8	109	2	Q5M419_STRT2	Q5M419_streptococc	1350	6	1.8	118	1	VATG2_PIG	Q9BT66_sus scrofa
1278	6	1.8	109	2	Q4S7R3_TETNG	Q4S7R3_tetradoccon	1351	6	1.8	118	2	Q4LIC2_9MAXI	Q4LIC2_lepeophthei
1279	6	1.8	110	2	Q5V4P1_HAUMA	Q5V4P1_haemulon n	1352	6	1.8	118	2	Q7CX77_AGRYS	Q7CX77_agrobacteri
1280	6	1.8	110	2	Q7PE28_ANOCA	Q7PE28_anopheles g	1353	6	1.8	118	2	Q5LV31_SILPO	Q5LV31_silicibacte
1281	6	1.8	110	2	Q8T416_DROME	Q8T416_drosophila	1354	6	1.8	118	2	Q7Z406_DESVH	Q7Z406_desulfovibr
1282	6	1.8	110	2	Q5NBM6_ORYSA	Q5NBM6_oryza sativ	1355	6	1.8	118	2	Q8R2H0_RAT	Q8R2H0_rattus norv
1283	6	1.8	110	2	Q571P2_ABRPU	Q571P2_aeromonas p	1356	6	1.8	118	2	Q54A87_MOUSE	Q54A87_mus musculu
1284	6	1.8	110	2	Q4NPOS_5MICC	Q4NPOS_atrichobact	1357	6	1.8	118	2	Q9CRB3_MOUSE	Q9CRB3_mus muscu
1285	6	1.8	110	2	Q5RLB7_MOUSE	Q5RLB7_mus musculu	1358	6	1.8	118	2	Q5D9D6_SCHJA	Q5D9D6_schistosoma
1286	6	1.8	110	2	Q4Z454_TIRASC	Q4Z454_tiraechmys s	1359	6	1.8	119	2	Q7RG12_PLAYO	Q7RG12_plasmodium
1287	6	1.8	111	1	RBFA_HELPJ	Q9ZM45_helicobacte	1360	6	1.8	119	2	Q4UZ29_XANCP	Q4UZ29_xanthomonas
1288	6	1.8	111	1	RBFA_HELPJ	Q5Y688_helicobacte	1361	6	1.8	119	2	Q4UZ29_XANCP	Q4UZ29_xanthomonas
1289	6	1.8	111	2	Q9UY95_PYPAB	Q9UY95_pyrococcus	1362	6	1.8	119	2	Q4P020_9DELT	Q4P020_aeromonas
1290	6	1.8	111	2	Q8LHY8_ORYSA	Q8LHY8_oryza sativ	1363	6	1.8	119	2	Q7W7B7_BORPA	Q7W7B7_bordetella
1291	6	1.8	111	2	Q6LPTS_PHOPR	Q6LPTS_photobacter	1364	6	1.8	119	2	Q8PD07_XANCP	Q8PD07_xanthomonas
1292	6	1.8	111	2	Q9HW55_PSEAE	Q9HW55_pseudomonas	1365	6	1.8	119	2	Q8PD08_XANCP	Q8PD08_xanthomonas
1293	6	1.8	111	2	Q6N2H1_RHOPA	Q6N2H1_rhodopseudo	1366	6	1.8	119	2	Q5XW58_MOUSE	Q5XW58_mus musculu
1294	6	1.8	111	2	Q6FYF8_BAROV	Q6FYF8_baritonella	1367	6	1.8	120	1	CCL2_CAVPO	Q08782_cavia porce
1295	6	1.8	111	2	Q8L1A7_RAT	Q8L1A7_rattus norv	1368	6	1.8	120	1	Y5866_RHIME	Q92UG5_thizobium m
1296	6	1.8	112	2	Q8ZTR9_PYPAR	Q8ZTR9_pyrobaculum	1369	6	1.8	120	2	Q5BSF2_SCHJA	Q5BSF2_schistosoma
1297	6	1.8	112	2	Q03884_TIRAST	Q03884_saccharomyc	1370	6	1.8	120	2	Q86J35_DICDI	Q86J35_dicyosrelli
1298	6	1.8	112	2	Q7RQ76_PLAYO	Q7RQ76_plasmodium	1371	6	1.8	120	2	Q4QBS1_LEIMA	Q4QBS1_leishmania
1299	6	1.8	112	2	Q931B3_STANU	Q931B3_staphylococ	1372	6	1.8	120	2	Q6LHC6_PHOPR	Q6LHC6_photobacter
1300	6	1.8	112	2	Q8YOL8_RALSO	Q8YOL8_ralstonia s	1373	6	1.8	120	2	Q8C659_MOUSE	Q8C659_mus musculu
1301	6	1.8	113	1	MIH_CALSI	Q55321_callicnectes	1374	6	1.8	120	2	Q6IN12_XENLA	Q6IN12_xenopus lae
1302	6	1.8	113	2	Q7RGX8_PLAYO	Q7RGX8_plasmodium	1375	6	1.8	121	2	Q95TDD_DROME	Q95TDD_drosophila
1303	6	1.8	113	2	Q35015_MELAY	Q35015_meloidogyne	1376	6	1.8	121	2	Q6Z1P7_ORYSA	Q6Z1P7_oryza sativ
1304	6	1.8	113	2	Q8ROR1_LACAC	Q8ROR1_lactobacilli	1377	6	1.8	122	2	Q8U1X6_PYPFU	Q8U1X6_pyrococcus
1305	6	1.8	113	2	Q57PA7_SALCH	Q57PA7_salmoneella	1378	6	1.8	122	2	Q8PS76_METWA	Q8PS76_methanosarc
1306	6	1.8	113	2	Q4NM27_5MICC	Q4NM27_atrichobact	1379	6	1.8	122	2	Q8N8P7_HUMAN	Q8N8P7_homo sapien
1307	6	1.8	113	2	Q4ZX29_PSESY	Q4ZX29_pseudomonas	1380	6	1.8	122	2	Q9NV16_HUMAN	Q9NV16_homo sapien
1308	6	1.8	113	2	Q4KGU3_PSEFS	Q4KGU3_pseudomonas	1381	6	1.8	122	2	Q4VY08_HUMAN	Q4VY08_homo sapien
1309	6	1.8	113	2	Q5PN89_SALPA	Q5PN89_salmoneella	1382	6	1.8	122	2	Q6E2A0_ARATH	Q6E2A0_arabidopsis
1310	6	1.8	113	2	Q8UCV9_AGRIS	Q8UCV9_agrobacteri	1383	6	1.8	122	2	Q6K851_ORYSA	Q6K851_oryza sativ
1311	6	1.8	113	2	Q8ZPH6_SALTU	Q8ZPH6_salmoneella	1384	6	1.8	122	2	Q9AF23_9BACT	Q9AF23_uncultured
1312	6	1.8	113	2	Q7VXG6_BORPE	Q7VXG6_bordetella	1385	6	1.8	122	2	Q5SHK5_THET8	Q5SHK5_thermus the
1313	6	1.8	113	2	Q7W8U8_BORPA	Q7W8U8_bordetella	1386	6	1.8	122	2	Q89YH2_BACTN	Q89YH2_bacteroides
1314	6	1.8	113	2	Q7WKS8_BORBR	Q7WKS8_bordetella	1387	6	1.8	122	2	Q9HZU9_PSBAB	Q9HZU9_pseudomonas
1315	6	1.8	113	2	Q886Z6_PSESM	Q886Z6_pseudomonas	1388	6	1.8	122	2	Q8CTD7_MOUSE	Q8CTD7_mus musculu
1316	6	1.8	114	2	Q8IWS4_HUMAN	Q8IWS4_homo sapien	1389	6	1.8	123	1	Y5489_RHIME	Q92V09_thizobium m
1317	6	1.8	114	2	Q8U957_AGRIS	Q8U957_agrobacteri	1390	6	1.8	123	2	Q6AK73_9ACAR	Q6AK73_campylobact
1318	6	1.8	114	2	Q7US46_RHOBA	Q7US46_rhodopirelli	1391	6	1.8	123	2	Q6OMN6_CABBR	Q6OMN6_caenorhabdi
1319	6	1.8	115	1	IR02_HGVVA	PI6802_human cytom	1392	6	1.8	123	2	Q7ONT2_GIALA	Q7ONT2_giardia lam
1320	6	1.8	115	2	Q57VG1_9TRYV	Q57VG1_rypanosoma	1393	6	1.8	123	2	Q6U6O8_9MOLL	Q6U6O8_cryptosporax
1321	6	1.8	115	2	Q4QI14_LEIMA	Q4QI14_leishmania	1394	6	1.8	123	2	Q6Z440_ORYSA	Q6Z440_oryza sativ
1322	6	1.8	115	2	Q5DYS5_VIBFI	Q5DYS5_vibriio fisc	1395	6	1.8	123	2	Q4HRB4_CAMPV	Q4HRB4_campylobact
1323	6	1.8	115	2	Q8CMN1_STAEP	Q8CMN1_staphylococ	1396	6	1.8	123	2	Q9RT46_DEIRA	Q9RT46_deltinococcus
1324	6	1.8	115	2	Q8YI66_BRUME	Q8YI66_brucella me	1397	6	1.8	123	2	Q90137_MARMO	Q90137_marmota mon
1325	6	1.8	115	2	Q4PRT7_WNV	Q4PRT7_west nile v	1398	6	1.8	123	2	Q9DDX9_XENLA	Q9DDX9_xenopus lae
1326	6	1.8	115	2	Q4PRT8_WNV	Q4PRT8_west nile v	1399	6	1.8	124	1	AP0C4_RABIT	P55057_oryctolagus
1327	6	1.8	115	2	Q4PRT9_WNV	Q4PRT9_west nile v	1400	6	1.8	124	1	KABI_ODAPF	P56254_oryctolagus
1328	6	1.8	115	2	Q4PRU0_WNV	Q4PRU0_west nile v	1401	6	1.8	124	2	Q6XHS7_DROVA	P6XHS7_drosophila
1329	6	1.8	115	2	Q4PRU1_WNV	Q4PRU1_west nile v	1402	6	1.8	124	2	Q69MW8_ORYSA	Q69MW8_oryza sativ
1330	6	1.8	115	2	Q4PRU2_WNV	Q4PRU2_west nile v	1403	6	1.8	124	2	Q7WPD6_BORBR	Q7WPD6_bordetella
1331	6	1.8	115	2	Q4PRU3_WNV	Q4PRU3_west nile v	1404	6	1.8	124	2	Q9ZB29_LISIN	Q9ZB29_listeria in
1332	6	1.8	115	2	Q4TUA9_WNV	Q4TUA9_west nile v	1405	6	1.8	124	2	Q65085_9PRIC	Q65085_foot-and-im
1333	6	1.8	115	2	Q7ZEU9_SHIVI	Q7ZEU9_human immun	1406	6	1.8	124	2	Q4S4Y0_TETNG	Q4S4Y0_tetradodon n
1334	6	1.8	116	2	Q6C7T9_YARLI	Q6C7T9_yarivlloa ii	1407	6	1.8	125	1	CCL2_RABIT	P28232_oryctolagus
1335	6	1.8	116	2	Q4P2K6_USTMA	Q4P2K6_ustillago ma	1408	6	1.8	125	2	Q5TL98_CLAPU	P52198_clayiceps p
1336	6	1.8	116	2	Q6NVJ2_HUMAN	Q6NVJ2_homo sapien	1409	6	1.8	125	2	Q9DPZ6_XENLA	Q9DPZ6_xenopus lae
1337	6	1.8	116	2	Q7VYX3_CAREL	Q7VYX3_caenorhabdi	1410	6	1.8	126	1	NU0A_BIFAP	Q8K9P7_bufo xenoap ap
1338	6	1.8	116	2	Q8Z3C0_CHLCV	Q8Z3C0_chlamydomphi	1411	6	1.8	126	1	YIGF_ECOLI	P27842_escherichia
1339	6	1.8	116	2	Q8XJV0_CLOPE	Q8XJV0_clostridium	1412	6	1.8	126	1	YIGF_SALTY	P0418_salmoneella
1340	6	1.8	117	2	Q59ZS2_CANAL	Q59ZS2_candida alb	1413	6	1.8	126	1	YIGF_SALTY	P0418_salmoneella
1341	6	1.8	117	2	Q7Q0Q5_ANOCA	Q7Q0Q5_anopheles g	1414	6	1.8	126	2	P95861_SULSO	P95861_sulfolobus
1342	6	1.8	117	2	Q7N3M9_PHOGL	Q7N3M9_photobacter	1415	6	1.8	126	2	Q9YEE3_AARPE	Q9YEE3_aeropyrum p
1343	6	1.8	117	2	Q8YUUI_RALSO	Q8YUUI_ralstonia s	1416	6	1.8	126	2	Q7YIC7_ORYSA	Q7YIC7_oryza sativ
1344	6	1.8	117	2	Q63063_PANT	Q63063_rattus norv	1417	6	1.8	126	2	Q83JWS_SHITL	Q83JWS_shigella fl
1345	6	1.8	118	1	VATG1_CANFA	Q5W709_canis famli	1418	6	1.8	127	2	Q5QLW7_ORYSA	Q5QLW7_oryza sativ

1419	6	1.8	127	2	Q8E1W3_SHEON	Q8E1W3_sheonella
1420	6	1.8	127	2	O10457_VIRU	O10457_venezuelan
1421	6	1.8	127	2	O10460_VIRU	O10460_venezuelan
1422	6	1.8	127	2	O10461_VIRU	O10461_venezuelan
1423	6	1.8	127	2	O39813_EMCV	O39813_encephalomy
1424	6	1.8	127	2	Q9DDY1_XENLA	Q9DDY1_xenopus lae
1425	6	1.8	128	1	MERT_STNAU	P08656_etaphylococ
1426	6	1.8	128	1	US384_GAHVG	O05102_gallid herp
1427	6	1.8	128	1	Y739_PASMU	Q9C6M3_pasteurella
1428	6	1.8	128	2	Q4J7E1_SULAC	Q4J7E1_sulfolobus
1429	6	1.8	128	2	Q5UX97_HAAMA	Q5UX97_haloarcula
1430	6	1.8	128	2	Q617P1_BOMKO	Q617P1_bomdix mori
1431	6	1.8	128	2	Q9B030_VIRU	Q9B030_bacterioph
1432	6	1.8	128	2	Q94163_ORYSA	Q94163_oryza sativ
1433	6	1.8	128	2	Q7X3J9_PSEPU	Q7X3J9_pseudomonas
1434	6	1.8	128	2	Q7N0X8_PHOIL	Q7N0X8_photorhabd
1435	6	1.8	128	2	Q928A1_LISTIN	Q928A1_listeria in
1436	6	1.8	128	2	Q9RVX6_DEIRA	Q9RVX6_dielnococcus
1437	6	1.8	128	2	Q71MT6_LISMF	Q71MT6_listeria mo
1438	6	1.8	128	2	Q8Y4F2_LISMO	Q8Y4F2_listeria mo
1439	6	1.8	128	2	Q8C2V3_MOUSE	Q8C2V3_mus muscu
1440	6	1.8	129	2	Q8TR81_MERTAC	Q8TR81_methanosarc
1441	6	1.8	129	2	Q86KX5_DICDI	Q86KX5_dicystosell
1442	6	1.8	129	2	Q862M3_BOVIN	Q862M3_bos taurus
1443	6	1.8	129	2	Q71J88_LACDL	Q71J88_lactobacill
1444	6	1.8	129	2	Q84GY0_PHOIL	Q84GY0_photorhabd
1445	6	1.8	129	2	Q6N0D2_RHOPA	Q6N0D2_rhodospirib
1446	6	1.8	129	2	Q8NNM5_TORGL	Q8NNM5_corynebacte
1447	6	1.8	129	2	Q70WH4_PLAFB	Q70WH4_platichthys
1448	6	1.8	130	1	Y6524_BACAN	Q9N06_bacillus an
1449	6	1.8	130	2	Q5BKK3_SCHUA	Q5BKK3_schistosoma
1450	6	1.8	131	2	Q5LKT1_SILPO	Q5LKT1_silicibacte
1451	6	1.8	131	2	Q6A8N0_PROAC	Q6A8N0_propionibac
1452	6	1.8	132	2	Q7Y7V2_92YGO	Q7Y7V2_cunningham
1453	6	1.8	132	2	Q7Q0Q9_GIALA	Q7Q0Q9_giardia lam
1454	6	1.8	132	2	Q8T9B2_DROME	Q8T9B2_drosophila
1455	6	1.8	132	2	Q9W2M6_DROME	Q9W2M6_drosophila
1456	6	1.8	132	2	Q5H2N3_XANOR	Q5H2N3_xanthomonas
1457	6	1.8	132	2	Q9A895_CAUCR	Q9A895_caulobacter
1458	6	1.8	132	2	Q9RT34_DEIRA	Q9RT34_dielnococcus
1459	6	1.8	132	2	Q9KA40_BACHD	Q9KA40_bacillus ha
1460	6	1.8	132	2	Q39815_EMCV	Q39815_encephalomy
1461	6	1.8	132	2	Q55212_9STRE	Q55212_streptococc
1462	6	1.8	133	2	Q7UVZ6_RHOBA	Q7UVZ6_rhodospirib
1463	6	1.8	133	2	Q4TG08_TETNG	Q4TG08_tetradodon n
1464	6	1.8	133	2	Q64A03_9ARCH	Q64A03_uncultured
1465	6	1.8	134	2	Q64EF7_9ARCH	Q64EF7_uncultured
1466	6	1.8	134	2	Q4WZU9_ASPFU	Q4WZU9_aeropyrum
1467	6	1.8	134	2	Q61MW7_DROME	Q61MW7_drosophila
1468	6	1.8	134	2	Q4FV15_BGAMM	Q4FV15_psychrobact
1469	6	1.8	134	2	Q69567_MYCLE	Q69567_mycobacteri
1470	6	1.8	134	2	Q7V2U6_PROMP	Q7V2U6_prochloroco
1471	6	1.8	134	2	Q6X779_MNV	Q6X779_kunjin viru
1472	6	1.8	134	2	Q9DDX4_XENLA	Q9DDX4_xenopus lae
1473	6	1.8	134	2	Q4RA94_TETNG	Q4RA94_tetradodon n
1474	6	1.8	134	2	Q6ZTT9_HOMAN	Q6ZTT9_homo sapien
1475	6	1.8	135	2	Q54LD6_DICDI	Q54LD6_dicystosell
1476	6	1.8	135	2	Q29049_PIG	Q29049_sus scrofa
1477	6	1.8	135	2	Q701P0_PASMU	Q701P0_pasteurella
1478	6	1.8	135	2	P95012_MYCTU	P95012_mycobacteri
1479	6	1.8	135	2	Q7TYC5_MYCBO	Q7TYC5_mycobacteri
1480	6	1.8	135	2	Q9CBH3_MYCBL	Q9CBH3_mycobacteri
1481	6	1.8	135	2	Q91380_PSEAB	Q91380_pseudomonas
1482	6	1.8	135	2	Q84VRS_STYRM	Q84VRS_streptococc
1483	6	1.8	136	1	YEDX_SALTY	Q84VRS_salmonella
1484	6	1.8	136	1	YEDX_SALTY	Q84VRS_salmonella
1485	6	1.8	136	1	YEDX_SALTY	Q84VRS_salmonella
1486	6	1.8	136	1	YEDX_SALTY	Q84VRS_salmonella
1487	6	1.8	136	2	Q61HUB_DROME	Q61HUB_drosophila
1488	6	1.8	136	2	Q65382_CABEL	Q65382_cenothabidi
1489	6	1.8	136	2	Q6WNAO_CYNVA	Q6WNAO_cynocophalu
1490	6	1.8	136	2	Q6YU24_ORYSA	Q6YU24_oryza sativ
1491	6	1.8	136	2	Q6YU24_ORYSA	Q6YU24_oryza sativ

1492	6	1.8	136	2	Q57Q08_SALCH	Q57Q08_salmonella
1493	6	1.8	136	2	Q4VVA5_SALDU	Q4VVA5_salmonella
1494	6	1.8	136	2	Q4KGB3_PSEPS	Q4KGB3_pseudomonas
1495	6	1.8	136	2	Q5PGAS_SALPA	Q5PGAS_salmonella
1496	6	1.8	136	2	Q7P116_CHRYO	Q7P116_chromobacte
1497	6	1.8	136	2	Q9COK5_MOUSE	Q9COK5_mus muscu
1498	6	1.8	136	2	Q6X767_MNV	Q6X767_kunjin viru
1499	6	1.8	136	2	Q6X768_MNV	Q6X768_kunjin viru
1500	6	1.8	136	2	Q6X769_MNV	Q6X769_kunjin viru
ALIGNMENTS						
RESULT 1						
SLAF7_HUMAN						
ID	SLAF7_HUMAN	STANDARD;	PRT;	335 AA.		
AC	Q9N0Z5; Q8N6Y8; Q8ND32; Q9NV08; Q9NV23;					
DT	13-SEP-2005 (Rel. 48, Created)					
DT	13-SEP-2005 (Rel. 48, Last sequence update)					
DT	13-SEP-2005 (Rel. 48, Last annotation update)					
DE	SLAM family member 7 precursor (CD2-like receptor activating cytotoxic cell) (CRACC) (Protein 19A) (Membrane protein FOAP-12) (CD2 subunit 1) (Novel Ly9).					
DE	Name=SLAF7; Synonyms=CS1; ORFNames=UHQ576/PRO138;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Eumarchontoglires; Primates; Catarrhini; Homidae;					
OC	Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	NCBLOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND TISSUE SPECIFICITY.					
RX	MEDLINE=21151549; PubMed=11220635; DOI=10.1007/s002510000274;					
RA	Boles K.S., Mathew P.A.;					
RT	"Molecular cloning of CS1, a novel human natural killer cell receptor belonging to the CD2 subset of the immunoglobulin superfamily.";					
RL	Immunogenetics 52:302-307(2001).					
RN	[2]					
RP	NCBLOTIDE SEQUENCE [MRNA] (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY.					
RX	PubMed=1169418;					
RA	Bouchon A., Cella M., Grierson H.L., Cohen J.I., Colonna M.;					
RT	"Activation of NK cell-mediated cytotoxicity by a SAP-independent receptor of the CD2 family.";					
RL	J. Immunol. 167:5517-5521(2001).					
RN	[3]					
RP	NCBLOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 3), FUNCTION, AND TISSUE SPECIFICITY.					
RX	MEDLINE=21661458; PubMed=11802771; DOI=10.1042/0264-6021.3610431;					
RA	Murphy J.J., Hobby P., Villarino-Varela J., Bishop B., Iordanidou P., Sutton B.J., Norton J.D.;					
RT	"A novel immunoglobulin superfamily receptor (19A) related to CD2 is expressed on activated lymphocytes and promotes homotypic B-cell adhesion.";					
RL	Biochem. J. 361:431-436(2002).					
RN	[4]					
RP	NCBLOTIDE SEQUENCE [MRNA] (ISOFORM 1).					
RC	TISSUE=Macrophage;					
RA	Fujii Y., Kawayama K., Tsuritani K., Yajima Y., Amemiya T., Ukai Y., Naito K., Kawaguchi A.;					
RT	"Homo sapiens mRNA for FOAP-12 protein, complete cds.";					
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.					
RN	[5]					
RP	NCBLOTIDE SEQUENCE [LARGE SCALE MRNA]					
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;					
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J., Chen D., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Batton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M.R., Robbie R., Sanchez C., Schoenfeld J., Sehnagiri S., Simmons L., Singh J., Smith V., Stinson J., Vages A., Vanden R.L., Watanabe C., Wleand D., Woods K., Xie M.-H., Yanesura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,					

RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RT J. Genomics Res. 13:2265-2270(2003).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RC TISSUE=Lymph node;
RG The German cDNA consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG Human chromosome 1 international sequencing consortium;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC TISSUE=Petal lung, and Fetal spleen;
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullanb S.J.,
RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley K.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rutterfield Y.C., Grimwood J., Schmitt J., Myers R.M.,
RA Rutterfield Y.C., Schmitt J., Skalska J., Smalms D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP PROTEIN SEQUENCE OF 23-37.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [10]
RP ALTERNATIVE SPLICING.
RX PubMed=15368295; DOI=10.1002/eji.200424917;
RA Lee J.K., Boles K.S., Mathew P.A.;
RT "Molecular and functional characterization of a CSI (CRACC) splice
RT variant expressed in human NK cells that does not contain
RT immunoreceptor tyrosine-based switch motifs.";
RL Eur. J. Immunol. 34:2791-2799(2004).
RN [11]
RP TISSUE SPECIFICITY, AND SAP-BINDING.
RX MEDLINE=22226696; PubMed=12242590; DOI=10.1007/s00251-002-0483-3;
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Plazuela P.,
RA Bosch J., Terhorst C., Engel P.;
RT "Mouse novel Iy9: a new member of the expanding CD150 (SLAM) family of
RT leukocyte cell surface receptors.";
RL Immunogenetics 54:394-402(2002).
RN [12]
RP FUNCTION: Isoform 1 mediates NK cell activation through a SAP-
RP independent extracellular signal-regulated ERK-mediated pathway.
RP May play a role in lymphocyte adhesion. Isoform 3 does not mediate
RP any activation. SAP can bind the cytoplasmic tail of isoform 1
RP when phosphorylated in the presence of Fyn (in vitro).
RN [13]
RP SUBCELLULAR LOCATION: Type I membrane protein.
RN [14]
RP Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=19A, CSI-L;
CC IsoId=09NQ25-1; Sequence=Displayed;
CC Name=2;
CC IsoId=09NQ25-2; Sequence=VSP_013781;

CC Note=No experimental confirmation available;
CC Name=3; Synonyms=19A2, CSI-S;
CC IsoId=09NQ25-3; Sequence=VSP_013782;
CC -1- TISSUE SPECIFICITY: Expressed in spleen, lymph node, peripheral
CC blood leukocytes, bone marrow, small intestine, stomach, appendix,
CC lung and trachea. Expression was detected in NK cells, activated
CC B-cells, NK-cell line but not in promyelocytic, B-, or T-cell
CC lines. The isoform 3 is expressed at much lower level than isoform
CC 1.
CC -1- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.
CC -1- CAUTION: Ref.3 (CAB76561) sequence differs from that shown due to
CC framehifts.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AF291815; AAK1549.1; -; mRNA.
CC EMBL: AF390894; AAL26389.1; -; mRNA.
CC EMBL: AJ271669; CAB76561.1; ALT FRAME; mRNA.
CC EMBL: AJ276429; CAB81950.2; -; mRNA.
CC EMBL: AB027233; BAB61022.1; -; mRNA.
CC EMBL: AY358512; AAC88676.1; -; mRNA.
CC EMBL: AL834424; CAD39085.1; -; mRNA.
CC EMBL: AL121985; CAC005079.1; -; Genomic DNA.
CC EMBL: AL121985; CAH73507.1; -; Genomic DNA.
CC EMBL: AL121985; CAH73508.1; -; Genomic DNA.
CC EMBL: BC027867; AAH27867.1; -; mRNA.
CC EMBL: ENSG0000026751; Homo sapiens.
CC HGNC: HGNC:21394; SLAMF7.
CC MIM: 606625; -.
CC DR GO: GO:0016020; C:membrane; NAS.
CC DR GO: GO:0007155; P:cell adhesion; NAS.
CC DR GO: GO:0030101; P:natural killer cell activation; NAS.
CC DR GO: GO:0042267; P:natural killer cell mediated cytotoxicity; NAS.
CC DR InterPro: IPR007110; Ig-like.
CC DR PROSITE: PSS0835; IG_LIKE; 1.
CC KW Alternative splicing; Direct protein sequencing; Glycoprotein;
CC Immunoglobulin domain; Receptor; Signal; Transmembrane.
CC FT SIGNAL 1 22
FT CHAIN 23 335 SLAM family member 7.
FT TOPO_DOM 23 226 Extracellular (Potential).
FT TRANSMEM 227 247 Potential.
FT TOPO_DOM 248 335 Cytoplasmic (Potential).
FT DOMAIN 131 206 Ig-like C2-type.
FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 176 176 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 204 204 N-linked (GlcNAc...) (Potential).
FT DISULFID 145 215 Potential.
FT DISULFID 151 195 By similarity.
FT DISULFID 151 195 Missing (in isoform 2).
FT VARSPIC 19 125 /FTid=VSP_013781.
FT VARSPIC 258 296 YIEKKRVDCRETPNCPHSGNTEYDTIPHTNRITLK
FT -> NNRKGRSKYGLHCGNTEBDGSKPLRAHARHTKALC
FT L (in isoform 3).
FT FTid=VSP_013782.
FT M -> L (in Ref. 3).
SQ SEQUENCE 335 AA; 37421 MW; D09ABBCFF7ABEBD4 CRC64;
Query Match 100.0%; Score 335; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 7; 5e-312; Indels 0; Gaps 0;
Matches 335; Conservative 0; Mismatches 0;
Oy 1 MAGSPCTLTITITIMOLTGSAAGPYKELVGSVGAATPPLKSKVKQVDSIWTPTPTPL 60
Db 1 MAGSPCTLTITITIMOLTGSAAGPYKELVGSVGAATPPLKSKVKQVDSIWTPTPTPL 60

QY 61 VTIOPEGGTTIVTQNRNRERVPDGGYSLKSLKLNKDSIYYGYSSSLQOPSTQEX 120
 DB 61 VTIOPEGGTTIVTQNRNRERVPDGGYSLKSLKLNKDSIYYGYSSSLQOPSTQEX 120
 QY 121 VLAHYEHLSKRTKMTGLOSNNGGTCVNTLTCMEHGEEDVYTWKALGOANBESHNGSL 180
 DB 121 VLAHYEHLSKRTKMTGLOSNNGGTCVNTLTCMEHGEEDVYTWKALGOANBESHNGSL 180
 QY 181 PISMRGSDMTFTICVANRPVSRNPSPIRLAKLCEGAADPDSSMTVLCILVPLILSL 240
 DB 181 PISMRGSDMTFTICVANRPVSRNPSPIRLAKLCEGAADPDSSMTVLCILVPLILSL 240
 QY 241 FVLGLFLWFLKROEYIEBKRAVDICRETPNICPHSGENTEXTDPTPTNRITLKEDPA 300
 DB 241 FVLGLFLWFLKROEYIEBKRAVDICRETPNICPHSGENTEXTDPTPTNRITLKEDPA 300
 QY 241 FVLGLFLWFLKROEYIEBKRAVDICRETPNICPHSGENTEXTDPTPTNRITLKEDPA 300
 DB 241 FVLGLFLWFLKROEYIEBKRAVDICRETPNICPHSGENTEXTDPTPTNRITLKEDPA 300
 QY 301 NTAVSTVAIPKRMENPHSLTMPDTPRLFAVENYI 335
 DB 301 NTAVSTVAIPKRMENPHSLTMPDTPRLFAVENYI 335
 RESULT 2
 QYCY18 AERPE PRELIMINARY; PRT; 156 AA.
 AC QYCY18;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Hypothetical protein ABE1433;
 GN OrderedLocusNames=ABE1433;
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
 OC Desulfurococcaceae; Aeropyrum.
 CX NCBI_TaxID=56636;
 RN [1]
 RP NCBILOTIDE SEQUENCE.
 RC STRAIN=K1;
 RX MEDLINE=99310339, PubMed=10382966;
 RA Kawanabe Y., Hino Y., Horikawa H., Yamazaki S., Hatake Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankael A., Kosugi H.,
 RA Hotoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamaya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RA "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Rep. 6:83-101(1999).
 DR EMBL; BA000002; BAA0430.1; -; Genomic_DNA.
 DR PIR; H72621; H72621.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 156 AA; 15954 MW; 73BBB5C99PBB453D CRC64;
 Query Match 2.7%; Score 9; DB 2; Length 156;
 Best Local Similarity 100.0%; Pred. No. 7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 LTGSAAAGP 25
 DB 105 LTGSAAAGP 113
 RESULT 3
 SLAF7_MOUSE STANDARD; PRT; 333 AA.
 AC Q8BHK6; Q8BTL2; Q8CJ63; Q8CJ64; Q8CJ65; Q91XA0;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE SLAM family member 7 precursor (Leukocyte cell-surface antigen) (Novel
 Ly9).
 GN Name=Slamf7; (Mouse).
 OS Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP NCBILOTIDE SEQUENCE [MRNA] (ISOFORMS 2 AND 3).
 RC STRAIN=BALB/c, and C57BL/6; TISSUE=Thymus;
 RX MEDLINE=2228696; PubMed=1242590; DOI=10.1007/s00251-002-0483-3;
 RA Toxar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
 RA Bosch J., Terhorst C., Engel P.;
 RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
 RT leukocyte cell-surface receptors.";
 RL Immunogenetics 54:394-402(2002).
 RN [2]
 RP NCBILOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).
 RC STRAIN=C57BL/6J; TISSUE=Aorta, Testis, and Vain;
 RX MEDLINE=22354683; PubMed=12468851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kaenkawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaio I., Osato N., Saito R., Suzuki H., Yamanka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojouri T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chohtia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.D., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedziarski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrosky N., Pillai R., Pontius J.O., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wallestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yangisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazawa N., Sato K.,
 RA Shiraki T., Waki K., Kawai T., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino Y.,
 RA Binyon E., Hayashino M.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [3]
 RP NCBILOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 4).
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshitsuki S., Cavalcanti P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Hyers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalela E., Smalins D.E.,
 RA Scherf A., Schein J.B., Jones S.J.M., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 -I- FUNCTION: Mediates NK cell activation through a SAP-independent
 CC extracellular signal-regulated ERK-mediated pathway. May play a
 CC role in lymphocyte adhesion (By similarity). Isoform 1 does not
 CC bind SAP (in vitro).
 CC

```
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=Q8BHK6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8BHK6-2; Sequence=VSP_013784;
CC Name=3;
CC IsoId=Q8BHK6-3; Sequence=VSP_013783, VSP_013784;
CC Name=4;
CC IsoId=Q8BHK6-4; Sequence=VSP_013783;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Expressed in spleen, lymph node, bone marrow
CC and testis. Lower levels detected in thymus. Expressed in NK cells
CC and B-cells.
CC -1- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.
CC -1- CAUTION: Ref.3 sequence differs from that shown due to a
CC frameshift in position 255.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC The European Bioinformatics Institute. There are no restrictions on items
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, AF467909; AAN63158.1; -; mRNA.
CC EMBL, AF467910; AAN63159.1; -; mRNA.
CC EMBL, AF467911; AAN63160.1; -; mRNA.
CC EMBL, AK030135; BAC26801.1; -; mRNA.
CC EMBL, AK030148; BAC26810.1; -; mRNA.
CC EMBL, AK040678; BAC30665.1; -; mRNA.
CC EMBL, AK089525; BAC40914.1; -; mRNA.
CC EMBL, BC011154; AAH1154.1; ALT PRIME; mRNA.
CC Ensemble; ENSMUSG0000038179; Mus musculus.
CC MGI; MGI:1922595; Slamf7.
CC CO; GO:0016021; C:integral to membrane; TAS.
CC DR InterPro; IPRO07110; Ig-Like.
CC DR PROSITE; PS50835; IG_LIKE; 1.
CC KW Alternative splicing; Glycoprotein; Immunoglobulin domain; Receptor;
CC Signal; Transmembrane.
CC FT SIGNAL 1 22 By similarity.
CC FT CHAIN 23 333 SLAM family member 7.
CC FT TOPO_DOM 23 224 Extracellular (Potential).
CC FT TRANSMEM 225 245 Potential.
CC FT TOPO_DOM 246 333 Cytoplasmic (Potential).
CC FT DOMAIN 128 203 Ig-like C2-type.
CC FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 156 156 N-linked (GlcNAc...) (Potential).
CC FT DISULFID 142 212 Potential.
CC FT DISULFID 148 192 By similarity.
CC FT VASPLPCL 255 289 Missing (in isoform 3 and isoform 4).
CC FT VASPLPCL 312 333 /FtId=VSP_013783.
CC VARSPPLIC 312 333 LPSGLPAKFLVPSLSIFENYI -> RSCPAREHLTCOPLS
CC FT FT KDHRAO (in isoform 2 and isoform 3).
CC FT FT /FtId=VSP_013784.
CC FT CONFLICT 118 118 V -> A (in Ref. 1; AAN63158).
CC FT CONFLICT 248 248 T -> M (in Ref. 1; AAN63158 and 2).
CC FT CONFLICT 253 253 G -> R (in Ref. 1; AAN63159 and 3).
CC SO SEQUENCE 333 AA; 37187 MW; 8D40B8237EBE7129 CRC64;
Query Match 2.7%; Score 9; DB 1; Length 333;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 138 OSNKGITCV 146
DB 135 OSNKGITCV 143
```

RESULT 4

OS5NS1_CRYNE	PRELIMINARY;	PRT;	572 AA.
ID	Q5NS1_1		
AC	Q5NS1_1		
DT	13-SEP-2005 (TREMBLrel. 31, Created)		
DT	13-SEP-2005 (TREMBLrel. 31, Last sequence update)		
DT	13-SEP-2005 (TREMBLrel. 31, Last annotation update)		
DE	Hypothetical protein.		
GN	ORFNames=CNBH0180;		
OS	Cryptococcus neoformans var. neoformans B-3501A.		
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;		
OC	Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.		
OX	NCBI_TaxID=283643;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=B-3501A;		
RA	Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,		
RA	Wicks B.L., Fu J., Davis R.W.;		
RT	"Cryptococcus neoformans serotype D sequencing."		
RL	Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.		
CC	-1- CAUTION: The sequence shown here is derived from an		
CC	EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is		
CC	preliminary data.		
DR	EMBL; AAEX0100041; EAL19324.1; -; Genomic_DNA.		
DQ	Hypothetical protein.		
SK	SEQUENCE 572 AA; 63774 MW; A78BFC0EACCB812B CRC64;		
Query Match	2.7%; Score 9; DB 2; Length 572;		
Best Local Similarity	100.0%; Pred. No. 19;		
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Cy	232 LTVPLLLSL 240		
Db	481 LTVPLLLSL 489		
RESULT 5			
MAP1B_MOUSE			
ID	MAP1B_MOUSE	STANDARD;	PRT; 2464 AA.
AC	P14873;		
DT	01-APR-1990 (Rel. 14, Created)		
DT	01-APR-1990 (Rel. 14, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Microtubule-associated protein 1B (MAP1B) (MAP1.2) (MAP1(X))		
GN	[Contains: MAP1 light chain Lc1].		
GN	Name=Map1b; Synonyms=Mtcap1b, Mtap5;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE, AND DOMAIN.		
RC	STRAIN=Swiss Webster; TISSUE=Brain;		
RA	MEDLINE=90094539; Pubmed=2480963; DOI=10.1083/jcb.109.6.3367;		
RA	NOBLE M., Lewis S.A., Cowan N.J.;		
RT	"The microtubule binding domain of microtubule-associated protein		
RT	MAP1B contains a repeated sequence motif unrelated to that of MAP2 and		
RL	tau."		
RL	J. Cell Biol. 109:3367-3376 (1989).		
RN	[2]		
RP	PHOSPHORYLATION SITES SER-828; SER-829; SER-1247; SER-1255; SER-1260;		
RP	SER-1307; SER-1317; TYR-1331; SER-1334; SER-1371; SER-1373; SER-1382;		
RP	SER-1384; SER-1391; SER-1395; SER-1616; SER-1621; SER-1768; SER-1775;		
RP	SER-1778; SER-1781; THR-1784; SER-1793; THR-1806; SER-1877; SER-1911;		
RP	SER-2030 AND SER-2034.		
RX	Pubmed=15572359; DOI=10.1074/jbc.M411220200;		
RA	Collins M.O., Yu L., Caba M.P., Husi H., Campuzano I.,		
RA	Blackstock W.P., Choudhary J.S., Grant S.G.;		
RT	"Proteomic analysis of in vivo phosphorylated synaptic proteins."		
RL	J. Biol. Chem. 280:5972-5982(2005).		
CC	-1- FUNCTION: The function of brain MAPs is essentially unknown.		
CC	phosphorylated MAP1B may play a role in the cytoskeletal changes		

CC that accompany neurite extension. Possibly MAP1B binds to at least
 CC two tubulin subunits in the polymer, and this bridging of subunits
 CC might be involved in nucleating microtubule polymerization and in
 CC stabilizing microtubules.
 CC -1 SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
 CC with MAP1A and MAP1B proteins.
 CC -1 DOMAIN: Has a highly basic region with many copies of the sequence
 CC KKEE and KKEI/V, repeated but not at fixed intervals, which is
 CC responsible for the binding of MAP1B to microtubules.
 CC -1 PPM: LC1 is coexpressed with MAP1B. It is a polypeptide generated
 CC from MAP1B by proteolytic processing. It is free to associate with
 CC both MAP1A and MAP1B. It interacts with the amino-terminal region
 CC of MAP1B.
 CC -1 SIMILARITY: Belongs to the MAP1A/MAP1B family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, X51396, CA35761.1, -, mRNA.
 CC PIR, S07549; QRMSP1.
 CC DR Ensembl; ENSMUSG0000052727; Mus musculus.
 CC DR MGI; MGI:1306778; Mmap1b.
 CC DR GO; GO:0005875; C:microtubule associated complex; TAS.
 CC DR GO; GO:0005519; F:cytoskeletal regulatory protein binding; TAS.
 CC DR GO; GO:0016338; P:dendrite morphogenesis; IMP.
 CC DR GO; GO:0001578; P:microtubule bundle formation; IMP.
 CC DR GO; GO:0007017; P:microtubule-based process; TAS.
 CC DR InterPro; IPR00102; MAP1B neuraxin.
 CC DR Pfam; PF00414; MAP1B neuraxin; 10.
 CC DR PROSITE; PS00230; MAP1B-NEURAXIN; 7.
 CC KM Microtubule; Phosphorylation; Repeat.
 CC FT CHAIN ? 2464 Microtubule-associated protein 1B.
 CC FT REPEAT 1 1890 MAP1B 1.
 CC FT REPEAT 1891 1907 MAP1B 2.
 CC FT REPEAT 1908 1924 MAP1B 3.
 CC FT REPEAT 1925 1941 MAP1B 4.
 CC FT REPEAT 1942 1958 MAP1B 5.
 CC FT REPEAT 1959 1975 MAP1B 6.
 CC FT REPEAT 1993 2009 MAP1B 7.
 CC FT REPEAT 2010 2026 MAP1B 8.
 CC FT REPEAT 2027 2043 MAP1B 9.
 CC FT REPEAT 2044 2060 MAP1B 10.
 CC FT COMPBIA5 589 787 Lys-rich (highly basic, contains many
 CC KKEE and KKEI/V repeats).
 CC FT MOD_RES 828 828 Phosphoserine.
 CC FT MOD_RES 829 829 Phosphoserine.
 CC FT MOD_RES 1247 1247 Phosphoserine.
 CC FT MOD_RES 1255 1255 Phosphoserine.
 CC FT MOD_RES 1260 1260 Phosphoserine.
 CC FT MOD_RES 1307 1307 Phosphoserine.
 CC FT MOD_RES 1317 1317 Phosphoserine.
 CC FT MOD_RES 1331 1331 Phosphotyrosine.
 CC FT MOD_RES 1334 1334 Phosphoserine.
 CC FT MOD_RES 1371 1371 Phosphoserine.
 CC FT MOD_RES 1373 1373 Phosphoserine.
 CC FT MOD_RES 1382 1382 Phosphoserine.
 CC FT MOD_RES 1384 1384 Phosphoserine.
 CC FT MOD_RES 1391 1391 Phosphoserine.
 CC FT MOD_RES 1395 1395 Phosphoserine.
 CC FT MOD_RES 1616 1616 Phosphoserine.
 CC FT MOD_RES 1621 1621 Phosphoserine.
 CC FT MOD_RES 1768 1768 Phosphoserine.
 CC FT MOD_RES 1775 1775 Phosphoserine.
 CC FT MOD_RES 1778 1778 Phosphoserine.
 CC FT MOD_RES 1781 1781 Phosphoserine.
 CC FT MOD_RES 1784 1784 Phosphothreonine.
 CC FT MOD_RES 1793 1793 Phosphoserine.
 CC FT MOD_RES 1806 1806 Phosphothreonine.
 CC FT MOD_RES 1877 1877 Phosphoserine.

FT MOD_RES 1911 1911 Phosphoserine.
 FT MOD_RES 2030 2030 Phosphoserine.
 FT MOD_RES 2094 2094 Phosphoserine.
 SQ SEQUENCE 2464 AA; 270411 MW; FBD3DD9CFDDBA87 CRC64;
 Query Match 2.7%; Score 9; DB 1; Length 2464;
 Best Local Similarity 100.0%; Pred. No.53;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 21 AASGPVKEL 29
 Db 812 AASGPVKEL 820
 RESULT 6
 0884T6_PSESM
 ID 0884T6_PSESM PRELIMINARY; PRT; 83 AA.
 AC 0884T6;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Prevent-host-death family protein.
 GN OrderedLocustNames=PSPT02000;
 OS Pseudomonas syringae (pv. tomato).
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=323;
 RN [1]
 RP Nucleotide Sequence [LARGE SCALE GENOMIC DNA].
 RC STPAIN=DC3000;
 RX MEDLINE=22844015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
 RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
 RA Gwyn M.L., Dodson R.V., Deboy R.T., Durkin A.S., Kolonay J.F.,
 RA Madupu R., Daugherty S.C., Brinkac L.M., Beaman M.J., Haft D.H.,
 RA Nelson W.C., Daviden T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
 RA Khouir H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
 RA Uterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
 RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
 RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
 RA Bender C.L., White O., Fraser C.M., Collier A.;
 RT "The complete genome sequence of the Arabidopsis and tomato pathogen
 RT Pseudomonas syringae pv. tomato DC3000."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
 DR EMBL; A016853; AAO55518.1; -, Genomic_DNA.
 DR TIGR; PSPTO2000; -;
 DR InterPro; IPR006442; Phd.
 DR TIGRFAMs; TIGR01552; phd_fam; 1.
 KM Complete proteome.
 SQ SEQUENCE 83 AA; 8993 MW; ED9080CB44BCD3BE CRC64;
 Query Match 2.4%; Score 8; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No.39;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 16 QLTGSAAS 23
 Db 46 QLTGSAAS 53
 RESULT 7
 081VU0_HUMAN
 ID 081VU0_HUMAN PRELIMINARY; PRT; 129 AA.
 AC 081VU0;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE PAPLN protein.
 GN Name=PAPLN;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 CC Homo.
 OX NCBI_TaxID=9606;

```

RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL, BC042057; AA042057.1; -; mRNA.
DR HSSP; P07996; 1.LSL.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR Pfam; PF00090; TSP_1; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00209; TSP1.1.
DR PROSITE; PS50092; TSP1.1.
SQ SEQUENCE 129 AA; 14368 MW; D5144A94C12B3B CRC64;

Query March 2.4%; Score 8; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 231 LLLVLL 238
Db 4 LLLVLL 11

RESULT 8
Q54WZ7 D1CD1 PRELIMINARY; PRT; 136 AA.
ID Q54WZ7 D1CD1 PRELIMINARY; PRT; 136 AA.
AC Q54WZ7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD80205707;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachbat J.A., Gloeckner G., Rajandream M.-A.,
RA Stengard R., Bertram M., Song J., Olsen R., Szafarski K., Xu Q.,
RA Jungblut B., Kummerfeld S., Madera M., Kontorov B.A., Rivero F.,
RA Bankler A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Plitcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Karhounou A., Nie X., Hall N., Anjard C., Hemphill L., Basom N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,

```

```

RA Wardrop A., Falder M., Thangavelu M., Johnson D., Knights A.,
RA Louibeged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Munkler T., Tanaka Y.,
RA Shinkley G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platter M., Kay R.A.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuapa A.,
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -1 CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA01000059; EAL67798.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 136 AA; 15218 MW; C227B91721529F55 CRC64;

Query March 2.4%; Score 8; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 NGSLIPIS 183
Db 77 NGSLIPIS 84

RESULT 9
ID Q5YY9 NOCPA PRELIMINARY; PRT; 139 AA.
AC Q5YY9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedListNames=nfa17560;
OS Nocardia farcinica.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardia.
OX NCBI_TaxID=37329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFW 10152;
RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RA Shiba T., Hattori M.;
RT "The complete genomic sequence of Nocardia farcinica IFW 10152.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR EMBL; AP006618; BAD56602.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 139 AA; 14684 MW; E8A7E23F33C3BE7C CRC64;

Query March 2.4%; Score 8; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 240 LFFVGLFL 247
Db 48 LFFVGLFL 55

RESULT 10
ID Q6ERB1 ORYZA PRELIMINARY; PRT; 155 AA.
AC Q6ERB1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein P0448B1.30.
GN Name=P0448B1.30;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.

```

```

OX NCB1_TaxID=39947;
RN NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, PAC
   clone: P0448B11."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005585; BAD28809.1; -; Genomic_DNA.
DR Genbank; O6ERB1; -.
DR GO; GO:0000150; F:recombinase activity; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR06118; Recombinase_S.
DR PROSITE; PS00397; RECOMBINASE_1; 1.
KM Hypothetical protein.
SQ SEQUENCE 155 AA; 16880 MW; 3A8A2D4D9B82B87 CRC64;

Query Match 2.4%; Score 8; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 LLSLFVL 243
Db 18 LLSLFVL 25

RESULT 11
O55866 SYN3 PRELIMINARY; PRT; 173 AA.
ID O55866 SYN3
AC O55866;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Yc36 protein.
GN Name=Yc36; OrderedLocustNames=s110584;
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCB1_TaxID=1148;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97061201; Pubmed=8905231;
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiyama M., Sasamoto S., Kimura T.,
RA Hoshouchi T., Matsuno A., Muraki A., Nakazaki N., Naro K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
   Synechocystis sp. strain PCC6803. II. Sequence determination of the
   entire genome and assignment of potential protein-coding regions."
RL DNA Rep. 3:109-136(1996).
DR EMBL; BA000022; BA010625.1; -; Genomic_DNA.
DR PIR; S7681; S7681.
DR InterPro; IPR009631; DUF1230.
DR Pfam; PF06799; DUF1230; 1.
KM Complete proteome.
SQ SEQUENCE 173 AA; 19933 MW; 666079BBE094111 CRC64;

Query Match 2.4%; Score 8; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 LLSLFVL 243
Db 85 LLSLFVL 92

RESULT 12
Q7V2B6 PROMP PRELIMINARY; PRT; 202 AA.
ID Q7V2B6 PROMP
AC Q7V2B6;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.

```

```

GN OrderedLocustNames=PM00564;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCB1_TaxID=59919;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22825698; Pubmed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Lattimer P.W., Lamerdin J.B., Malfatti S., Chait P.,
RA Aalgreen N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb B.A., Zinner B.R., Christol S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
   niche differentiation."
RL Nature 424:1042-1047(2003).
DR EMBL; BX572091; CAE19023.1; -; Genomic_DNA.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 202 AA; 23132 MW; FF35586196F7P2E CRC64;

Query Match 2.4%; Score 8; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 LSKLKND 99
Db 122 LSKLKND 129

RESULT 13
Q9S488 PROS9 PRELIMINARY; PRT; 211 AA.
ID Q9S488 PROS9
AC Q9S488;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Prochlorococcus sp. (strain PCC 9511).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCB1_TaxID=100363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=PCC 9511;
RX MEDLINE=21142517; Pubmed=11208789; DOI=10.1126/JB.183.3.915-920.2001;
RA Holtzendorff J., Partensky F., Jacquet S., Bryant F., Marie D.,
RA Gatzertek L., Mary I., Valot D., Hess W.R.;
RT "Diurnal expression of cell cycle-related genes in synchronized cultures
   of Prochlorococcus sp. strain PCC 9511."
RL J. Bacteriol. 183:915-920(2001).
DR EMBL; AF158628; AAD45694.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 211 AA; 24129 MW; 6228068FF04673F2 CRC64;

Query Match 2.4%; Score 8; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 LSKLKND 99
Db 131 LSKLKND 138

RESULT 14
Q5VID5 HALMA PRELIMINARY; PRT; 230 AA.
ID Q5VID5 HALMA
AC Q5VID5;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Proteasome subunit alpha.
GN Name=psm1; OrderedLocustNames=trnAC1772;
OS Haloarcula marismortui (Haloacterium marismortui).

```

OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halorcula.
 OX NCBI_TaxID=2238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 43049;
 RX PubMed=15520287; DOI=10.1101/gr.2700304;
 RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
 RA Deutch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
 RA Date S.V., Marcotte E., Hood L., Ng W.V.;
 RT "Genome sequence of Halorcula marismortui: a halophilic archaeon from
 the Dead Sea."
 RL Genome Res. 14:2221-2234(2004).
 DR EMBL; AY596297; AAY46667.1; -; Genomic_DNA.
 DR GO; GO:0005829; C:cytosol; IEA.
 DR GO; GO:0005839; C:proteasome core complex (sensu Eukaryota); IEA.
 DR GO; GO:0004298; F:chreonine endopeptidase activity; IEA.
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
 DR InterPro; IPR000243; Pept_T1A_subB.
 DR InterPro; IPR001353; Proteasome_A_B.
 DR Pfam; PF00227; Proteasome; 1.
 DR PRINTS; PR00141; PROTEASOME.
 KM Complete proteome; Proteasome.
 SQ SEQUENCE 230 AA; 24274 MW; A97828C417B98407 CRC64;

Query Match 2.4%; Score 8; DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 LVGSVGA 36
 |||||
 Db 81 LVGSVGA 88

RESULT 15

OSV4S6 HALMA PRELIMINARY; PRT; 240 AA.
 ID OSV4S6 HALMA PRELIMINARY;
 AC OSV4S6;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Proteasome subunit alpha.
 GN Name=psmA3; OrderedLocNames=trnAC0442;
 OS Halorcula marismortui (Halobacterium marismortui).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halorcula.
 OX NCBI_TaxID=2238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 43049;
 RX PubMed=15520287; DOI=10.1101/gr.2700304;
 RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
 RA Deutch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
 RA Date S.V., Marcotte E., Hood L., Ng W.V.;
 RT "Genome sequence of Halorcula marismortui: a halophilic archaeon from
 the Dead Sea."
 RL Genome Res. 14:2221-2234(2004).
 DR EMBL; AY596297; AAY45476.1; -; Genomic_DNA.
 DR GO; GO:0005829; C:cytosol; IEA.
 DR GO; GO:0005839; C:proteasome core complex (sensu Eukaryota); IEA.
 DR GO; GO:0004298; F:chreonine endopeptidase activity; IEA.
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
 DR InterPro; IPR000243; Pept_T1A_subB.
 DR InterPro; IPR001353; Proteasome_A_B.
 DR Pfam; PF00227; Proteasome; 1.
 DR PRINTS; PR00141; PROTEASOME.
 KM Complete proteome; Proteasome.
 SQ SEQUENCE 240 AA; 25261 MW; 9274753670576304 CRC64;

Query Match 2.4%; Score 8; DB 2; Length 240;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 LVGSVGA 36
 |||||
 Db 92 LVGSVGA 99

Search completed: December 16, 2005, 11:57:47
 Job time : 234 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 11:49:55 ; Search time 47 Seconds
(without alignments)
589,284 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 335
Sequence: 1 MASPTCTLYIYLQITGS.....PHSLTTPDPRLPAYENV1 335

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1500 summaries

Database :

- 1: /cgn2_6/ptodata/1/1aa/5.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/6.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/PCrUS.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RB.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	335	100.0	335	2	US-09-991-181-253
2	335	100.0	335	2	US-09-990-444-253
3	335	100.0	335	2	US-09-997-333-253
4	335	100.0	335	2	US-09-992-598-253
5	97	29.0	97	2	US-09-513-999C-4472
6	8	2.4	289	2	US-09-466-778-8
7	8	2.4	360	2	US-09-907-794A-213
8	8	2.4	360	2	US-09-905-125A-213
9	8	2.4	360	2	US-09-902-775A-213
10	8	2.4	360	2	US-09-906-700-213
11	8	2.4	360	2	US-09-903-603A-213
12	8	2.4	360	2	US-09-904-920A-213
13	8	2.4	360	2	US-09-909-064-213
14	8	2.4	360	2	US-09-905-381A-213
15	8	2.4	360	2	US-09-906-618-213
16	8	2.4	360	2	US-09-906-646-213
17	8	2.4	360	2	US-09-904-462-213
18	8	2.4	360	2	US-09-902-736A-213
19	8	2.4	360	2	US-09-906-722A-213
20	8	2.4	410	2	US-09-252-991A-31174
21	8	2.4	1105	2	US-09-949-016-8227
22	8	2.4	1117	2	US-09-949-016-6148
23	7	2.1	63	2	US-09-646-681B-10
24	7	2.1	67	2	US-09-543-681A-4733
25	7	2.1	84	2	US-09-270-767-60733
26	7	2.1	85	2	US-09-248-796A-22136
27	7	2.1	97	2	US-09-886-319A-29

28	7	2.1	98	2	US-08-613-822-4	Sequence 4, Appl1
29	7	2.1	98	2	US-08-852-212-2	Sequence 2, Appl1
30	7	2.1	98	2	US-09-479-729B-4	Sequence 4, Appl1
31	7	2.1	98	2	US-09-261-201A-4	Sequence 4, Appl1
32	7	2.1	98	2	US-09-717-209-4	Sequence 4, Appl1
33	7	2.1	98	2	US-09-545-894-2	Sequence 2, Appl1
34	7	2.1	98	2	US-09-834-795A-25	Sequence 25, Appl1
35	7	2.1	98	2	US-10-164-621-4	Sequence 4, Appl1
36	7	2.1	98	2	US-10-125-451-4	Sequence 4, Appl1
37	7	2.1	137	2	US-09-270-767-33253	Sequence 33253, A
38	7	2.1	137	2	US-09-270-767-48470	Sequence 48470, A
39	7	2.1	156	2	US-09-270-767-45241	Sequence 45241, A
40	7	2.1	132	2	US-08-486-099-107	Sequence 107, App
41	7	2.1	132	2	US-08-360-107B-117	Sequence 117, App
42	7	2.1	192	2	US-08-484-223B-107	Sequence 107, App
43	7	2.1	192	2	US-08-919-597-107	Sequence 107, App
44	7	2.1	192	2	US-08-475-668A-107	Sequence 107, App
45	7	2.1	192	2	US-08-485-551A-107	Sequence 107, App
46	7	2.1	192	2	US-08-471-913A-107	Sequence 107, App
47	7	2.1	192	2	US-08-485-264A-107	Sequence 107, App
48	7	2.1	192	2	US-08-474-349A-107	Sequence 107, App
49	7	2.1	192	2	US-08-470-896-107	Sequence 107, App
50	7	2.1	192	2	US-08-485-546A-107	Sequence 107, App
51	7	2.1	192	2	US-08-487-266A-107	Sequence 107, App
52	7	2.1	192	2	US-08-484-741-107	Sequence 107, App
53	7	2.1	208	1	US-08-680-726A-72	Sequence 72, Appl1
54	7	2.1	208	1	US-09-092-409-72	Sequence 72, Appl1
55	7	2.1	229	2	US-09-078-691-4	Sequence 4, Appl1
56	7	2.1	244	2	US-09-328-352-4316	Sequence 4316, Ap
57	7	2.1	262	2	US-10-104-047-2006	Sequence 2006, Ap
58	7	2.1	264	2	US-09-069-023-7	Sequence 7, Appl1
59	7	2.1	266	2	US-09-107-433-2900	Sequence 2900, Ap
60	7	2.1	276	2	US-09-302-540-11303	Sequence 11303, A
61	7	2.1	277	2	US-09-583-110-2944	Sequence 2944, Ap
62	7	2.1	290	2	US-09-107-433-4262	Sequence 4262, Ap
63	7	2.1	300	2	US-09-099-041A-4	Sequence 4, Appl1
64	7	2.1	300	2	US-09-245-281-4	Sequence 4, Appl1
65	7	2.1	300	2	US-09-207-359B-4	Sequence 4, Appl1
66	7	2.1	300	2	US-09-340-620B-4	Sequence 4, Appl1
67	7	2.1	300	2	US-09-865-364-4	Sequence 4, Appl1
68	7	2.1	300	2	US-09-728-721-4	Sequence 4, Appl1
69	7	2.1	301	2	US-09-583-110-3523	Sequence 3523, Ap
70	7	2.1	303	2	US-09-632-947B-5	Sequence 5, Appl1
71	7	2.1	316	2	US-09-078-691-2	Sequence 2, Appl1
72	7	2.1	318	2	US-09-107-532A-6372	Sequence 6372, Ap
73	7	2.1	332	2	US-09-543-681A-6622	Sequence 6622, Ap
74	7	2.1	337	2	US-09-252-991A-32265	Sequence 32265, A
75	7	2.1	335	2	US-09-134-000C-4818	Sequence 4818, Ap
76	7	2.1	408	1	US-09-014-969-13	Sequence 13, Appl1
77	7	2.1	419	1	US-08-997-080-125	Sequence 125, App
78	7	2.1	419	1	US-08-997-362-125	Sequence 125, App
79	7	2.1	419	2	US-09-095-855-125	Sequence 125, App
80	7	2.1	419	2	US-09-324-542-125	Sequence 125, App
81	7	2.1	419	2	US-09-205-426-125	Sequence 125, App
82	7	2.1	427	2	US-09-134-000C-4837	Sequence 4837, Ap
83	7	2.1	433	2	US-10-152-886-11	Sequence 11, Appl1
84	7	2.1	439	2	US-09-282-305-6	Sequence 6, Appl1
85	7	2.1	439	2	US-09-883-720-6	Sequence 6, Appl1
86	7	2.1	448	2	US-09-724-797-44	Sequence 4, Appl1
87	7	2.1	472	2	US-09-489-039A-11144	Sequence 11144, A
88	7	2.1	472	2	US-09-107-532A-6117	Sequence 6117, Ap
89	7	2.1	478	2	US-09-069-023-4	Sequence 4, Appl1
90	7	2.1	478	2	US-09-502-540-10474	Sequence 10474, A
91	7	2.1	493	2	US-09-720-529A-2	Sequence 2, Appl1
92	7	2.1	522	2	US-09-605-703B-1378	Sequence 1378, Ap
93	7	2.1	530	2	US-09-069-023-3	Sequence 3, Appl1
94	7	2.1	531	2	US-09-069-023-1	Sequence 1, Appl1
95	7	2.1	539	2	US-09-800-170-16	Sequence 16, Appl1
96	7	2.1	540	2	US-09-019-842-1	Sequence 1, Appl1
97	7	2.1	540	2	US-09-099-041A-2	Sequence 2, Appl1
98	7	2.1	540	2	US-09-069-023-27	Sequence 27, Appl1
99	7	2.1	540	2	US-09-245-281-2	Sequence 2, Appl1
100	7	2.1	540	2	US-09-470-271-1	Sequence 1, Appl1

101	7	2.1	540	2	US-09-207-359B-2	Sequence 2, Appl1	174	6	1.8	28	4	PCT-US92-04537-6	Sequence 6, Appl1
102	7	2.1	540	2	US-09-340-620A-2	Sequence 2, Appl1	175	6	1.8	29	1	US-07-927-391-8	Sequence 8, Appl1
103	7	2.1	540	2	US-09-345-473E-28	Sequence 28, Appl1	176	6	1.8	30	1	US-08-619-198-7	Sequence 7, Appl1
104	7	2.1	540	2	US-09-865-364-2	Sequence 2, Appl1	177	6	1.8	33	2	US-07-927-391-9	Sequence 9, Appl1
105	7	2.1	540	2	US-09-748-537-1	Sequence 1, Appl1	178	6	1.8	33	2	US-08-789-333F-15	Sequence 15, Appl1
106	7	2.1	540	2	US-09-981-397A-14	Sequence 14, Appl1	179	6	1.8	33	2	US-09-169-015-25	Sequence 25, Appl1
107	7	2.1	540	2	US-09-862-027-28	Sequence 28, Appl1	180	6	1.8	33	2	US-09-133-944-15	Sequence 15, Appl1
108	7	2.1	540	2	US-09-728-721-2	Sequence 2, Appl1	181	6	1.8	33	2	US-09-208-827-16	Sequence 16, Appl1
109	7	2.1	550	2	US-09-771-161A-184	Sequence 184, App	182	6	1.8	33	2	US-08-787-738B-15	Sequence 15, Appl1
110	7	2.1	540	2	US-09-248-796A-20760	Sequence 20760, A	183	6	1.8	33	2	US-09-157-748-18	Sequence 18, Appl1
111	7	2.1	646	2	US-09-252-991A-18949	Sequence 18949, A	184	6	1.8	33	2	US-09-800-170-68	Sequence 68, Appl1
112	7	2.1	650	2	US-09-310-463-2	Sequence 2, Appl1	185	6	1.8	33	2	US-09-626-581B-28	Sequence 28, Appl1
113	7	2.1	650	2	US-08-842-248A-2	Sequence 2, Appl1	186	6	1.8	33	2	US-09-415-765E-28	Sequence 28, Appl1
114	7	2.1	650	2	US-09-949-002-390	Sequence 390, App	187	6	1.8	33	2	US-09-626-580C-28	Sequence 28, Appl1
115	7	2.1	650	2	US-10-104-047-3395	Sequence 3395, App	188	6	1.8	33	2	US-09-749-959-24	Sequence 24, Appl1
116	7	2.1	651	2	US-08-985-950-22	Sequence 22, Appl1	189	6	1.8	33	2	US-10-043-074-16	Sequence 16, Appl1
117	7	2.1	651	2	US-09-546-049-22	Sequence 22, Appl1	190	6	1.8	33	2	US-09-285-912A-78	Sequence 78, Appl1
118	7	2.1	652	2	US-09-310-463-4	Sequence 4, Appl1	191	6	1.8	33	2	US-09-578-030-19	Sequence 19, Appl1
119	7	2.1	652	2	US-08-842-248A-4	Sequence 4, Appl1	192	6	1.8	33	2	US-09-916-940-15	Sequence 15, Appl1
120	7	2.1	670	1	US-08-997-080-178	Sequence 178, App	193	6	1.8	33	2	US-09-419-381-62	Sequence 62, Appl1
121	7	2.1	670	1	US-08-997-362-178	Sequence 178, App	194	6	1.8	33	2	US-10-142-662-29	Sequence 29, Appl1
122	7	2.1	670	1	US-09-095-855-178	Sequence 178, App	195	6	1.8	33	2	US-09-308-992B-13	Sequence 13, Appl1
123	7	2.1	670	2	US-09-324-542-178	Sequence 178, App	196	6	1.8	33	2	US-09-308-992B-24	Sequence 24, Appl1
124	7	2.1	670	2	US-09-205-426-178	Sequence 178, App	197	6	1.8	33	2	US-09-308-992B-25	Sequence 25, Appl1
125	7	2.1	672	1	US-09-949-002-416	Sequence 416, App	198	6	1.8	33	2	US-10-096-550-15	Sequence 15, Appl1
126	7	2.1	722	1	US-08-997-080-174	Sequence 174, App	199	6	1.8	33	2	US-09-062-330-11	Sequence 11, Appl1
127	7	2.1	722	1	US-08-997-362-174	Sequence 174, App	200	6	1.8	33	2	US-10-226-877A-20	Sequence 20, Appl1
128	7	2.1	722	2	US-09-095-855-174	Sequence 174, App	201	6	1.8	33	2	US-10-177-725-144	Sequence 144, App
129	7	2.1	722	2	US-09-324-542-174	Sequence 174, App	202	6	1.8	36	2	US-09-308-992B-22	Sequence 22, Appl1
130	7	2.1	722	2	US-09-205-426-174	Sequence 174, App	203	6	1.8	40	2	US-08-776-971-113	Sequence 113, App
131	7	2.1	728	2	US-09-949-016-9813	Sequence 9813, App	204	6	1.8	40	2	US-09-576-290-113	Sequence 113, App
132	7	2.1	734	2	US-09-949-016-9115	Sequence 9115, App	205	6	1.8	40	2	US-09-716-147-113	Sequence 113, App
133	7	2.1	743	2	US-10-104-047-2340	Sequence 2340, App	206	6	1.8	43	1	US-07-998-003A-57	Sequence 57, Appl1
134	7	2.1	816	2	US-09-949-016-9116	Sequence 9116, App	207	6	1.8	43	1	US-08-453-274B-57	Sequence 57, Appl1
135	7	2.1	943	2	US-09-583-110-4794	Sequence 4794, App	208	6	1.8	43	1	US-08-453-695A-57	Sequence 57, Appl1
136	7	2.1	945	2	US-09-107-433-3340	Sequence 3340, App	209	6	1.8	43	1	US-08-268-161A-57	Sequence 57, Appl1
137	7	2.1	963	1	US-08-537-002A-3	Sequence 3, Appl1	210	6	1.8	43	1	US-08-453-702A-57	Sequence 57, Appl1
138	7	2.1	963	2	US-08-863-010-3	Sequence 3, Appl1	211	6	1.8	43	1	US-09-099-639-57	Sequence 57, Appl1
139	7	2.1	963	2	US-09-024-429-3	Sequence 3, Appl1	212	6	1.8	43	4	PCT-US93-1258B-57	Sequence 57, Appl1
140	7	2.1	964	2	US-09-543-681A-5035	Sequence 5035, App	213	6	1.8	43	4	PCT-US95-08071-57	Sequence 57, Appl1
141	7	2.1	972	2	US-09-489-039A-11867	Sequence 11867, A	214	6	1.8	46	2	US-09-471-276-1047	Sequence 1047, App
142	7	2.1	1019	1	US-08-271-364A-7	Sequence 7, Appl1	215	6	1.8	47	2	US-09-391-799-6	Sequence 6, Appl1
143	7	2.1	1019	1	US-08-222-715B-26	Sequence 26, Appl1	216	6	1.8	47	2	US-09-471-276-955	Sequence 955, App
144	7	2.1	1085	1	US-08-431-080-28	Sequence 28, Appl1	217	6	1.8	49	2	US-09-208-140-7	Sequence 7, Appl1
145	7	2.1	1085	1	US-08-938-534-28	Sequence 28, Appl1	218	6	1.8	49	2	US-09-308-140-31	Sequence 19, Appl1
146	7	2.1	1085	2	US-09-345-294-28	Sequence 28, Appl1	219	6	1.8	49	2	US-09-208-140-31	Sequence 31, Appl1
147	7	2.1	1161	2	US-09-252-991A-22872	Sequence 22872, A	220	6	1.8	49	2	US-09-208-140-32	Sequence 32, Appl1
148	7	2.1	1290	2	US-09-150-460B-6	Sequence 6, Appl1	221	6	1.8	56	2	US-09-621-976-5480	Sequence 5480, App
149	7	2.1	1291	2	US-09-150-460B-10	Sequence 10, Appl1	222	6	1.8	56	2	US-09-621-976-6983	Sequence 6983, App
150	7	2.1	1291	2	US-09-220-641-5	Sequence 5, Appl1	223	6	1.8	60	2	US-09-513-999E-5781	Sequence 5781, App
151	7	2.1	1566	2	US-09-581-472B-2	Sequence 2, Appl1	224	6	1.8	61	2	US-09-248-796A-25070	Sequence 25070, A
152	7	2.1	1581	2	US-09-110-517-2	Sequence 2, Appl1	225	6	1.8	62	2	US-09-621-976-4988	Sequence 4988, App
153	7	2.1	1607	2	US-09-902-540-16765	Sequence 16765, A	226	6	1.8	65	2	US-09-543-681A-5670	Sequence 5670, App
154	7	2.1	6239	2	US-09-914-286-4	Sequence 4, Appl1	227	6	1.8	65	2	US-09-513-999C-6592	Sequence 6592, App
155	6	1.8	8	2	US-09-248-588-66	Sequence 66, Appl1	228	6	1.8	67	2	US-09-621-976-6567	Sequence 6567, App
156	6	1.8	12	2	US-08-836-075A-130	Sequence 130, App	229	6	1.8	67	2	US-09-270-767-37915	Sequence 37915, A
157	6	1.8	18	2	US-09-470-830A-2	Sequence 2, Appl1	230	6	1.8	67	2	US-09-270-767-53132	Sequence 53132, A
158	6	1.8	19	2	US-08-848-580-8	Sequence 8, Appl1	231	6	1.8	67	2	US-09-248-796A-25766	Sequence 25766, A
159	6	1.8	19	2	US-08-488-123-8	Sequence 8, Appl1	232	6	1.8	67	2	US-09-513-999E-5199	Sequence 5199, App
160	6	1.8	19	2	US-09-470-830A-3	Sequence 3, Appl1	233	6	1.8	69	2	US-09-621-976-6740	Sequence 6740, App
161	6	1.8	19	2	US-09-470-830A-4	Sequence 4, Appl1	234	6	1.8	69	2	US-09-270-767-39496	Sequence 39496, A
162	6	1.8	19	4	PCT-US92-04537-4	Sequence 4, Appl1	235	6	1.8	69	2	US-09-270-767-58217	Sequence 58217, A
163	6	1.8	20	2	US-09-470-830A-43	Sequence 43, Appl1	236	6	1.8	71	2	US-09-370-767-58217	Sequence 58217, A
164	6	1.8	21	2	US-08-848-580-9	Sequence 9, Appl1	237	6	1.8	71	2	US-09-370-767-62067	Sequence 62067, A
165	6	1.8	21	2	US-08-488-123-9	Sequence 9, Appl1	238	6	1.8	72	2	US-09-370-767-36918	Sequence 36918, A
166	6	1.8	21	2	US-09-471-276-950	Sequence 950, App	239	6	1.8	72	2	US-09-270-767-52135	Sequence 52135, A
167	6	1.8	21	4	PCT-US92-04537-5	Sequence 5, Appl1	240	6	1.8	73	2	US-09-543-681A-4655	Sequence 4655, App
168	6	1.8	23	2	US-07-927-391-7	Sequence 7, Appl1	241	6	1.8	74	2	US-08-305-223-294	Sequence 294, App
169	6	1.8	25	2	US-09-690-454-200	Sequence 200, App	242	6	1.8	78	2	US-08-305-223-296	Sequence 296, App
170	6	1.8	28	2	US-08-848-580-10	Sequence 10, Appl1	243	6	1.8	79	2	US-09-621-976-5293	Sequence 5293, App
171	6	1.8	28	2	US-09-149-476-322	Sequence 322, App	244	6	1.8	79	2	US-09-370-767-58410	Sequence 58410, A
172	6	1.8	28	2	US-09-149-476-509	Sequence 509, App	245	6	1.8	80	2	US-09-328-352-5464	Sequence 5464, App
173	6	1.8	28	2	US-08-488-123-10	Sequence 10, Appl1	246	6	1.8	80	2	US-09-540-236-3087	Sequence 3087, App

247	6	1.8	81	2	US-09-248-796A-23117	Sequence 23117, A	320	6	1.8	99	1	US-08-347-492B-8	Sequence 8, Appl1
248	6	1.8	81	2	US-09-248-796A-27993	Sequence 27993, A	321	6	1.8	99	1	US-08-480-449-18	Sequence 18, Appl1
249	6	1.8	82	2	US-09-489-039A-13580	Sequence 13580, A	322	6	1.8	99	1	US-08-480-449-19	Sequence 19, Appl1
250	6	1.8	83	2	US-08-776-971-45	Sequence 45, Appl1	323	6	1.8	99	1	US-08-479-126B-5	Sequence 5, Appl1
251	6	1.8	83	2	US-08-776-971-124	Sequence 124, App	324	6	1.8	99	1	US-08-421-144A-5	Sequence 5, Appl1
252	6	1.8	83	2	US-08-776-971-137	Sequence 137, App	325	6	1.8	99	1	US-08-726-830A-5	Sequence 5, Appl1
253	6	1.8	83	2	US-09-576-290-45	Sequence 45, Appl1	326	6	1.8	99	1	US-08-660-542-18	Sequence 18, Appl1
254	6	1.8	83	2	US-09-576-290-124	Sequence 124, App	327	6	1.8	99	1	US-08-660-542-19	Sequence 19, Appl1
255	6	1.8	83	2	US-09-576-290-137	Sequence 137, App	328	6	1.8	99	1	US-08-798-143-8	Sequence 8, Appl1
256	6	1.8	83	2	US-09-716-147-45	Sequence 45, Appl1	329	6	1.8	99	2	US-07-927-391-24	Sequence 24, Appl1
257	6	1.8	83	2	US-09-716-147-124	Sequence 124, App	330	6	1.8	99	2	US-08-995-156A-5	Sequence 5, Appl1
258	6	1.8	83	2	US-09-716-147-137	Sequence 137, App	331	6	1.8	99	2	US-09-044-856A-5	Sequence 5, Appl1
259	6	1.8	83	2	US-10-012-819-250	Sequence 250, App	332	6	1.8	99	2	US-09-044-855A-5	Sequence 5, Appl1
260	6	1.8	84	2	US-09-248-796A-24714	Sequence 24714, A	333	6	1.8	99	2	US-08-613-822-18	Sequence 18, Appl1
261	6	1.8	84	2	US-09-248-796A-26339	Sequence 26339, A	334	6	1.8	99	2	US-08-928-183B-14	Sequence 14, Appl1
262	6	1.8	84	2	US-09-248-796A-27934	Sequence 27934, A	335	6	1.8	99	2	US-09-133-521-5	Sequence 5, Appl1
263	6	1.8	85	2	US-09-328-352-6104	Sequence 6104, App	336	6	1.8	99	2	US-08-679-493A-152	Sequence 152, App
264	6	1.8	86	2	US-10-178-213-230	Sequence 230, App	337	6	1.8	99	2	US-08-479-603-18	Sequence 18, Appl1
265	6	1.8	87	2	US-09-288-143-96	Sequence 96, Appl1	338	6	1.8	99	2	US-08-479-603-19	Sequence 19, Appl1
266	6	1.8	87	2	US-09-270-767-34042	Sequence 34042, A	339	6	1.8	99	2	US-09-419-281-5	Sequence 5, Appl1
267	6	1.8	87	2	US-09-270-767-49259	Sequence 49259, A	340	6	1.8	99	2	US-09-479-729B-18	Sequence 18, Appl1
268	6	1.8	89	2	US-09-543-681A-6121	Sequence 6121, App	341	6	1.8	99	2	US-09-366-887A-10	Sequence 10, Appl1
269	6	1.8	91	2	US-09-270-767-34720	Sequence 34720, A	342	6	1.8	99	2	US-08-939-107-18	Sequence 18, Appl1
270	6	1.8	91	2	US-09-270-767-49937	Sequence 49937, A	343	6	1.8	99	2	US-08-939-107-19	Sequence 19, Appl1
271	6	1.8	92	2	US-09-366-887A-14	Sequence 14, Appl1	344	6	1.8	99	2	US-09-886-319A-30	Sequence 30, Appl1
272	6	1.8	92	2	US-09-252-991A-28334	Sequence 28334, A	345	6	1.8	99	2	US-09-886-319A-30	Sequence 30, Appl1
273	6	1.8	92	2	US-09-621-976-5285	Sequence 5285, App	346	6	1.8	99	2	US-09-717-209-18	Sequence 18, Appl1
274	6	1.8	92	2	US-09-248-796A-22331	Sequence 22331, A	347	6	1.8	99	2	US-09-545-894-5	Sequence 5, Appl1
275	6	1.8	92	2	US-09-248-796A-26769	Sequence 26769, A	348	6	1.8	99	2	US-09-545-894-7	Sequence 7, Appl1
276	6	1.8	92	2	US-09-517-204-14	Sequence 14, Appl1	349	6	1.8	99	2	US-09-834-795A-27	Sequence 27, Appl1
277	6	1.8	93	2	US-09-248-796A-27221	Sequence 27221, A	350	6	1.8	99	2	US-09-834-795A-28	Sequence 28, Appl1
278	6	1.8	94	1	US-08-150-203A-5	Sequence 5, Appl1	351	6	1.8	99	2	US-09-067-447B-18	Sequence 18, Appl1
279	6	1.8	94	1	US-08-949-788-5	Sequence 5, Appl1	352	6	1.8	99	2	US-09-67-447B-19	Sequence 19, Appl1
280	6	1.8	94	2	US-09-621-976-6341	Sequence 6341, App	353	6	1.8	99	2	US-09-513-599C-7700	Sequence 7700, App
281	6	1.8	94	2	US-09-198-452A-1220	Sequence 1220, App	354	6	1.8	99	2	US-08-437-306-2	Sequence 2, Appl1
282	6	1.8	95	2	US-09-621-976-5712	Sequence 5712, App	355	6	1.8	99	2	US-08-479-620-18	Sequence 18, Appl1
283	6	1.8	95	2	US-09-366-887A-9	Sequence 9, Appl1	356	6	1.8	99	2	US-08-479-620-19	Sequence 19, Appl1
284	6	1.8	96	2	US-09-248-796A-18136	Sequence 18136, A	357	6	1.8	99	2	US-10-054-960-5	Sequence 5, Appl1
285	6	1.8	96	2	US-09-645-593-9	Sequence 9, Appl1	358	6	1.8	99	2	US-10-141-865-5	Sequence 5, Appl1
286	6	1.8	96	2	US-09-517-204-9	Sequence 9, Appl1	359	6	1.8	99	2	US-09-537-859D-1	Sequence 1, Appl1
287	6	1.8	96	2	US-08-467-822-40	Sequence 40, Appl1	360	6	1.8	99	2	US-09-537-859D-2	Sequence 2, Appl1
288	6	1.8	97	2	US-09-472-971-4	Sequence 4, Appl1	361	6	1.8	99	2	US-10-125-451-18	Sequence 18, Appl1
289	6	1.8	97	2	US-08-432-697-40	Sequence 40, Appl1	362	6	1.8	99	2	US-09-104-1087-5	Sequence 5, Appl1
290	6	1.8	97	2	US-08-466-248-40	Sequence 40, Appl1	363	6	1.8	99	4	PCT-US96-10087-5	Patent No. 5212073
291	6	1.8	97	2	US-09-886-319A-21	Sequence 21, Appl1	364	6	1.8	99	6	US-10-104-047-2869	Sequence 2869, App
292	6	1.8	97	2	US-09-545-894-13	Sequence 13, Appl1	365	6	1.8	100	2	US-08-894-173-77	Sequence 77, Appl1
293	6	1.8	97	2	US-09-545-894-16	Sequence 16, Appl1	366	6	1.8	100	2	US-09-358-193-77	Sequence 77, Appl1
294	6	1.8	97	2	US-08-776-971-1	Sequence 1, Appl1	367	6	1.8	103	2	US-09-084-303B-198	Sequence 198, App
295	6	1.8	98	2	US-08-776-971-115	Sequence 115, App	368	6	1.8	103	2	US-09-248-796A-24695	Sequence 24695, A
296	6	1.8	98	2	US-08-776-971-117	Sequence 117, App	369	6	1.8	104	2	US-09-543-681A-4881	Sequence 4881, App
297	6	1.8	98	2	US-08-776-971-122	Sequence 122, App	370	6	1.8	104	2	US-09-545-894-4	Sequence 4, Appl1
298	6	1.8	98	2	US-08-776-971-131	Sequence 131, App	371	6	1.8	104	2	US-09-489-039A-13803	Sequence 13803, A
299	6	1.8	98	2	US-08-776-971-136	Sequence 136, App	372	6	1.8	105	2	US-09-270-767-48695	Sequence 48695, A
300	6	1.8	98	2	US-09-248-796A-23678	Sequence 23678, A	373	6	1.8	106	2	US-09-489-039A-13627	Sequence 13627, A
301	6	1.8	98	2	US-09-576-290-44	Sequence 44, Appl1	374	6	1.8	107	2	US-09-830-230A-41	Sequence 41, Appl1
302	6	1.8	98	2	US-09-576-290-115	Sequence 115, App	375	6	1.8	107	2	US-07-927-391-16	Sequence 16, Appl1
303	6	1.8	98	2	US-09-576-290-117	Sequence 117, App	376	6	1.8	109	1	US-08-421-144A-7	Sequence 7, Appl1
304	6	1.8	98	2	US-09-576-290-131	Sequence 131, App	377	6	1.8	109	1	US-08-679-493A-153	Sequence 153, App
305	6	1.8	98	2	US-09-716-147-44	Sequence 44, Appl1	378	6	1.8	109	2	US-09-886-319A-71	Sequence 71, Appl1
306	6	1.8	98	2	US-09-716-147-115	Sequence 115, App	379	6	1.8	110	2	US-09-366-887A-13	Sequence 13, Appl1
307	6	1.8	98	2	US-09-716-147-117	Sequence 117, App	380	6	1.8	110	2	US-09-540-336-2945	Sequence 2945, App
308	6	1.8	98	2	US-09-716-147-122	Sequence 122, App	381	6	1.8	110	2	US-09-517-204-13	Sequence 13, Appl1
309	6	1.8	98	2	US-09-716-147-131	Sequence 131, App	382	6	1.8	110	2	US-09-489-039A-12524	Sequence 12524, A
310	6	1.8	98	2	US-09-716-147-136	Sequence 136, App	383	6	1.8	112	2	US-08-894-173-97	Sequence 97, Appl1
311	6	1.8	98	2	US-09-716-147-144	Sequence 44, Appl1	384	6	1.8	114	2	US-09-398-193-97	Sequence 97, Appl1
312	6	1.8	98	2	US-09-716-147-115	Sequence 115, App	385	6	1.8	114	2	US-09-312-833C-121	Sequence 121, App
313	6	1.8	98	2	US-09-716-147-117	Sequence 117, App	386	6	1.8	114	2	US-09-489-039A-8566	Sequence 8566, App
314	6	1.8	98	2	US-09-716-147-122	Sequence 122, App	387	6	1.8	116	2	US-09-098-789-1	Sequence 1, Appl1
315	6	1.8	98	2	US-09-716-147-131	Sequence 131, App	388	6	1.8	116	2	US-09-312-833C-121	Sequence 121, App
316	6	1.8	98	2	US-09-716-147-136	Sequence 136, App	389	6	1.8	116	2	US-09-489-039A-8566	Sequence 8566, App
317	6	1.8	99	1	US-08-127-499A-35	Sequence 35, Appl1	390	6	1.8	118	2	US-09-312-833C-121	Sequence 121, App
318	6	1.8	99	1	US-08-482-847-35	Sequence 35, Appl1	391	6	1.8	118	2	US-09-312-833C-121	Sequence 121, App
319	6	1.8	99	1	US-08-482-847-35	Sequence 35, Appl1	392	6	1.8	118	2	US-09-312-833C-121	Sequence 121, App

393	6	1.8	122	1	US-09-109-266-8	Sequence 8, Appl1	466	6	1.8	159	2	US-09-489-039A-12575	Sequence 12575, A
394	6	1.8	122	2	US-09-424-840B-24	Sequence 24, Appl1	467	6	1.8	159	2	US-09-248-796A-18945	Sequence 18945, A
395	6	1.8	122	2	US-09-949-016-9711	Sequence 9711, Ap	468	6	1.8	160	2	US-09-270-767-42891	Sequence 42891, A
396	6	1.8	124	2	US-09-134-001C-2930	Sequence 2930, Ap	469	6	1.8	165	2	US-09-270-767-46481	Sequence 46481, A
397	6	1.8	125	1	US-08-473-981A-10	Sequence 10, Appl1	470	6	1.8	165	2	US-09-302-540-15344	Sequence 15344, A
398	6	1.8	125	1	US-08-474-087-10	Sequence 10, Appl1	471	6	1.8	166	2	US-08-916-5768-6	Sequence 6, Appl1
399	6	1.8	125	2	US-09-543-681A-4730	Sequence 4730, Ap	472	6	1.8	166	2	US-09-213-2930-18	Sequence 18, Appl1
400	6	1.8	127	2	US-09-513-999C-4184	Sequence 4184, Ap	473	6	1.8	166	2	US-10-078-337-6	Sequence 6, Appl1
401	6	1.8	127	2	US-09-513-999C-4185	Sequence 4185, Ap	474	6	1.8	168	1	US-08-193-977-9	Sequence 9, Appl1
402	6	1.8	128	2	US-09-461-325-165	Sequence 165, App	475	6	1.8	170	2	US-09-205-258-1011	Sequence 1011, Ap
403	6	1.8	128	2	US-10-012-542-165	Sequence 165, App	476	6	1.8	170	2	US-10-004-860-1011	Sequence 1011, Ap
404	6	1.8	128	2	US-10-115-123-165	Sequence 165, App	477	6	1.8	171	2	US-09-646-028-9	Sequence 9, Appl1
405	6	1.8	129	2	US-09-509-559B-713	Sequence 13, Appl1	478	6	1.8	172	2	US-09-252-991A-23876	Sequence 23876, A
406	6	1.8	130	2	US-09-248-796A-27313	Sequence 27313, A	479	6	1.8	172	2	US-09-198-452A-1195	Sequence 1195, Ap
407	6	1.8	130	2	US-09-605-703B-2870	Sequence 2870, Ap	480	6	1.8	174	1	US-08-768-964-13	Sequence 13, Appl1
408	6	1.8	131	2	US-09-248-796A-26343	Sequence 26343, A	481	6	1.8	174	2	US-09-005-299-13	Sequence 13, Appl1
409	6	1.8	131	2	US-09-640-211A-673	Sequence 673, App	482	6	1.8	174	2	US-09-515-331-13	Sequence 13, Appl1
410	6	1.8	132	2	US-09-513-999C-4373	Sequence 4373, Ap	483	6	1.8	174	2	US-09-640-211A-768	Sequence 768, App
411	6	1.8	133	2	US-09-252-991A-31726	Sequence 31726, A	484	6	1.8	175	2	US-09-270-767-32147	Sequence 32147, A
412	6	1.8	134	2	US-09-252-991A-18396	Sequence 18396, A	485	6	1.8	175	2	US-09-270-767-47384	Sequence 47384, A
413	6	1.8	134	2	US-09-759-143-910	Sequence 910, App	486	6	1.8	175	2	US-09-902-540-11358	Sequence 2, Appl1
414	6	1.8	134	2	US-10-012-896-910	Sequence 910, App	487	6	1.8	176	2	US-09-309-317-2	Sequence 2, Appl1
415	6	1.8	136	2	US-09-205-258-465	Sequence 465, App	488	6	1.8	176	2	US-09-949-016-6706	Sequence 6706, Ap
416	6	1.8	136	2	US-09-270-767-31783	Sequence 31783, A	489	6	1.8	176	2	US-09-902-540-11336	Sequence 11336, A
417	6	1.8	136	2	US-09-270-767-47000	Sequence 47000, A	490	6	1.8	177	2	US-09-252-991A-20614	Sequence 20614, A
418	6	1.8	136	2	US-10-004-860-465	Sequence 465, App	491	6	1.8	177	2	US-09-893-737-30	Sequence 30, Appl1
419	6	1.8	137	2	US-09-205-258-308	Sequence 308, App	492	6	1.8	179	2	US-09-438-185A-444	Sequence 444, App
420	6	1.8	137	2	US-10-004-860-308	Sequence 308, App	493	6	1.8	180	2	US-09-270-767-32273	Sequence 32273, A
421	6	1.8	137	2	US-10-104-047-3766	Sequence 3766, Ap	494	6	1.8	180	2	US-09-270-767-47490	Sequence 47490, A
422	6	1.8	140	2	US-09-543-681A-6438	Sequence 6438, Ap	495	6	1.8	182	2	US-09-107-532A-5701	Sequence 5701, Ap
423	6	1.8	141	2	US-09-248-796A-22756	Sequence 22756, A	496	6	1.8	183	2	US-08-858-207A-401	Sequence 401, App
424	6	1.8	141	2	US-09-902-540-13787	Sequence 13787, A	497	6	1.8	186	2	US-09-248-796A-21757	Sequence 21757, A
425	6	1.8	142	2	US-09-270-767-37079	Sequence 37079, A	498	6	1.8	186	2	US-09-949-016-9722	Sequence 9722, Ap
426	6	1.8	142	2	US-09-270-767-52296	Sequence 52296, A	499	6	1.8	187	2	US-09-583-110-5246	Sequence 5246, Ap
427	6	1.8	143	2	US-09-270-767-60539	Sequence 60539, A	500	6	1.8	187	2	US-09-949-016-11428	Sequence 11428, A
428	6	1.8	145	2	US-09-338-352-7720	Sequence 7720, Ap	501	6	1.8	188	2	US-09-270-767-43077	Sequence 43077, A
429	6	1.8	146	2	US-09-732-210-621	Sequence 621, App	502	6	1.8	188	2	US-09-902-540-13118	Sequence 13118, A
430	6	1.8	146	2	US-09-270-767-72099	Sequence 72099, A	503	6	1.8	190	2	US-09-605-703B-950	Sequence 950, App
431	6	1.8	146	2	US-09-270-767-47316	Sequence 47316, A	504	6	1.8	190	2	US-09-605-703B-952	Sequence 952, App
432	6	1.8	146	2	US-09-640-211A-680	Sequence 680, App	505	6	1.8	191	2	US-08-671-548C-30	Sequence 30, Appl1
433	6	1.8	147	2	US-09-355-160D-7	Sequence 7, Appl1	506	6	1.8	191	2	US-09-350-841A-1593	Sequence 1593, Ap
434	6	1.8	147	2	US-10-092-219-7	Sequence 7, Appl1	507	6	1.8	191	2	US-08-284-667A-30	Sequence 30, Appl1
435	6	1.8	148	2	US-09-270-767-35815	Sequence 35815, A	508	6	1.8	193	2	US-08-671-548C-20	Sequence 20, Appl1
436	6	1.8	148	2	US-09-270-767-51032	Sequence 51032, A	509	6	1.8	193	2	US-08-671-548C-36	Sequence 36, Appl1
437	6	1.8	149	2	US-08-836-075A-30	Sequence 30, Appl1	510	6	1.8	193	2	US-08-284-667A-20	Sequence 20, Appl1
438	6	1.8	149	2	US-08-635-886C-283	Sequence 283, App	511	6	1.8	193	2	US-08-284-667A-36	Sequence 36, Appl1
439	6	1.8	149	2	US-08-974-690C-283	Sequence 283, App	512	6	1.8	194	2	US-08-671-548C-26	Sequence 26, Appl1
440	6	1.8	149	2	US-09-270-767-37973	Sequence 37973, A	513	6	1.8	194	2	US-08-284-667A-26	Sequence 26, Appl1
441	6	1.8	149	2	US-09-270-767-54940	Sequence 54940, A	514	6	1.8	196	2	US-08-981-392-35	Sequence 35, Appl1
442	6	1.8	151	2	US-09-564-329A-15	Sequence 15, Appl1	515	6	1.8	196	2	US-09-328-352-5098	Sequence 5098, Ap
443	6	1.8	151	2	US-09-270-767-35961	Sequence 35961, A	516	6	1.8	196	2	US-09-908-322-35	Sequence 35, Appl1
444	6	1.8	151	2	US-09-270-767-51178	Sequence 51178, A	517	6	1.8	196	2	US-09-605-703B-1914	Sequence 1914, Ap
445	6	1.8	151	2	US-09-963-620-15	Sequence 15, Appl1	518	6	1.8	199	1	US-08-768-964-12	Sequence 12, Appl1
446	6	1.8	151	2	US-09-855-632-15	Sequence 15, Appl1	519	6	1.8	199	2	US-09-005-299-12	Sequence 12, Appl1
447	6	1.8	151	2	US-09-934-773-15	Sequence 15, Appl1	520	6	1.8	199	2	US-09-515-431-12	Sequence 12, Appl1
448	6	1.8	151	2	US-09-855-153-15	Sequence 15, Appl1	521	6	1.8	199	2	US-09-252-991A-30003	Sequence 30003, A
449	6	1.8	151	2	US-10-224-720-15	Sequence 15, Appl1	522	6	1.8	201	2	US-09-902-540-14022	Sequence 14022, A
450	6	1.8	152	2	US-09-270-767-33006	Sequence 33006, A	523	6	1.8	204	1	US-08-185-432-8	Sequence 8, Appl1
451	6	1.8	152	2	US-09-270-767-48223	Sequence 48223, A	524	6	1.8	205	2	US-09-134-000C-3393	Sequence 3313, Ap
452	6	1.8	153	2	US-09-270-767-44655	Sequence 44655, A	525	6	1.8	205	2	US-09-270-767-43874	Sequence 43874, A
453	6	1.8	153	2	US-09-605-703B-1634	Sequence 1634, Ap	526	6	1.8	206	2	US-09-562-737-51	Sequence 51, Appl1
454	6	1.8	154	2	US-09-583-110-4155	Sequence 4155, Ap	527	6	1.8	206	2	US-09-562-737-55	Sequence 55, Appl1
455	6	1.8	155	2	US-09-107-532A-6942	Sequence 6942, Ap	528	6	1.8	206	2	US-09-562-737-57	Sequence 57, Appl1
456	6	1.8	156	2	US-09-646-028-4	Sequence 4, Appl1	529	6	1.8	206	2	US-09-562-737-58	Sequence 58, Appl1
457	6	1.8	156	2	US-09-148-545-136	Sequence 136, App	530	6	1.8	206	2	US-09-538-092-795	Sequence 795, App
458	6	1.8	156	2	US-09-949-016-9452	Sequence 9452, Ap	531	6	1.8	206	2	US-09-489-847-285	Sequence 285, App
459	6	1.8	156	2	US-09-621-011-136	Sequence 136, App	532	6	1.8	207	2	US-09-270-767-32689	Sequence 32689, A
460	6	1.8	157	2	US-08-872-855-6	Sequence 6, Appl1	533	6	1.8	207	2	US-09-270-767-47906	Sequence 47906, A
461	6	1.8	157	2	US-08-981-392-68	Sequence 68, Appl1	534	6	1.8	207	2	US-08-657-7490-21	Sequence 21, Appl1
462	6	1.8	157	2	US-09-252-991A-22516	Sequence 22516, A	535	6	1.8	208	2	US-08-235-836C-32	Sequence 32, Appl1
463	6	1.8	157	2	US-09-908-322-68	Sequence 68, Appl1	536	6	1.8	209	2	US-09-697-367-10	Sequence 10, Appl1
464	6	1.8	157	2	US-09-310-685-20	Sequence 20, Appl1	537	6	1.8	210	2	US-09-134-001C-4790	Sequence 4790, Ap
465	6	1.8	158	2	US-09-252-991A-26205	Sequence 26205, A	538	6	1.8	210	2		

539	6	1.8	210	2	US-09-918-909A-10	Sequence 10, Appl	612	6	1.8	251	2	US-09-248-796A-18124	Sequence 18124, A
540	6	1.8	211	2	US-09-252-991A-25965	Sequence 25965, A	613	6	1.8	252	2	US-09-949-016-10380	Sequence 10380, A
541	6	1.8	212	1	US-08-158-353-4	Sequence 4, Appl1	614	6	1.8	253	2	US-09-252-991A-17553	Sequence 17553, A
542	6	1.8	212	1	US-08-763-121-1	Sequence 1, Appl1	615	6	1.8	253	2	US-09-310-463-36	Sequence 36, Appl
543	6	1.8	212	1	US-08-878-957-34	Sequence 34, Appl	616	6	1.8	253	2	US-09-370-167-42144	Sequence 42144, A
544	6	1.8	212	2	US-09-196-293-11	Sequence 11, Appl	617	6	1.8	254	2	US-09-240-915-7	Sequence 7, Appl1
545	6	1.8	212	2	US-08-209-603E-11	Sequence 11, Appl	618	6	1.8	254	2	US-09-591-435-7	Sequence 7, Appl1
546	6	1.8	212	2	US-08-235-836C-34	Sequence 34, Appl	619	6	1.8	254	2	US-10-098-600B-7	Sequence 7, Appl1
547	6	1.8	212	2	US-09-216-066-11	Sequence 11, Appl1	620	6	1.8	256	2	US-09-543-681A-4882	Sequence 4282, Ap
548	6	1.8	212	2	US-09-711-546-11	Sequence 11, Appl	621	6	1.8	257	1	US-07-781-355-2	Sequence 2, Appl1
549	6	1.8	212	2	US-09-270-767-56499	Sequence 36499, A	622	6	1.8	257	1	US-08-287-959-4	Sequence 4, Appl1
550	6	1.8	212	2	US-09-767-51716	Sequence 51716, A	623	6	1.8	258	2	US-09-252-991A-25067	Sequence 25067, A
551	6	1.8	212	2	US-09-270-767-38211	Sequence 38211, A	624	6	1.8	258	2	US-09-252-991A-29435	Sequence 29435, A
552	6	1.8	212	2	US-09-270-767-53428	Sequence 53428, A	625	6	1.8	260	2	US-09-252-991A-22230	Sequence 23230, A
553	6	1.8	212	2	US-09-974-992B-7	Sequence 7, Appl1	626	6	1.8	261	2	US-09-902-540-10632	Sequence 10632, A
554	6	1.8	212	2	US-10-289-795-11	Sequence 11, Appl	627	6	1.8	263	1	US-08-768-964-2	Sequence 2, Appl1
555	6	1.8	213	1	US-08-763-121-3	Sequence 3, Appl1	628	6	1.8	263	2	US-09-005-299-2	Sequence 2, Appl1
556	6	1.8	213	2	US-09-216-066-3	Sequence 3, Appl1	629	6	1.8	263	2	US-09-515-431-2	Sequence 2, Appl1
557	6	1.8	213	2	US-09-902-540-13705	Sequence 13705, A	630	6	1.8	263	2	US-09-198-452A-1063	Sequence 1063, Ap
558	6	1.8	214	2	US-09-187-789-9	Sequence 9, Appl1	631	6	1.8	263	2	US-09-438-185A-785	Sequence 785, App
559	6	1.8	214	2	US-09-989-903-9	Sequence 9, Appl1	632	6	1.8	263	2	US-10-104-047-3558	Sequence 3558, Ap
560	6	1.8	215	2	US-09-583-110-5435	Sequence 3435, Ap	633	6	1.8	265	2	US-09-310-463-34	Sequence 34, Appl
561	6	1.8	216	2	US-09-489-039A-7265	Sequence 7265, Ap	634	6	1.8	266	2	US-07-857-224B-40	Sequence 40, Appl
562	6	1.8	217	2	US-09-630-454-196	Sequence 196, App	635	6	1.8	266	2	US-09-147-550-11	Sequence 11, Appl
563	6	1.8	217	2	US-09-252-991A-30641	Sequence 30641, A	636	6	1.8	266	2	US-09-557-917-11	Sequence 11, Appl
564	6	1.8	218	1	US-08-463-115-92	Sequence 92, Appl	637	6	1.8	266	2	US-09-543-681A-5904	Sequence 5904, Ap
565	6	1.8	218	1	US-08-463-388-92	Sequence 92, Appl	638	6	1.8	267	2	US-09-134-000C-5723	Sequence 5723, Ap
566	6	1.8	219	2	US-09-270-767-41489	Sequence 41489, A	639	6	1.8	269	2	US-09-270-767-44310	Sequence 44310, A
567	6	1.8	219	2	US-09-248-796A-21540	Sequence 21540, A	640	6	1.8	272	2	US-08-690-095-1	Sequence 1, Appl1
568	6	1.8	221	2	US-09-583-110-3352	Sequence 3352, Ap	641	6	1.8	272	2	US-09-510-367C-19	Sequence 19, Appl
569	6	1.8	221	2	US-09-107-433-3993	Sequence 3993, Ap	642	6	1.8	274	2	US-09-5252-991A-27466	Sequence 27466, A
570	6	1.8	222	2	US-09-589-733C-11	Sequence 11, Appl	643	6	1.8	274	2	US-09-915-524-19	Sequence 19, Appl
571	6	1.8	222	2	US-10-104-047-3510	Sequence 3510, Ap	644	6	1.8	274	2	US-09-934-634-19	Sequence 19, Appl
572	6	1.8	223	1	US-08-394-189B-22	Sequence 22, Appl	645	6	1.8	274	2	US-09-917-278-19	Sequence 19, Appl
573	6	1.8	223	2	US-09-465-901-12	Sequence 12, Appl	646	6	1.8	274	6	5489533-2	Patent No. 5489533
574	6	1.8	223	2	US-09-888-243-22	Sequence 22, Appl	647	6	1.8	274	6	5512660-2	Patent No. 5512660
575	6	1.8	226	2	US-09-869-388-10	Sequence 10, Appl	648	6	1.8	275	2	US-09-248-796A-18804	Sequence 18804, A
576	6	1.8	227	2	US-09-593-887-16	Sequence 16, Appl	649	6	1.8	276	2	US-09-270-767-44216	Sequence 44216, A
577	6	1.8	227	2	US-09-869-388-7	Sequence 7, Appl1	650	6	1.8	278	2	US-09-570-367C-2	Sequence 2, Appl1
578	6	1.8	229	2	US-09-764-803B-4	Sequence 4, Appl1	651	6	1.8	278	2	US-09-570-367C-21	Sequence 21, Appl
579	6	1.8	230	2	US-09-187-789-7	Sequence 7, Appl1	652	6	1.8	278	2	US-09-915-524-2	Sequence 2, Appl1
580	6	1.8	230	2	US-09-989-903-7	Sequence 7, Appl1	653	6	1.8	278	2	US-09-915-524-21	Sequence 21, Appl1
581	6	1.8	231	2	US-09-252-991A-25675	Sequence 25675, A	654	6	1.8	278	2	US-09-915-524-21	Sequence 21, Appl1
582	6	1.8	232	1	US-08-425-763-2	Sequence 2, Appl1	655	6	1.8	278	2	US-09-934-634-21	Sequence 21, Appl
583	6	1.8	232	1	US-07-934-373C-32	Sequence 32, Appl	656	6	1.8	278	2	US-09-917-278-2	Sequence 2, Appl1
584	6	1.8	232	2	US-08-437-642B-32	Sequence 32, Appl	657	6	1.8	278	2	US-09-917-278-21	Sequence 21, Appl
585	6	1.8	232	2	US-08-811-757-2	Sequence 2, Appl1	658	6	1.8	278	2	US-09-917-278-21	Sequence 21, Appl
586	6	1.8	232	2	US-09-249-230-2	Sequence 2, Appl1	659	6	1.8	282	2	US-09-247-890-16	Sequence 16, Appl
587	6	1.8	232	4	PCT-US93-07832-32	Sequence 32, Appl1	660	6	1.8	282	2	US-09-724-852-16	Sequence 16, Appl
588	6	1.8	233	2	US-09-107-433-8676	Sequence 2676, Ap	661	6	1.8	282	2	US-09-724-852-16	Sequence 16, Appl
589	6	1.8	234	2	US-09-270-767-56898	Sequence 56898, A	662	6	1.8	282	2	US-09-134-000C-4468	Sequence 4468, Ap
590	6	1.8	237	2	US-09-107-532A-6553	Sequence 6553, Ap	663	6	1.8	283	2	US-09-904-615-106	Sequence 106, App
591	6	1.8	237	2	US-09-710-219-162	Sequence 162, App	664	6	1.8	283	2	US-10-054-988-106	Sequence 106, App
592	6	1.8	238	1	US-08-768-964-7	Sequence 7, Appl1	665	6	1.8	285	2	US-09-583-110-4775	Sequence 4775, Ap
593	6	1.8	238	2	US-09-005-299-7	Sequence 7, Appl1	666	6	1.8	287	2	US-09-310-463-32	Sequence 32, Appl1
594	6	1.8	238	2	US-09-515-431-7	Sequence 7, Appl1	667	6	1.8	287	2	US-09-252-991A-30447	Sequence 30447, A
595	6	1.8	238	2	US-09-149-476-485	Sequence 485, App	668	6	1.8	287	2	US-09-489-039A-14187	Sequence 14187, A
596	6	1.8	238	2	US-09-949-016-11628	Sequence 11628, A	669	6	1.8	287	2	US-09-949-016-7477	Sequence 7477, Ap
597	6	1.8	241	2	US-09-489-039A-7888	Sequence 7888, Ap	670	6	1.8	288	2	US-09-489-039A-12218	Sequence 12218, Ap
598	6	1.8	242	2	US-09-187-789-5	Sequence 5, Appl1	671	6	1.8	292	2	US-09-107-433-3232	Sequence 3232, Ap
599	6	1.8	242	2	US-09-252-991A-24652	Sequence 24652, A	672	6	1.8	293	2	US-09-252-991A-26267	Sequence 26267, A
600	6	1.8	242	2	US-09-764-803B-25	Sequence 25, Appl	673	6	1.8	294	2	US-09-270-767-56859	Sequence 56859, A
601	6	1.8	242	2	US-09-764-803B-25	Sequence 25, Appl	674	6	1.8	295	2	US-09-902-540-13497	Sequence 13497, A
602	6	1.8	242	2	US-09-764-803B-26	Sequence 26, Appl	675	6	1.8	297	2	US-09-632-847B-4	Sequence 4, Appl1
603	6	1.8	242	2	US-09-989-903-5	Sequence 5, Appl1	676	6	1.8	298	2	US-09-232-160-17	Sequence 17, Appl
604	6	1.8	242	2	US-09-851-873-105	Sequence 105, App	677	6	1.8	298	2	US-09-252-991A-23700	Sequence 23700, A
605	6	1.8	244	2	US-09-724-623-82	Sequence 82, Appl1	678	6	1.8	298	2	US-09-800-729-87	Sequence 87, Appl
606	6	1.8	245	2	US-09-413-814-6	Sequence 6, Appl1	679	6	1.8	298	2	US-09-800-729-121	Sequence 121, App
607	6	1.8	245	2	US-08-425-630-24	Sequence 20, Appl	680	6	1.8	298	2	US-09-582-934-2	Sequence 2, Appl1
608	6	1.8	246	2	US-09-198-452A-22	Sequence 22, Appl	681	6	1.8	298	2	US-09-248-796A-27392	Sequence 27392, A
609	6	1.8	246	2	US-09-438-185A-13	Sequence 13, Appl	682	6	1.8	298	2	US-10-000-489-22	Sequence 22, Appl
610	6	1.8	248	2	US-09-482-273-126	Sequence 126, App	683	6	1.8	298	2	US-09-832-129-50	Sequence 50, Appl
611	6	1.8	251	2	US-09-602-787A-434	Sequence 434, App	684	6	1.8	298	2	US-10-104-047-2809	Sequence 2809, Ap

685	6	1.8	299	2	US-09-310-463-30	Sequence 30, Appl	758	6	1.8	332	1	US-08-442-281-7	Sequence 7, Appl1
686	6	1.8	300	2	US-09-343-681A-6670	Sequence 6670, Ap	759	6	1.8	332	1	US-08-939-727-7	Sequence 7, Appl1
687	6	1.8	301	2	US-09-107-532A-4953	Sequence 4953, Ap	760	6	1.8	333	2	US-09-198-452A-652	Sequence 652, App
688	6	1.8	301	2	US-09-582-934-1	Sequence 1, Appl1	761	6	1.8	334	2	US-09-252-991A-18120	Sequence 18120, A
689	6	1.8	302	2	US-09-874-923-122	Sequence 122, App	762	6	1.8	334	2	US-09-252-991A-22395	Sequence 22395, A
690	6	1.8	303	1	US-08-185-432-5	Sequence 5, Appl1	763	6	1.8	335	1	US-07-947-130-3	Sequence 3, Appl1
691	6	1.8	304	2	US-09-632-947B-7	Sequence 7, Appl1	764	6	1.8	335	1	US-08-421-822-3	Sequence 3, Appl1
692	6	1.8	304	2	US-09-489-039A-11906	Sequence 11906, A	765	6	1.8	335	1	US-08-421-823-3	Sequence 3, Appl1
693	6	1.8	305	2	US-09-540-236-5603	Sequence 3603, Ap	766	6	1.8	335	2	US-09-543-681A-7733	Sequence 7733, Ap
694	6	1.8	306	2	US-09-902-540-15500	Sequence 15500, A	767	6	1.8	335	2	US-09-438-185A-615	Sequence 615, App
695	6	1.8	307	2	US-09-949-016-9817	Sequence 9817, Ap	768	6	1.8	337	1	US-09-013-634-4	Sequence 7, Appl1
696	6	1.8	307	2	US-09-949-016-9818	Sequence 9818, Ap	769	6	1.8	339	2	US-10-169-048-40	Sequence 40, Appl
697	6	1.8	307	2	US-09-303-518D-404	Sequence 404, App	770	6	1.8	340	2	US-09-543-681A-5967	Sequence 5967, Ap
698	6	1.8	307	2	US-09-303-518D-406	Sequence 406, App	771	6	1.8	342	2	US-09-071-035-104	Sequence 104, App
699	6	1.8	307	2	US-09-303-518D-408	Sequence 408, App	772	6	1.8	342	2	US-10-206-576-104	Sequence 104, App
700	6	1.8	308	2	US-09-252-991A-20337	Sequence 20337, A	773	6	1.8	344	2	US-09-110-116-4	Sequence 4, Appl1
701	6	1.8	308	2	US-09-710-279-1072	Sequence 1072, Ap	774	6	1.8	344	2	US-10-121-576-20	Sequence 20, Appl
702	6	1.8	308	2	US-09-710-279-7706	Sequence 2706, Ap	775	6	1.8	345	2	US-09-252-991A-16669	Sequence 16669, A
703	6	1.8	308	2	US-10-014-269-31	Sequence 31, Appl	776	6	1.8	346	2	US-09-724-224-6	Sequence 6, Appl1
704	6	1.8	308	2	US-10-002-974-31	Sequence 31, Appl	777	6	1.8	346	2	US-10-093-317-6	Sequence 6, Appl1
705	6	1.8	309	1	US-08-729-202-1	Sequence 1, Appl1	778	6	1.8	346	4	PCT-US96-10602-2	Sequence 2, Appl1
706	6	1.8	309	1	US-08-896-371-1	Sequence 1, Appl1	779	6	1.8	347	2	PCT-US96-10602-2	Sequence 2, Appl1
707	6	1.8	309	2	US-08-996-338-22	Sequence 22, Appl	780	6	1.8	348	2	US-08-857-076-100	Sequence 100, App
708	6	1.8	309	2	US-09-556-972-22	Sequence 22, Appl	781	6	1.8	349	1	US-09-270-767-46628	Sequence 46628, A
709	6	1.8	309	2	US-09-902-540-13383	Sequence 13383, A	782	6	1.8	349	4	PCT-US93-08528-7	Sequence 7, Appl1
710	6	1.8	310	2	US-09-252-991A-16314	Sequence 16314, A	783	6	1.8	350	2	US-09-161-241-9	Sequence 9, Appl1
711	6	1.8	310	2	US-09-270-767-52725	Sequence 35725, A	784	6	1.8	350	2	US-09-907-794A-236	Sequence 236, App
712	6	1.8	311	2	US-09-222-939-8	Sequence 8, Appl1	785	6	1.8	350	2	US-09-905-125A-236	Sequence 236, App
713	6	1.8	311	2	US-09-252-991A-28068	Sequence 28068, A	786	6	1.8	350	2	US-09-902-775A-236	Sequence 236, App
714	6	1.8	311	2	US-09-543-681A-4963	Sequence 4963, Ap	787	6	1.8	350	2	US-09-906-700-236	Sequence 236, App
715	6	1.8	311	2	US-10-023-528-8	Sequence 8, Appl1	788	6	1.8	350	2	US-09-903-603A-236	Sequence 236, App
716	6	1.8	311	2	US-10-423-330-8	Sequence 8, Appl1	789	6	1.8	350	2	US-09-904-920A-236	Sequence 236, App
717	6	1.8	312	1	US-08-808-931-52	Sequence 22, Appl	790	6	1.8	350	2	US-09-909-064-236	Sequence 236, App
718	6	1.8	312	2	US-08-808-333-22	Sequence 22, Appl	791	6	1.8	350	2	US-09-905-381A-236	Sequence 236, App
719	6	1.8	312	2	US-09-050-603A-22	Sequence 22, Appl	792	6	1.8	350	2	US-09-906-618-236	Sequence 236, App
720	6	1.8	312	2	US-09-102-420B-22	Sequence 22, Appl	793	6	1.8	350	2	US-09-906-646-236	Sequence 236, App
721	6	1.8	312	2	US-09-487-688-22	Sequence 22, Appl	794	6	1.8	350	2	US-09-904-462-236	Sequence 236, App
722	6	1.8	312	2	US-09-107-532A-6219	Sequence 6219, Ap	795	6	1.8	350	2	US-09-902-736A-236	Sequence 236, App
723	6	1.8	312	2	US-09-730-525-22	Sequence 22, Appl	796	6	1.8	350	2	US-09-906-722A-236	Sequence 236, App
724	6	1.8	313	2	US-09-347-803-25	Sequence 25, Appl	797	6	1.8	352	1	US-08-933-750C-46	Sequence 46, Appl1
725	6	1.8	313	2	US-09-252-991A-22411	Sequence 22411, A	798	6	1.8	352	2	US-09-234-613-46	Sequence 46, Appl1
726	6	1.8	313	2	US-09-252-991A-24305	Sequence 24305, A	799	6	1.8	352	2	US-09-252-991A-25209	Sequence 25209, A
727	6	1.8	313	2	US-09-248-796A-20918	Sequence 20918, A	800	6	1.8	353	2	US-09-543-681A-7190	Sequence 7190, Ap
728	6	1.8	314	2	US-09-107-532A-4919	Sequence 4919, Ap	801	6	1.8	353	2	US-09-949-016-7210	Sequence 7210, Ap
729	6	1.8	315	1	US-07-757-390-8	Sequence 8, Appl1	802	6	1.8	354	1	US-08-394-189B-20	Sequence 20, Appl
730	6	1.8	315	1	US-08-442-282-8	Sequence 8, Appl1	803	6	1.8	354	2	US-09-888-243-20	Sequence 20, Appl
731	6	1.8	315	1	US-08-442-281-8	Sequence 8, Appl1	804	6	1.8	356	2	US-09-198-452A-526	Sequence 526, App
732	6	1.8	315	1	US-08-939-727-8	Sequence 8, Appl1	805	6	1.8	358	2	US-09-934-901-8	Sequence 8, Appl1
733	6	1.8	315	2	US-09-252-991A-25763	Sequence 25763, A	806	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
734	6	1.8	316	2	US-09-311-021-56	Sequence 26, Appl	807	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
735	6	1.8	316	2	US-09-252-991A-18629	Sequence 18629, A	808	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
736	6	1.8	317	2	US-09-252-991A-22489	Sequence 22489, A	809	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
737	6	1.8	318	2	US-09-134-001C-3852	Sequence 3852, Ap	810	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
738	6	1.8	318	2	US-09-902-540-11076	Sequence 11076, A	811	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
739	6	1.8	319	2	US-09-134-000C-5242	Sequence 5242, Ap	812	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
740	6	1.8	319	2	US-09-438-185A-989	Sequence 989, App	813	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
741	6	1.8	320	2	US-09-248-796A-20977	Sequence 20977, A	814	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
742	6	1.8	320	2	US-09-107-433-6282	Sequence 4282, Ap	815	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
743	6	1.8	324	2	US-09-252-991A-24664	Sequence 24664, A	816	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
744	6	1.8	325	2	US-09-248-796A-25600	Sequence 25600, A	817	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
745	6	1.8	328	2	US-09-270-767-58409	Sequence 38409, A	818	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
746	6	1.8	328	2	US-09-270-767-53626	Sequence 53626, A	819	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
747	6	1.8	328	2	US-09-477-962-124	Sequence 124, App	820	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
748	6	1.8	329	1	US-08-225-477B-3	Sequence 3, Appl1	821	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
749	6	1.8	329	1	US-08-562-535C-4	Sequence 4, Appl1	822	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
750	6	1.8	329	1	US-08-742-605D-4	Sequence 4, Appl1	823	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
751	6	1.8	329	2	US-09-259-294-4	Sequence 4, Appl1	824	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
752	6	1.8	329	2	US-09-489-039A-10276	Sequence 10276, A	825	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
753	6	1.8	329	4	PCT-US91-04353-3	Sequence 4, Appl1	826	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
754	6	1.8	329	4	PCT-US91-04353-3	Sequence 4, Appl1	827	6	1.8	358	2	US-09-934-868-18	Sequence 18, Appl
755	6	1.8	331	1	US-08-356-180-3	Sequence 3, Appl1	828	6	1.8	370	2	US-10-093-317-2	Sequence 2, Appl1
756	6	1.8	332	1	US-07-757-390-7	Sequence 7, Appl1	829	6	1.8	371	1	US-08-225-477B-8	Sequence 8, Appl1
757	6	1.8	332	1	US-08-442-282-7	Sequence 7, Appl1	830	6	1.8	371	2	US-09-148-545-259	Sequence 259, App

831	6	1.8	371	2	US-09-621-011-259	Sequence 259, App	904	6	1.8	414	2	US-09-248-796A-19046	Sequence 19046, A
832	6	1.8	371	4	PCT-US95-04353-8	Sequence 8, Appli	905	6	1.8	414	2	US-09-908-992B-10	Sequence 10, Appli
833	6	1.8	372	2	US-09-071-035-102	Sequence 102, App	906	6	1.8	415	1	US-07-757-390-5	Sequence 5, Appli
834	6	1.8	372	2	US-09-252-991A-28586	Sequence 28586, A	907	6	1.8	415	1	US-08-442-282-5	Sequence 5, Appli
835	6	1.8	372	2	US-09-252-991A-30132	Sequence 30132, A	908	6	1.8	415	1	US-08-442-281-5	Sequence 5, Appli
836	6	1.8	372	2	US-09-270-767-45792	Sequence 45792, A	909	6	1.8	415	1	US-08-939-727-5	Sequence 5, Appli
837	6	1.8	372	2	US-10-206-576-102	Sequence 102, App	910	6	1.8	415	2	US-09-886-319A-23	Sequence 23, Appli
838	6	1.8	375	2	US-09-949-016-7856	Sequence 7856, Ap	911	6	1.8	417	2	US-09-489-039A-12272	Sequence 12272, A
839	6	1.8	375	2	US-09-949-016-7857	Sequence 7857, Ap	912	6	1.8	419	2	US-08-974-691-3	Sequence 3, Appli
840	6	1.8	375	2	US-09-949-016-7858	Sequence 7858, Ap	913	6	1.8	419	2	US-09-705-448-10	Sequence 10, Appli
841	6	1.8	375	2	US-09-902-540-12456	Sequence 12456, A	914	6	1.8	421	2	US-09-543-681A-791	Sequence 7791, Ap
842	6	1.8	376	2	US-09-270-767-44454	Sequence 44454, A	915	6	1.8	423	1	US-08-290-731C-10	Sequence 10, Appli
843	6	1.8	377	2	US-08-888-077A-27	Sequence 27, Appli	916	6	1.8	423	1	US-08-290-731C-11	Sequence 11, Appli
844	6	1.8	377	2	US-09-665-479A-16	Sequence 16, Appli	917	6	1.8	423	2	US-08-855-910-13	Sequence 13, Appli
845	6	1.8	377	2	US-09-710-279-2926	Sequence 2926, Ap	918	6	1.8	424	2	US-09-328-352-4199	Sequence 4199, Ap
846	6	1.8	378	4	PCT-US95-04353-9	Sequence 9, Appli	919	6	1.8	426	2	US-09-252-991A-20025	Sequence 20025, A
847	6	1.8	378	4	PCT-US95-04353-9	Sequence 9, Appli	920	6	1.8	426	2	US-10-332-795-14	Sequence 14, Appli
848	6	1.8	379	2	US-09-489-039A-11991	Sequence 11991, A	921	6	1.8	427	2	US-09-134-000C-5142	Sequence 5142, Ap
849	6	1.8	379	2	US-09-724-797-54	Sequence 54, Appli	922	6	1.8	427	2	US-08-956-171B-5244	Sequence 5244, Ap
850	6	1.8	380	2	US-09-710-279-1402	Sequence 1402, Ap	923	6	1.8	430	2	US-08-781-986A-5244	Sequence 5244, Ap
851	6	1.8	380	2	US-09-902-540-16242	Sequence 16242, A	924	6	1.8	430	2	US-09-248-796A-14556	Sequence 14556, A
852	6	1.8	382	2	US-09-029-333-2	Sequence 2, Appli	925	6	1.8	433	2	US-09-252-991A-20728	Sequence 20728, A
853	6	1.8	382	2	US-09-270-767-42344	Sequence 42344, A	926	6	1.8	433	2	US-09-302-540-15313	Sequence 15313, A
854	6	1.8	383	2	US-09-248-796A-19589	Sequence 19589, A	927	6	1.8	436	2	US-09-252-991A-22081	Sequence 22081, A
855	6	1.8	384	2	US-08-946-026-27	Sequence 27, Appli	928	6	1.8	437	2	US-09-248-796A-20561	Sequence 20561, A
856	6	1.8	386	2	US-09-724-623-70	Sequence 70, Appli	929	6	1.8	437	2	US-09-252-991A-32048	Sequence 32048, A
857	6	1.8	386	2	US-10-154-515A-2	Sequence 2, Appli	930	6	1.8	438	2	US-09-583-110-4975	Sequence 4975, Ap
858	6	1.8	386	2	US-10-122-706-2	Sequence 2, Appli	931	6	1.8	440	1	US-08-808-931-24	Sequence 24, Appli
859	6	1.8	387	1	US-08-123-161A-10	Sequence 10, Appli	932	6	1.8	440	2	US-08-808-323-24	Sequence 24, Appli
860	6	1.8	387	1	US-08-123-161A-12	Sequence 12, Appli	933	6	1.8	440	2	US-09-050-603A-24	Sequence 24, Appli
861	6	1.8	387	1	US-08-483-278-10	Sequence 10, Appli	934	6	1.8	440	2	US-09-102-420B-24	Sequence 24, Appli
862	6	1.8	387	1	US-08-483-278-12	Sequence 12, Appli	935	6	1.8	440	2	US-09-497-698-24	Sequence 24, Appli
863	6	1.8	387	2	US-09-134-001C-3625	Sequence 3625, Ap	936	6	1.8	440	2	US-09-730-525-24	Sequence 24, Appli
864	6	1.8	389	2	US-09-248-796A-17305	Sequence 17305, A	937	6	1.8	442	2	US-09-252-991A-30607	Sequence 30607, A
865	6	1.8	390	1	US-07-817-920-6	Sequence 6, Appli	938	6	1.8	443	2	US-09-107-433-5150	Sequence 5150, Ap
866	6	1.8	390	1	US-08-117-006-6	Sequence 6, Appli	939	6	1.8	446	2	US-09-370-767-57633	Sequence 57633, A
867	6	1.8	390	1	US-08-216-594-6	Sequence 6, Appli	940	6	1.8	446	2	US-09-302-540-12677	Sequence 12677, A
868	6	1.8	390	1	US-08-461-812-4	Sequence 4, Appli	941	6	1.8	446	2	US-09-489-039A-12786	Sequence 12786, A
869	6	1.8	390	1	US-08-157-185-15	Sequence 15, Appli	942	6	1.8	448	2	US-09-489-039A-9246	Sequence 9246, Ap
870	6	1.8	390	2	US-08-281-526B-15	Sequence 15, Appli	943	6	1.8	452	2	US-09-328-352-5528	Sequence 5528, Ap
871	6	1.8	390	2	US-09-450-790A-15	Sequence 15, Appli	944	6	1.8	453	2	US-09-370-767-44567	Sequence 44567, A
872	6	1.8	390	2	US-09-332-837-15	Sequence 15, Appli	945	6	1.8	454	1	US-07-934-373C-22	Sequence 22, Appli
873	6	1.8	390	2	US-09-371-705-4	Sequence 4, Appli	946	6	1.8	454	2	US-08-437-642B-22	Sequence 22, Appli
874	6	1.8	390	2	US-09-826-509-427	Sequence 427, App	947	6	1.8	454	2	US-08-929-329-8	Sequence 8, Appli
875	6	1.8	390	4	PCT-US93-00149-6	Sequence 6, Appli	948	6	1.8	454	2	US-08-146-206C-22	Sequence 22, Appli
876	6	1.8	392	2	US-09-949-016-9728	Sequence 9728, Ap	949	6	1.8	454	2	US-09-705-686-22	Sequence 22, Appli
877	6	1.8	394	2	US-09-270-767-43783	Sequence 43783, A	950	6	1.8	454	2	US-09-705-392A-22	Sequence 22, Appli
878	6	1.8	395	2	US-09-328-352-6660	Sequence 6660, Ap	951	6	1.8	454	2	US-09-902-540-12301	Sequence 12301, A
879	6	1.8	395	2	US-09-543-681A-6203	Sequence 6, Appli	952	6	1.8	454	2	US-09-302-540-12301	Sequence 22, Appli
880	6	1.8	398	1	US-07-757-390-6	Sequence 6, Appli	953	6	1.8	454	4	PCT-US93-07832-22	Sequence 22, Appli
881	6	1.8	398	1	US-08-370-542-6	Sequence 6, Appli	954	6	1.8	455	2	US-09-540-236-2325	Sequence 2325, Ap
882	6	1.8	398	1	US-08-442-282-6	Sequence 6, Appli	955	6	1.8	456	2	US-09-328-352-6174	Sequence 6174, Ap
883	6	1.8	398	1	US-08-542-358-6	Sequence 6, Appli	956	6	1.8	459	1	US-08-870-518-4	Sequence 4, Appli
884	6	1.8	398	1	US-08-442-281-6	Sequence 6, Appli	957	6	1.8	459	2	US-08-836-567-4	Sequence 4, Appli
885	6	1.8	398	1	US-08-939-727-6	Sequence 6, Appli	958	6	1.8	459	2	US-09-606-304-4	Sequence 4, Appli
886	6	1.8	398	2	US-09-018-351-6	Sequence 6, Appli	959	6	1.8	460	2	US-09-647-540A-2	Sequence 2, Appli
887	6	1.8	398	2	US-09-328-352-6411	Sequence 6411, Ap	960	6	1.8	460	2	US-10-119-600C-2	Sequence 2, Appli
888	6	1.8	399	2	US-09-134-000C-4500	Sequence 4500, Ap	961	6	1.8	460	2	US-09-198-452A-7	Sequence 7, Appli
889	6	1.8	402	2	US-09-252-991A-31178	Sequence 31178, A	962	6	1.8	460	2	US-10-119-651-2	Sequence 2, Appli
890	6	1.8	403	2	US-09-710-279-1522	Sequence 1522, Ap	963	6	1.8	460	2	US-09-438-185A-1071	Sequence 1071, Ap
891	6	1.8	406	2	US-09-134-001C-3544	Sequence 3544, Ap	964	6	1.8	461	2	US-09-949-016-8839	Sequence 8839, Ap
892	6	1.8	409	2	US-09-258-754-449	Sequence 449, App	965	6	1.8	461	2	US-10-104-047-3865	Sequence 3865, Ap
893	6	1.8	409	2	US-09-676-475A-449	Sequence 449, App	966	6	1.8	462	1	US-08-865-597A-2	Sequence 2, Appli
894	6	1.8	410	2	US-09-252-991A-22340	Sequence 22340, A	967	6	1.8	463	2	US-09-252-991A-29065	Sequence 29065, A
895	6	1.8	411	2	US-09-543-681A-7404	Sequence 7404, Ap	968	6	1.8	463	2	US-09-489-039A-13721	Sequence 13721, A
896	6	1.8	412	1	US-08-349-696-21	Sequence 21, Appli	969	6	1.8	463	2	US-09-979-775A-3	Sequence 3, Appli
897	6	1.8	412	1	US-08-233-009-21	Sequence 21, Appli	970	6	1.8	464	2	US-09-902-540-12021	Sequence 12021, A
898	6	1.8	412	1	US-08-560-231-21	Sequence 21, Appli	971	6	1.8	466	1	US-07-882-202A-4	Sequence 4, Appli
899	6	1.8	412	2	US-09-080-704A-21	Sequence 21, Appli	972	6	1.8	466	1	US-08-021-615A-4	Sequence 4, Appli
900	6	1.8	412	2	US-09-800-274-5	Sequence 2, Appli	973	6	1.8	466	1	US-08-321-777-4	Sequence 4, Appli
901	6	1.8	413	2	US-09-252-991A-20866	Sequence 20866, A	974	6	1.8	466	2	US-09-009-217-14	Sequence 14, Appli
902	6	1.8	414	2	US-09-543-681A-4320	Sequence 4320, Ap	975	6	1.8	466	2	US-09-009-656-14	Sequence 14, Appli
903	6	1.8	414	2	US-09-489-039A-10428	Sequence 10428, A	976	6	1.8	466	2	US-09-270-767-42346	Sequence 42346, A

977	6	1.8	466	4	PCT-US93-04493-4	Sequence 4, Appli	1050	6	1.8	503	2	US-09-888-243-2	Sequence 2, Appli
978	6	1.8	467	2	US-09-086-463A-6	Sequence 6, Appli	1051	6	1.8	503	2	US-09-888-243-29	Sequence 2, Appli
979	6	1.8	467	2	US-09-580-212-6	Sequence 6, Appli	1052	6	1.8	503	4	PCT-US93-05701-19	Sequence 19, Appli
980	6	1.8	467	2	US-09-273-871A-11	Sequence 11, Appli	1053	6	1.8	503	4	PCT-US93-05705-2	Sequence 2, Appli
981	6	1.8	467	2	US-09-769-402-6	Sequence 6, Appli	1054	6	1.8	505	1	US-08-394-189B-5	Sequence 5, Appli
982	6	1.8	467	2	US-10-083-452-11	Sequence 11, Appli	1055	6	1.8	505	2	US-09-888-243-5	Sequence 5, Appli
983	6	1.8	468	2	US-09-013-895A-2	Sequence 2, Appli	1056	6	1.8	505	4	PCT-US93-05701-20	Sequence 20, Appli
984	6	1.8	468	2	US-09-134-001C-3999	Sequence 3999, Ap	1057	6	1.8	505	4	PCT-US93-05705-5	Sequence 5, Appli
985	6	1.8	468	2	US-09-565-918-2	Sequence 2, Appli	1058	6	1.8	507	2	US-09-252-991A-23432	Sequence 23432, A
986	6	1.8	468	2	US-09-448-868-2	Sequence 2, Appli	1059	6	1.8	507	2	US-09-248-796A-15836	Sequence 15836, A
987	6	1.8	468	2	US-09-602-787A-324	Sequence 324, Ap	1060	6	1.8	509	1	US-08-665-926-8	Sequence 8, Appli
988	6	1.8	468	2	US-09-949-016-6423	Sequence 6423, Ap	1061	6	1.8	509	2	US-08-740-223A-10	Sequence 10, Appli
989	6	1.8	468	2	US-10-175-902-2	Sequence 2, Appli	1062	6	1.8	509	2	US-09-202-491-3	Sequence 2, Appli
990	6	1.8	468	2	US-10-226-286-2	Sequence 2, Appli	1063	6	1.8	509	2	US-09-202-491-3	Sequence 3, Appli
991	6	1.8	473	2	US-09-720-529A-4	Sequence 4, Appli	1064	6	1.8	509	2	US-09-709-188-10	Sequence 10, Appli
992	6	1.8	474	2	US-09-328-352-5724	Sequence 5724, Ap	1065	6	1.8	509	2	US-09-328-352-6488	Sequence 6488, Ap
993	6	1.8	474	2	US-09-540-236-3598	Sequence 3598, Ap	1066	6	1.8	509	2	US-09-602-787A-12	Sequence 12, Appli
994	6	1.8	477	2	US-09-248-796A-19976	Sequence 19976, A	1067	6	1.8	509	2	US-10-225-060-10	Sequence 10, Appli
995	6	1.8	479	2	US-09-489-039A-10571	Sequence 10571, A	1068	6	1.8	509	2	US-10-018-386-5	Sequence 5, Appli
996	6	1.8	479	2	US-09-540-236-2292	Sequence 2292, Ap	1069	6	1.8	509	2	US-10-215-224-2	Sequence 2, Appli
997	6	1.8	479	2	US-09-908-992B-28	Sequence 28, Appli	1070	6	1.8	509	2	US-10-215-224-3	Sequence 3, Appli
998	6	1.8	480	2	US-09-908-992B-8	Sequence 8, Appli	1071	6	1.8	509	2	US-10-214-812-2	Sequence 2, Appli
999	6	1.8	480	2	US-09-908-992B-12	Sequence 12, Appli	1072	6	1.8	509	2	US-10-214-812-3	Sequence 3, Appli
1000	6	1.8	480	2	US-09-902-540-10711	Sequence 10711, A	1073	6	1.8	510	1	US-08-278-635B-4	Sequence 4, Appli
1001	6	1.8	481	1	US-08-472-028A-6	Sequence 6, Appli	1074	6	1.8	510	2	US-08-471-961-4	Sequence 4, Appli
1002	6	1.8	481	1	US-08-808-931-6	Sequence 6, Appli	1075	6	1.8	510	2	US-09-345-1096-4	Sequence 4, Appli
1003	6	1.8	481	2	US-08-808-323-6	Sequence 6, Appli	1076	6	1.8	510	2	US-09-248-796A-20738	Sequence 20738, A
1004	6	1.8	481	2	US-09-050-603A-6	Sequence 6, Appli	1077	6	1.8	511	2	US-08-464-258B-4	Sequence 4, Appli
1005	6	1.8	481	2	US-09-102-420B-6	Sequence 6, Appli	1078	6	1.8	511	2	US-09-759-143-909	Sequence 909, App
1006	6	1.8	481	2	US-09-015-683-6	Sequence 6, Appli	1079	6	1.8	511	2	US-10-012-896-909	Sequence 909, App
1007	6	1.8	481	2	US-09-457-698-6	Sequence 6, Appli	1080	6	1.8	512	2	US-09-724-224-4	Sequence 4, Appli
1008	6	1.8	481	2	US-09-730-525-6	Sequence 6, Appli	1081	6	1.8	512	2	US-08-999-689A-7	Sequence 7, Appli
1009	6	1.8	483	2	US-09-071-286-6	Sequence 6, Appli	1082	6	1.8	512	2	US-10-093-317-4	Sequence 4, Appli
1010	6	1.8	483	2	US-09-136-268-6	Sequence 6, Appli	1083	6	1.8	512	2	US-09-902-540-16215	Sequence 16215, A
1011	6	1.8	483	2	US-09-191-998-6	Sequence 6, Appli	1084	6	1.8	513	2	US-09-645-337A-12	Sequence 12, Appli
1012	6	1.8	484	2	US-09-949-016-8523	Sequence 8523, Ap	1085	6	1.8	513	2	US-09-720-529A-7	Sequence 7, Appli
1013	6	1.8	484	2	US-09-328-352-4849	Sequence 4849, Ap	1086	6	1.8	514	2	US-08-688-988-35	Sequence 35, Appli
1014	6	1.8	484	2	US-10-142-231-56	Sequence 56, Appli	1087	6	1.8	515	1	US-09-073-362-3	Sequence 3, Appli
1015	6	1.8	485	2	US-10-130-419-1	Sequence 1, Appli	1088	6	1.8	515	1	US-09-243-920-3	Sequence 3, Appli
1016	6	1.8	487	2	US-09-724-224-8	Sequence 8, Appli	1089	6	1.8	515	2	US-09-949-016-6445	Sequence 6445, Ap
1017	6	1.8	487	2	US-09-620-412C-349	Sequence 349, App	1090	6	1.8	516	2	US-09-252-991A-29719	Sequence 29719, A
1018	6	1.8	487	2	US-09-598-419-349	Sequence 349, App	1091	6	1.8	517	2	US-09-282-305-8	Sequence 8, Appli
1019	6	1.8	487	2	US-09-489-039A-12980	Sequence 12980, A	1092	6	1.8	517	2	US-09-883-720-8	Sequence 8, Appli
1020	6	1.8	487	2	US-10-093-317-8	Sequence 8, Appli	1093	6	1.8	518	2	US-09-248-796A-20772	Sequence 20772, A
1021	6	1.8	487	2	US-09-825-414-56	Sequence 66, Appli	1094	6	1.8	518	2	US-09-248-796A-15238	Sequence 15238, A
1022	6	1.8	489	2	US-08-983-502-9	Sequence 9, Appli	1095	6	1.8	519	2	US-09-448-796A-20852	Sequence 20852, A
1023	6	1.8	489	2	US-09-516-747-9	Sequence 9, Appli	1096	6	1.8	520	2	US-09-068-740A-3	Sequence 3, Appli
1024	6	1.8	489	2	US-10-376-397B-4	Sequence 4, Appli	1097	6	1.8	520	2	US-09-527-073-3	Sequence 3, Appli
1025	6	1.8	489	4	PCT-US96-10521-9	Sequence 9, Appli	1098	6	1.8	521	1	US-08-878-563A-3	Sequence 3, Appli
1026	6	1.8	490	2	US-09-949-016-8784	Sequence 8784, Ap	1099	6	1.8	521	2	US-08-996-338-20	Sequence 20, Appli
1027	6	1.8	492	2	US-09-605-703B-1846	Sequence 1846, Ap	1100	6	1.8	521	2	US-09-270-117-3	Sequence 3, Appli
1028	6	1.8	495	2	US-09-328-352-4637	Sequence 4637, Ap	1101	6	1.8	521	2	US-08-956-322-4	Sequence 4, Appli
1029	6	1.8	495	2	US-10-154-515A-6	Sequence 6, Appli	1102	6	1.8	521	2	US-09-252-991A-30623	Sequence 30623, A
1030	6	1.8	495	2	US-10-122-706-6	Sequence 6, Appli	1103	6	1.8	521	2	US-09-556-972-20	Sequence 20, Appli
1031	6	1.8	498	2	US-08-657-749D-23	Sequence 23, Appli	1104	6	1.8	521	2	US-09-046-572-5	Sequence 5, Appli
1032	6	1.8	500	2	US-09-107-532A-4085	Sequence 4085, Ap	1105	6	1.8	522	2	US-09-198-452A-480	Sequence 480, App
1033	6	1.8	502	2	US-09-248-796A-16824	Sequence 16824, A	1106	6	1.8	522	2	US-09-502-540-11338	Sequence 11338, A
1034	6	1.8	503	1	US-08-394-189B-2	Sequence 2, Appli	1107	6	1.8	526	2	US-09-252-991A-27044	Sequence 27044, A
1035	6	1.8	503	2	US-08-258-287B-2	Sequence 2, Appli	1108	6	1.8	528	1	US-08-808-931-10	Sequence 10, Appli
1036	6	1.8	503	2	US-08-258-287B-35	Sequence 35, Appli	1109	6	1.8	528	2	US-08-808-323-10	Sequence 10, Appli
1037	6	1.8	503	2	US-08-258-287B-36	Sequence 36, Appli	1110	6	1.8	528	2	US-09-050-603A-10	Sequence 10, Appli
1038	6	1.8	503	2	US-08-368-704C-2	Sequence 2, Appli	1111	6	1.8	528	2	US-09-102-420B-10	Sequence 10, Appli
1039	6	1.8	503	2	US-08-368-704C-35	Sequence 35, Appli	1112	6	1.8	528	2	US-09-497-698-10	Sequence 10, Appli
1040	6	1.8	503	2	US-08-368-704C-36	Sequence 36, Appli	1113	6	1.8	528	2	US-09-010-147B-20	Sequence 20, Appli
1041	6	1.8	503	2	US-08-740-223A-11	Sequence 11, Appli	1114	6	1.8	528	2	US-09-730-525-10	Sequence 10, Appli
1042	6	1.8	503	2	US-09-709-188-11	Sequence 11, Appli	1115	6	1.8	528	2	US-10-188-495-71	Sequence 71, Appli
1043	6	1.8	503	2	US-08-724-378D-10	Sequence 10, Appli	1116	6	1.8	531	2	US-09-489-039A-9781	Sequence 9781, Ap
1044	6	1.8	503	2	US-08-999-689A-6	Sequence 6, Appli	1117	6	1.8	535	2	US-09-252-991A-31062	Sequence 31062, A
1045	6	1.8	503	2	US-09-291-289-12	Sequence 12, Appli	1118	6	1.8	536	1	US-08-808-931-20	Sequence 20, Appli
1046	6	1.8	503	2	US-09-895-263B-13	Sequence 13, Appli	1119	6	1.8	536	2	US-08-808-323-20	Sequence 20, Appli
1047	6	1.8	503	2	US-09-944-807-4	Sequence 4, Appli	1120	6	1.8	536	2	US-09-050-603A-20	Sequence 20, Appli
1048	6	1.8	503	2	US-10-225-060-11	Sequence 11, Appli	1121	6	1.8	536	2	US-09-102-420B-20	Sequence 20, Appli
1049	6	1.8	503	2	US-09-613-508B-13	Sequence 13, Appli	1122	6	1.8	536	2	US-09-497-698-20	Sequence 20, Appli

1123	6	1.8	536	2	US-09-328-352-4594	Sequence 4594, Ap	1196	6	1.8	580	2	US-09-489-039A-8096	Sequence 8096, Ap
1124	6	1.8	536	2	US-09-730-525-20	Sequence 20, Appl	1197	6	1.8	581	2	US-09-583-110-3011	Sequence 3011, Ap
1125	6	1.8	537	1	US-08-472-028A-2	Sequence 2, Appl1	1198	6	1.8	583	2	US-09-583-110-3011	Sequence 15800, A
1126	6	1.8	537	1	US-08-808-931-2	Sequence 2, Appl1	1199	6	1.8	589	1	US-08-937-540-6	Sequence 6, Appl1
1127	6	1.8	537	2	US-08-808-333-2	Sequence 2, Appl1	1200	6	1.8	590	2	US-09-398-395A-54	Sequence 54, Appl
1128	6	1.8	537	2	US-09-050-603A-2	Sequence 2, Appl1	1201	6	1.8	590	2	US-09-887-586A-54	Sequence 54, Appl
1129	6	1.8	537	2	US-09-102-420B-2	Sequence 2, Appl1	1202	6	1.8	590	2	US-09-895-752-54	Sequence 54, Appl
1130	6	1.8	537	2	US-09-071-296-2	Sequence 2, Appl1	1203	6	1.8	590	2	US-09-903-0128-54	Sequence 54, Appl
1131	6	1.8	537	2	US-09-196-268-2	Sequence 2, Appl1	1204	6	1.8	590	2	US-09-900-797-54	Sequence 54, Appl
1132	6	1.8	537	2	US-09-015-683-2	Sequence 2, Appl1	1205	6	1.8	590	2	US-09-893-820-54	Sequence 54, Appl
1133	6	1.8	537	2	US-09-191-998-2	Sequence 2, Appl1	1206	6	1.8	594	2	US-09-949-016-9261	Sequence 9261, Ap
1134	6	1.8	537	2	US-09-497-698-2	Sequence 2, Appl1	1207	6	1.8	595	2	US-09-107-433-2632	Sequence 2632, Ap
1135	6	1.8	537	2	US-09-730-525-2	Sequence 2, Appl1	1208	6	1.8	597	2	US-09-902-540-11095	Sequence 11095, A
1136	6	1.8	537	2	US-09-508-525-2	Sequence 2, Appl1	1209	6	1.8	608	2	US-09-134-001C-3855	Sequence 3855, Ap
1137	6	1.8	539	1	US-09-808-931-16	Sequence 16, Appl	1210	6	1.8	611	2	US-09-916-393A-81	Sequence 81, Appl
1138	6	1.8	539	2	US-08-808-333-16	Sequence 16, Appl	1211	6	1.8	611	2	US-09-662-254A-19	Sequence 19, Appl
1139	6	1.8	539	2	US-09-050-603A-16	Sequence 16, Appl	1212	6	1.8	613	1	US-08-915-207-2	Sequence 2, Appl1
1140	6	1.8	539	2	US-09-102-420B-16	Sequence 16, Appl	1213	6	1.8	613	1	US-09-238-555-2	Sequence 2, Appl1
1141	6	1.8	539	2	US-09-497-698-16	Sequence 16, Appl	1214	6	1.8	613	2	US-09-238-555-4	Sequence 4, Appl1
1142	6	1.8	539	2	US-09-730-525-16	Sequence 16, Appl	1215	6	1.8	616	1	US-08-453-695A-115	Sequence 9128, Ap
1143	6	1.8	540	2	US-09-583-110-3685	Sequence 3685, Ap	1216	6	1.8	616	1	US-08-268-161A-1195	Sequence 115, App
1144	6	1.8	541	1	US-08-604-333-2	Sequence 2, Appl1	1217	6	1.8	616	1	US-08-453-695A-115	Sequence 115, App
1145	6	1.8	541	2	US-09-110-618-2	Sequence 2, Appl1	1218	6	1.8	616	1	US-08-453-695A-115	Sequence 115, App
1146	6	1.8	541	2	US-09-173-151A-28	Sequence 28, Appl1	1219	6	1.8	616	1	US-08-453-695A-115	Sequence 115, App
1147	6	1.8	541	2	US-09-578-178-2	Sequence 2, Appl1	1220	6	1.8	616	4	PCT-US95-08071-115	Sequence 115, App
1148	6	1.8	541	2	US-09-577-806-2	Sequence 2, Appl1	1221	6	1.8	616	4	PCT-US95-08071-115	Sequence 115, App
1149	6	1.8	541	2	US-09-621-502-4	Sequence 4, Appl1	1222	6	1.8	617	2	US-09-603-208A-32	Sequence 32, Appl
1150	6	1.8	541	2	US-09-949-002-360	Sequence 360, App	1223	6	1.8	618	2	US-09-603-208A-34	Sequence 34, Appl
1151	6	1.8	543	1	US-08-808-931-12	Sequence 12, Appl	1224	6	1.8	618	2	US-09-949-016-6308	Sequence 6308, Ap
1152	6	1.8	543	2	US-08-808-333-12	Sequence 12, Appl	1225	6	1.8	619	2	US-09-949-016-6308	Sequence 10, Appl
1153	6	1.8	543	2	US-09-050-603A-12	Sequence 12, Appl	1226	6	1.8	620	2	US-09-602-787A-10	Sequence 6, Appl1
1154	6	1.8	543	2	US-09-102-420B-12	Sequence 12, Appl	1227	6	1.8	621	1	US-08-295-814E-6	Sequence 6, Appl1
1155	6	1.8	543	2	US-09-497-698-12	Sequence 12, Appl	1228	6	1.8	621	4	PCT-US93-01959-6	Sequence 839, App
1156	6	1.8	543	2	US-09-302-357-6	Sequence 6, Appl1	1229	6	1.8	626	2	US-09-198-452A-839	Sequence 791, App
1157	6	1.8	543	2	US-09-540-236-3630	Sequence 3630, Ap	1230	6	1.8	627	2	US-09-438-185A-791	Sequence 843, App
1158	6	1.8	543	2	US-09-730-525-12	Sequence 12, Appl	1231	6	1.8	629	2	US-09-198-452A-843	Sequence 6976, Ap
1159	6	1.8	543	2	US-09-697-719-6	Sequence 6, Appl1	1232	6	1.8	632	2	US-09-949-016-6976	Sequence 26, Appl
1160	6	1.8	545	2	US-09-270-767-39221	Sequence 39221, A	1233	6	1.8	632	2	US-09-438-185A-795	Sequence 795, App
1161	6	1.8	545	2	US-09-270-767-54338	Sequence 54338, A	1234	6	1.8	640	2	US-08-836-567-10	Sequence 10, Appl
1162	6	1.8	545	2	US-09-248-796A-15777	Sequence 15777, A	1235	6	1.8	641	2	US-09-606-304-10	Sequence 10, Appl
1163	6	1.8	546	2	US-09-107-532A-4759	Sequence 4759, Ap	1236	6	1.8	641	2	US-09-613-303-51	Sequence 51, Appl
1164	6	1.8	546	2	US-09-949-002-489	Sequence 489, App	1237	6	1.8	641	2	US-10-267-311-51	Sequence 51, Appl
1165	6	1.8	548	2	US-08-687-590-31	Sequence 31, Appl	1238	6	1.8	644	2	US-08-800-291E-8	Sequence 8, Appl1
1166	6	1.8	548	2	US-09-508-418A-2	Sequence 2, Appl1	1239	6	1.8	648	2	US-09-489-039A-10538	Sequence 10538, A
1167	6	1.8	552	2	US-09-949-016-9572	Sequence 9572, Ap	1240	6	1.8	648	2	US-09-489-039A-10538	Sequence 63, Appl
1168	6	1.8	552	2	US-09-955-732A-15	Sequence 15, Appl1	1241	6	1.8	649	2	US-10-188-495-63	Sequence 1, Appl1
1169	6	1.8	552	2	US-09-775-925-4	Sequence 2, Appl1	1242	6	1.8	650	2	US-09-443-795-1	Sequence 17330, A
1170	6	1.8	553	2	US-09-514-245-4	Sequence 4, Appl1	1243	6	1.8	650	2	US-09-252-991A-17330	Sequence 5, Appl1
1171	6	1.8	553	2	US-09-800-960-4	Sequence 4, Appl1	1244	6	1.8	652	1	US-08-318-931-8	Sequence 8, Appl1
1172	6	1.8	556	2	US-10-096-960-4	Sequence 4, Appl1	1245	6	1.8	652	1	US-09-110-116-1	Sequence 1, Appl1
1173	6	1.8	557	2	US-09-252-991A-22465	Sequence 22465, A	1246	6	1.8	652	2	US-08-956-322-2	Sequence 2, Appl1
1174	6	1.8	559	2	US-09-252-991A-28488	Sequence 28488, A	1247	6	1.8	652	2	US-09-949-016-8841	Sequence 8841, Ap
1175	6	1.8	560	1	US-08-808-931-18	Sequence 18, Appl	1248	6	1.8	654	2	US-09-949-016-8841	Sequence 422, App
1176	6	1.8	560	2	US-08-808-323-18	Sequence 18, Appl	1249	6	1.8	654	2	US-09-487-3588-422	Sequence 35, Appl1
1177	6	1.8	560	2	US-09-050-603A-18	Sequence 18, Appl	1250	6	1.8	661	2	US-09-595-684B-35	Sequence 3, Appl1
1178	6	1.8	560	2	US-09-102-420B-18	Sequence 18, Appl	1251	6	1.8	665	2	US-08-704-711A-3	Sequence 29, Appl
1179	6	1.8	560	2	US-09-497-698-18	Sequence 18, Appl	1252	6	1.8	669	2	US-09-521-220-3	Sequence 61, Appl
1180	6	1.8	560	2	US-09-730-525-18	Sequence 18, Appl	1253	6	1.8	676	2	US-09-583-110-4259	Sequence 4259, Ap
1181	6	1.8	563	2	US-09-289-180-9	Sequence 9, Appl1	1254	6	1.8	677	2	US-09-902-540-15691	Sequence 15691, A
1182	6	1.8	563	2	US-09-302-357-18	Sequence 18, Appl1	1255	6	1.8	680	2	US-09-107-433-3924	Sequence 3924, Ap
1183	6	1.8	563	2	US-09-978-709-9	Sequence 9, Appl1	1256	6	1.8	684	2	US-08-965-762-2	Sequence 2, Appl1
1184	6	1.8	563	2	US-09-697-719-18	Sequence 18, Appl1	1257	6	1.8	684	2	US-09-911-827-2	Sequence 2, Appl1
1185	6	1.8	564	2	US-09-211-704A-8	Sequence 8, Appl1	1258	6	1.8	684	2	US-09-911-882-2	Sequence 2, Appl1
1186	6	1.8	565	2	US-09-800-960-2	Sequence 2, Appl1	1259	6	1.8	684	2	US-09-911-882-2	Sequence 2, Appl1
1187	6	1.8	565	2	US-10-096-960-2	Sequence 2, Appl1	1260	6	1.8	684	2	US-09-911-882-2	Sequence 2, Appl1
1188	6	1.8	568	2	US-09-188-930-291	Sequence 291, App	1261	6	1.8	684	2	US-09-911-882-2	Sequence 2, Appl1
1189	6	1.8	568	2	US-09-312-283C-291	Sequence 291, App	1262	6	1.8	684	2	US-09-911-882-2	Sequence 2, Appl1
1190	6	1.8	568	2	US-09-902-540-13650	Sequence 13650, A	1263	6	1.8	684	2	US-09-911-882-2	Sequence 2, Appl1
1191	6	1.8	569	2	US-09-514-245-16	Sequence 16, Appl1	1264	6	1.8	684	2	US-09-911-882-2	Sequence 2, Appl1
1192	6	1.8	573	2	US-09-252-991A-26428	Sequence 26428, A	1265	6	1.8	694	2	US-09-252-991A-22481	Sequence 22481, A
1193	6	1.8	573	2	US-09-438-185A-489	Sequence 488, App	1266	6	1.8	699	2	US-09-252-991A-17077	Sequence 17077, A
1194	6	1.8	575	2	US-09-328-352-7529	Sequence 7529, Ap	1267	6	1.8	702	2	US-09-068-740A-4	Sequence 4, Appl1
1195	6	1.8	577	2	US-09-902-540-10734	Sequence 10734, A	1268	6	1.8	705	2	US-09-949-016-10464	Sequence 10464, A

1269	6	1.8	709	2	US-09-874-923-121	Sequence 121, App	1342	6	1.8	879	1	US-08-220-151-2	Sequence 2, Appli
1270	6	1.8	712	2	US-09-252-991A-20471	Sequence 20471, A	1343	6	1.8	879	1	US-08-220-151-3	Sequence 3, Appli
1271	6	1.8	719	2	US-09-763-902B-5	Sequence 5, Appli	1344	6	1.8	879	1	US-08-413-118-2	Sequence 2, Appli
1272	6	1.8	723	2	US-09-068-740A-9	Sequence 9, Appli	1345	6	1.8	879	1	US-08-413-118-3	Sequence 3, Appli
1273	6	1.8	723	2	US-09-423-753-27	Sequence 27, Appl	1346	6	1.8	879	1	US-08-413-118-106	Sequence 106, Appl
1274	6	1.8	723	2	US-09-641-612-6	Sequence 6, Appli	1347	6	1.8	879	2	US-08-473-446-2	Sequence 2, Appli
1275	6	1.8	725	2	US-09-350-457A-2	Sequence 2, Appli	1348	6	1.8	879	2	US-08-473-446-3	Sequence 3, Appli
1276	6	1.8	725	2	US-09-248-796A-20849	Sequence 20849, A	1349	6	1.8	879	2	US-08-473-446-106	Sequence 106, App
1277	6	1.8	727	2	US-09-350-457A-4	Sequence 4, Appli	1350	6	1.8	880	2	US-10-104-047-2834	Sequence 2834, Ap
1278	6	1.8	728	2	US-09-543-681A-6690	Sequence 6690, Ap	1351	6	1.8	883	2	US-09-248-796A-14418	Sequence 14418, A
1279	6	1.8	728	2	US-08-981-392-2	Sequence 2, Appli	1352	6	1.8	883	2	US-09-248-796A-18931	Sequence 18931, A
1280	6	1.8	728	2	US-09-908-332-2	Sequence 2, Appli	1353	6	1.8	883	2	US-10-195-970-3	Sequence 3, Appli
1281	6	1.8	728	2	US-09-310-685-11	Sequence 11, Appli	1354	6	1.8	883	2	US-10-195-970-6	Sequence 6, Appli
1282	6	1.8	729	2	US-08-872-855-8	Sequence 8, Appli	1355	6	1.8	883	2	US-10-188-495-72	Sequence 72, Appl
1283	6	1.8	733	2	US-09-270-767-44442	Sequence 44442, A	1356	6	1.8	884	1	US-07-718-575-12	Sequence 12, Appl
1284	6	1.8	737	1	US-08-185-432-2	Sequence 2, Appli	1357	6	1.8	884	1	US-08-481-206-12	Sequence 12, Appl
1285	6	1.8	737	1	US-08-185-432-4	Sequence 4, Appli	1358	6	1.8	884	1	US-08-486-269A-112	Sequence 12, Appl
1286	6	1.8	738	2	US-09-107-532A-5096	Sequence 5096, Ap	1359	6	1.8	892	2	US-09-540-236-2074	Sequence 2074, Ap
1287	6	1.8	739	2	US-09-022-983-2	Sequence 2, Appli	1360	6	1.8	906	2	US-09-717-364A-15	Sequence 15, Appl
1288	6	1.8	742	2	US-09-494-297A-4	Sequence 4, Appli	1361	6	1.8	908	2	US-09-635-872A-15	Sequence 15, Appl
1289	6	1.8	745	2	US-10-104-047-2955	Sequence 2955, Ap	1362	6	1.8	908	2	US-09-636-077A-15	Sequence 15, Appl
1290	6	1.8	745	2	US-10-104-047-2960	Sequence 2960, Ap	1363	6	1.8	908	2	US-09-636-060C-15	Sequence 15, Appl
1291	6	1.8	746	2	US-09-248-796A-20280	Sequence 20280, A	1364	6	1.8	908	2	US-09-986-552-15	Sequence 15, Appl
1292	6	1.8	749	2	US-09-562-737-94	Sequence 94, Appl	1365	6	1.8	908	2	US-09-636-596C-15	Sequence 15, Appl
1293	6	1.8	749	2	US-09-562-737-98	Sequence 98, Appl	1366	6	1.8	908	2	US-10-023-894-9	Sequence 9, Appli
1294	6	1.8	751	2	US-09-036-987A-24	Sequence 24, Appl	1367	6	1.8	908	2	US-10-306-686-15	Sequence 15, Appl
1295	6	1.8	751	2	US-09-370-700-24	Sequence 24, Appl	1368	6	1.8	908	2	US-09-895-072-15	Sequence 15, Appl
1296	6	1.8	751	2	US-09-603-207-24	Sequence 24, Appl	1369	6	1.8	908	2	US-10-023-888-9	Sequence 9, Appli
1297	6	1.8	766	4	PCT-US94-00198-6	Sequence 6, Appli	1370	6	1.8	908	4	PCT-US95-03747-3	Sequence 3, Appli
1298	6	1.8	769	2	US-09-902-540-16616	Sequence 16616, A	1371	6	1.8	909	2	US-09-425-383-2	Sequence 2, Appli
1299	6	1.8	772	1	US-08-524-757-12	Sequence 12, Appl	1372	6	1.8	911	2	US-09-902-540-12141	Sequence 12141, A
1300	6	1.8	784	2	US-09-902-540-14775	Sequence 14775, A	1373	6	1.8	912	4	PCT-US95-03747-2	Sequence 2, Appli
1301	6	1.8	785	2	US-09-252-991A-32952	Sequence 32952, A	1374	6	1.8	916	2	US-09-999-833A-390	Sequence 390, App
1302	6	1.8	794	2	US-09-710-279-1050	Sequence 1050, Ap	1375	6	1.8	916	2	US-10-020-4453-390	Sequence 390, App
1303	6	1.8	801	2	US-09-538-092-258	Sequence 258, App	1376	6	1.8	927	2	US-09-248-796A-16269	Sequence 16269, A
1304	6	1.8	802	2	US-09-252-991A-23824	Sequence 23824, A	1377	6	1.8	927	2	US-09-841-786-3	Sequence 3, Appli
1305	6	1.8	803	2	US-09-902-540-11475	Sequence 11475, A	1378	6	1.8	931	2	US-09-949-016-8987	Sequence 8987, Ap
1306	6	1.8	810	2	US-09-328-352-7181	Sequence 7181, Ap	1379	6	1.8	931	2	US-09-949-016-8988	Sequence 8988, Ap
1307	6	1.8	820	2	US-09-252-991A-23346	Sequence 23346, A	1380	6	1.8	932	2	US-09-949-016-8989	Sequence 8989, Ap
1308	6	1.8	821	2	US-09-556-877-195	Sequence 195, App	1381	6	1.8	933	1	US-08-682-847-2	Sequence 2, Appli
1309	6	1.8	821	2	US-09-620-412C-195	Sequence 195, App	1382	6	1.8	935	1	US-08-152-721B-2	Sequence 2, Appli
1310	6	1.8	821	2	US-09-598-419-195	Sequence 195, App	1383	6	1.8	935	2	US-09-512-250C-33	Sequence 33, Appl
1311	6	1.8	823	2	US-09-248-796A-16699	Sequence 16699, A	1384	6	1.8	935	2	US-09-252-991A-33037	Sequence 33037, A
1312	6	1.8	823	2	US-09-248-796A-19339	Sequence 19339, A	1385	6	1.8	933	2	US-08-911-321-4	Sequence 4, Appli
1313	6	1.8	829	2	US-09-949-016-5852	Sequence 6852, Ap	1386	6	1.8	950	2	US-09-914-259-69	Sequence 69, Appl
1314	6	1.8	829	2	US-09-949-016-57161	Sequence 7161, Ap	1387	6	1.8	952	2	US-09-270-767-14680	Sequence 14680, A
1315	6	1.8	830	2	US-09-562-737-34	Sequence 34, Appl	1388	6	1.8	956	2	US-09-902-540-10395	Sequence 10395, A
1316	6	1.8	831	2	US-09-702-705-1819	Sequence 1819, Ap	1389	6	1.8	958	2	US-09-171-891-6	Sequence 6, Appli
1317	6	1.8	831	2	US-09-736-457-1819	Sequence 1819, Ap	1390	6	1.8	960	2	US-09-422-936-45	Sequence 45, Appl
1318	6	1.8	831	2	US-09-671-325-1819	Sequence 1819, Ap	1391	6	1.8	961	2	US-09-540-236-2492	Sequence 2492, Ap
1319	6	1.8	831	2	US-10-017-754-1819	Sequence 1819, Ap	1392	6	1.8	962	2	US-09-134-001C-44497	Sequence 4497, Ap
1320	6	1.8	839	2	US-10-202-481-4	Sequence 4, Appli	1393	6	1.8	963	2	US-09-394-272-12	Sequence 12, Appl
1321	6	1.8	843	2	US-09-361-631-1	Sequence 1, Appli	1394	6	1.8	963	2	US-09-394-272-13	Sequence 13, Appl
1322	6	1.8	843	2	US-09-361-631-2	Sequence 2, Appli	1395	6	1.8	970	2	US-09-134-000C-4256	Sequence 4256, Ap
1323	6	1.8	843	2	US-09-252-991A-19886	Sequence 19886, A	1396	6	1.8	970	2	US-09-538-092-664	Sequence 664, App
1324	6	1.8	846	2	US-09-949-016-10381	Sequence 10381, A	1397	6	1.8	973	1	US-08-683-262B-75	Sequence 75, Appl
1325	6	1.8	848	2	US-09-543-681A-7615	Sequence 7615, Ap	1398	6	1.8	973	2	US-09-361-707-75	Sequence 75, Appl
1326	6	1.8	852	1	US-08-190-802A-59	Sequence 59, Appl	1399	6	1.8	973	2	US-09-430-723-2	Sequence 2, Appli
1327	6	1.8	852	1	US-08-190-802A-67	Sequence 67, Appl	1400	6	1.8	975	2	US-09-540-236-2304	Sequence 2304, Ap
1328	6	1.8	852	1	US-08-477-346-59	Sequence 59, Appl	1401	6	1.8	979	2	US-08-514-213A-2	Sequence 2, Appli
1329	6	1.8	852	2	US-08-477-346-57	Sequence 67, Appl	1402	6	1.8	979	2	US-09-015-399-5	Sequence 5, Appli
1330	6	1.8	852	2	US-08-473-089-59	Sequence 59, Appl	1403	6	1.8	985	1	US-08-680-326-41	Sequence 41, Appl
1331	6	1.8	852	2	US-08-473-089-67	Sequence 67, Appl	1404	6	1.8	999	2	US-09-438-185A-455	Sequence 455, App
1332	6	1.8	852	2	US-08-487-072A-59	Sequence 59, Appl	1405	6	1.8	1003	2	US-09-949-016-11260	Sequence 11260, A
1333	6	1.8	852	2	US-08-487-072A-67	Sequence 67, Appl	1406	6	1.8	1009	2	US-09-693-146-4	Sequence 4, Appli
1334	6	1.8	867	2	US-09-417-485D-2	Sequence 2, Appli	1407	6	1.8	1009	2	US-09-562-737-45	Sequence 45, Appli
1335	6	1.8	867	2	US-09-417-485D-4	Sequence 4, Appli	1408	6	1.8	1024	2	US-09-562-737-87	Sequence 87, Appl
1336	6	1.8	877	1	US-08-916-917-2	Sequence 2, Appli	1409	6	1.8	1034	2	US-09-543-681A-8172	Sequence 8172, Ap
1337	6	1.8	877	1	US-08-972-631-2	Sequence 2, Appli	1410	6	1.8	1038	2	US-09-902-540-11907	Sequence 11907, A
1338	6	1.8	877	1	US-08-972-632-2	Sequence 2, Appli	1411	6	1.8	1040	2	US-09-902-540-11105	Sequence 11105, A
1339	6	1.8	877	1	US-08-972-630-2	Sequence 2, Appli	1412	6	1.8	1041	1	US-08-220-151-4	Sequence 4, Appli
1340	6	1.8	877	1	US-08-672-211-2	Sequence 2, Appli	1413	6	1.8	1041	1	US-08-413-118-4	Sequence 4, Appli
1341	6	1.8	877	2	US-09-225-170-2	Sequence 2, Appli	1414	6	1.8	1041	2	US-08-473-446-4	Sequence 4, Appli

1415	6	1.8	1044	2	US-09-107-532A-5229	Sequence 5229, Ap
1416	6	1.8	1048	2	US-09-802-540-10865	Sequence 10845, A
1417	6	1.8	1051	2	US-09-252-991A-25332	Sequence 25233, A
1418	6	1.8	1072	2	US-09-248-796A-16400	Sequence 16400, A
1419	6	1.8	1073	2	US-10-104-047-2513	Sequence 2, Appl
1420	6	1.8	1089	1	US-08-375-300-2	Sequence 2, Appl
1421	6	1.8	1089	1	US-09-177-431-2	Sequence 2, Appl
1422	6	1.8	1089	4	PCT-US95-16930-2	Sequence 2, Appl
1423	6	1.8	1094	1	US-08-680-326-40	Sequence 40, Appl
1424	6	1.8	1096	2	US-09-252-991A-19328	Sequence 19328, A
1425	6	1.8	1098	2	US-10-104-047-3280	Sequence 3280, Ap
1426	6	1.8	1099	2	US-08-726-214-14	Sequence 14, Appl
1427	6	1.8	1114	2	US-08-811-583-2	Sequence 2, Appl
1428	6	1.8	1122	1	US-08-619-198-3	Sequence 3, Appl
1429	6	1.8	1125	2	US-09-900-920-60	Sequence 60, Appl
1430	6	1.8	1148	2	US-09-949-016-6798	Sequence 6798, Ap
1431	6	1.8	1194	2	US-09-092-508-2	Sequence 2, Appl
1432	6	1.8	1194	2	US-09-435-115-2	Sequence 2, Appl
1433	6	1.8	1194	2	US-09-069-023-26	Sequence 26, Appl
1434	6	1.8	1194	2	US-09-098-310-2	Sequence 2, Appl
1435	6	1.8	1194	2	US-09-538-092-825	Sequence 825, App
1436	6	1.8	1194	2	US-09-949-016-6030	Sequence 6030, Ap
1437	6	1.8	1196	2	US-09-949-016-10065	Sequence 10065, A
1438	6	1.8	1196	2	US-09-949-016-10065	Sequence 10065, A
1439	6	1.8	1205	2	US-09-092-508-16	Sequence 16, Appl
1440	6	1.8	1205	2	US-09-435-115-16	Sequence 16, Appl
1441	6	1.8	1237	2	US-09-949-016-6842	Sequence 6842, Ap
1442	6	1.8	1239	2	US-09-949-016-10063	Sequence 10063, A
1443	6	1.8	1239	2	US-09-949-016-10063	Sequence 10063, A
1444	6	1.8	1279	2	US-09-489-039A-13602	Sequence 13602, A
1445	6	1.8	1287	2	US-09-949-016-7826	Sequence 7826, Ap
1446	6	1.8	1289	1	US-08-853-659A-51	Sequence 51, Appl
1447	6	1.8	1294	2	US-09-338-352-6314	Sequence 6314, Ap
1448	6	1.8	1297	1	US-08-290-731C-4	Sequence 4, Appl
1449	6	1.8	1298	2	US-09-252-991A-30579	Sequence 30579, A
1450	6	1.8	1319	1	US-08-290-731C-2	Sequence 2, Appl
1451	6	1.8	1321	1	US-08-317-310A-64	Sequence 64, Appl
1452	6	1.8	1323	2	US-09-270-767-46728	Sequence 46728, A
1453	6	1.8	1326	2	US-09-147-236-5	Sequence 5, Appl
1454	6	1.8	1326	2	US-09-532-474-5	Sequence 5, Appl
1455	6	1.8	1333	2	US-09-356-952-2	Sequence 2, Appl
1456	6	1.8	1333	2	US-09-976-594-312	Sequence 312, App
1457	6	1.8	1336	1	US-08-290-731C-6	Sequence 6, Appl
1458	6	1.8	1346	2	US-09-949-016-0959	Sequence 9959, Ap
1459	6	1.8	1364	2	US-09-252-991A-26880	Sequence 26880, A
1460	6	1.8	1389	1	US-08-619-198-5	Sequence 5, Appl
1461	6	1.8	1431	2	US-09-902-540-10614	Sequence 10614, A
1462	6	1.8	1436	2	US-09-578-063-78	Sequence 78, Appl
1463	6	1.8	1449	2	US-09-303-518D-652	Sequence 652, App
1464	6	1.8	1454	2	US-09-673-896-2	Sequence 2, Appl
1465	6	1.8	1457	2	US-09-673-896-4	Sequence 4, Appl
1466	6	1.8	1457	2	US-09-303-518D-650	Sequence 650, App
1467	6	1.8	1468	2	US-09-303-518D-654	Sequence 654, App
1468	6	1.8	1509	2	US-09-676-519-27	Sequence 27, Appl
1469	6	1.8	1568	2	US-09-181-706-2	Sequence 2, Appl
1470	6	1.8	1568	2	US-09-458-791-2	Sequence 2, Appl
1471	6	1.8	1568	2	US-09-459-066-2	Sequence 2, Appl
1472	6	1.8	1568	2	US-09-459-065-2	Sequence 2, Appl
1473	6	1.8	1575	2	US-09-917-254-38	Sequence 98, Appl
1474	6	1.8	1608	2	US-09-964-956-61	Sequence 61, Appl
1475	6	1.8	1651	2	US-09-949-016-10643	Sequence 10643, A
1476	6	1.8	1666	2	US-09-902-540-15792	Sequence 15792, A
1477	6	1.8	1686	2	US-09-355-160D-2	Sequence 2, Appl
1478	6	1.8	1686	2	US-10-092-219-2	Sequence 2, Appl
1479	6	1.8	1729	2	US-09-696-115B-2	Sequence 2, Appl
1480	6	1.8	1753	2	US-09-248-796A-19154	Sequence 19154, A
1481	6	1.8	1776	2	US-09-556-877-179	Sequence 179, App
1482	6	1.8	1776	2	US-09-620-412C-179	Sequence 179, App
1483	6	1.8	1776	2	US-09-598-419-179	Sequence 179, App
1484	6	1.8	1780	2	US-09-949-016-6899	Sequence 6899, App
1485	6	1.8	1788	1	US-08-962-284-2	Sequence 2, Appl
1486	6	1.8	1788	2	US-09-964-956-60	Sequence 60, Appl
1487	6	1.8	1806	2	US-09-919-497-56	Sequence 56, Appl

1488

6

1.8

1872

1

US-08-188-582-14

Sequence 14, Appl

1489

6

1.8

1872

1

US-08-646-715-14

Sequence 14, Appl

1490

6

1.8

1884

2

US-09-949-016-7154

Sequence 7154, Ap

1491

6

1.8

1893

1

US-08-188-582-11

Sequence 11, Appl

1492

6

1.8

1893

1

US-08-646-715-11

Sequence 11, Appl

1493

6

1.8

1898

1

US-08-056-200-94

Sequence 94, Appl

1494

6

1.8

1898

1

US-08-800-644-94

Sequence 94, Appl

1495

6

1.8

1898

2

US-09-802-540-11251

Sequence 1280, Ap

1496

6

1.8

1990

2

US-09-538-092-1371

Sequence 1371, Ap

1497

6

1.8

2004

2

US-09-949-016-6756

Sequence 6756, Ap

1498

6

1.8

2165

1

US-08-514-975B-2

Sequence 2, Appl

1499

6

1.8

2165

1

US-09-368-076-29

Sequence 29, Appl

1500

6

1.8

2165

2

US-09-368-076-29

Sequence 29, Appl

RESULT 1

US-09-991-181-253

Sequence 253, Application US/09991181

Patent No. 691919

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gunney, Austin L.

APPLICANT: Kijavini, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumaas, Daniel

APPLICANT: Matanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC53

CURRENT APPLICATION NUMBER: US/09/991,181

CURRENT FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 3,6e-314;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTYILMQLGSAASGVKELNGSGAMTFPLKSKKQVDSIVMFTNTPL 60
DB 1 MAGSPCTCLTYILMQLGSAASGVKELNGSGAVTFPLKSKKQVDSIVMFTNTPL 60

OY 61 VTIOEGGTIVTQNRNERYDFPDGYSLLKSKLKNDGSGIYYVIGYSSSIQOPSTOY 120
DB 61 VTIOEGGTIVTQNRNERYDFPDGYSLLKSKLKNDGSGIYYVIGYSSSIQOPSTOY 120

OY 121 VLAHYEHLKSKPVMTGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGOANESHNGSIL 180
DB 121 VLAHYEHLKSKPVMTGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGOANESHNGSIL 180

OY 181 PISMRWGSMDTFCVARNPVSRNFSPTLARKLCEGAADPDSSMTLLCLLVPLLLSL 240
DB 181 PISMRWGSMDTFCVARNPVSRNFSPTLARKLCEGAADPDSSMTLLCLLVPLLLSL 240

OY 241 FVLGLFLMFLKREPOEXYIEEKRVDCRETPTNLCPHSGENTEXTTPTHTRTILKEDPA 300
DB 241 FVLGLFLMFLKREPOEXYIEEKRVDCRETPTNLCPHSGENTEXTTPTHTRTILKEDPA 300

OY 301 NTYYSTVEIPKKMENPHSLTMPDTPRLPAYENV 335
DB 301 NTYYSTVEIPKKMENPHSLTMPDTPRLPAYENV 335

RESULT 2
US-09-990-444-253
; Sequence 253, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Boetstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertjesen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, V. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532

;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089600
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02

;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 3.6e-314;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCTLIYIIMQLTGSAAGPVKELVGSVGAATVPLKSKVKOVDSIWTFTTTPPL 60
DB 1 MAGSPCTCTLIYIIMQLTGSAAGPVKELVGSVGAATVPLKSKVKOVDSIWTFTTTPPL 60
QY 61 VTTQPEGGTIIYQNRREBVDPPDGGYSLKSLKKNDSGIYYVGIYSSLIQPSIOEY 120
DB 61 VTTQPEGGTIIYQNRREBVDPPDGGYSLKSLKKNDSGIYYVGIYSSLIQPSIOEY 120
QY 121 VLAHYEHSKPKVTMGLQSNKNGTCVNTLTCMEHGEDEVIYTWKALGOANESHNGSIL 180
DB 121 VLAHYEHSKPKVTMGLQSNKNGTCVNTLTCMEHGEDEVIYTWKALGOANESHNGSIL 180
QY 181 PISWRGESDMTF CVARNPVSNRFSPIIARKLCBGAADDPSSMWLLCLLIVPLLSTL 240
DB 181 PISWRGESDMTF CVARNPVSNRFSPIIARKLCBGAADDPSSMWLLCLLIVPLLSTL 240
QY 241 FVLGLFLWFLKREOEYIEKKRVDCRETPNICPSGENTEXTDTPHTNRITLKEDPA 300
DB 241 FVLGLFLWFLKREOEYIEKKRVDCRETPNICPSGENTEXTDTPHTNRITLKEDPA 300
QY 301 NTVYSTVEIRPKMENPHSLTMDPTPRLPAYENVY 335
DB 301 NTVYSTVEIRPKMENPHSLTMDPTPRLPAYENVY 335

RESULT 3
US-09-997-333-253
; Sequence 253, Application us/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C27
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694

;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090662
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 2; Length 335;

Best Local Similarity 100.0%; Pred. No. 3,6e-314;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTLYIIMQLTGSAAGVVKELVSGVGAVFPPKSKVKQVDSIVMTFNTPL 60
DB 1 MAGSPCTCLTLYIIMQLTGSAAGVVKELVSGVGAVFPPKSKVKQVDSIVMTFNTPL 60
QY 61 VTIOBGGTIIVTQNRNRERVDPPDGYSLKLSKLNKNSGIYYVGISSSLQPSITGEY 120
DB 61 VTIOBGGTIIVTQNRNRERVDPPDGYSLKLSKLNKNSGIYYVGISSSLQPSITGEY 120
QY 121 VLAHYEHLSKPKVTMGLOSNKNGTCVTNLTCCMEHGEEDVITYWKALGOANESHNGSIL 180
DB 121 VLAHYEHLSKPKVTMGLOSNKNGTCVTNLTCCMEHGEEDVITYWKALGOANESHNGSIL 180
QY 181 PISRWGESDWTFCVARNPVSRNPSBPIARKLCEGAADPDSSMTLCLLVPILSL 240
DB 181 PISRWGESDWTFCVARNPVSRNPSBPIARKLCEGAADPDSSMTLCLLVPILSL 240
QY 241 FVLGLFPLFKREROEYIEBKKEVDICRETPNICPHSGENTEXYDTIPHTNRITLIKEDPA 300
DB 241 FVLGLFPLFKREROEYIEBKKEVDICRETPNICPHSGENTEXYDTIPHTNRITLIKEDPA 300
QY 301 NTVYSTVEIPKKNPHSLTMPDTPRLFAVENYI 335
DB 301 NTVYSTVEIPKKNPHSLTMPDTPRLFAVENYI 335

RESULT 4
US-09-992-598-253
; Sequence 253, Application US/099925398
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Batson, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas P.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C20
;; CURRENT APPLICATION NUMBER: US/09/992,598
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087609
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088021
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088028
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088030
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088655
;; PRIOR FILING DATE: 1998-06-09
;; PRIOR APPLICATION NUMBER: 60/088734

PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 3,6e-314;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAGSPCTCTTITITIMOLTGSAASGPVKEIVGSGAVTFPLKSKVKQVDSITWTFNTPL 60
1 MAGSPCTCTTITITIMOLTGSAASGPVKEIVGSGAVTFPLKSKVKQVDSITWTFNTPL 60
VTIQPEGGTTIVTONRRRERVDPPDGGYSILSLKLNKNDSGIYYVGIIYSSSIQO PSTQEX 120
VTIQPEGGTTIVTONRRRERVDPPDGGYSILSLKLNKNDSGIYYVGIIYSSSIQO PSTQEX 120
VIAHYEHLSPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVITYTKALQOANESHNGSIL 180
VIAHYEHLSPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVITYTKALQOANESHNGSIL 180
PISWRGSDMTFCVARNPVSRRFSSPILARKLCEGAADPPDSMTLLCLLVPILLSL 240
PISWRGSDMTFCVARNPVSRRFSSPILARKLCEGAADPPDSMTLLCLLVPILLSL 240
PISWRGSDMTFCVARNPVSRRFSSPILARKLCEGAADPPDSMTLLCLLVPILLSL 240
PISWRGSDMTFCVARNPVSRRFSSPILARKLCEGAADPPDSMTLLCLLVPILLSL 240
FVLGLFLMPLKREOEYIEKKRVDCRETPTNCPHSGENTEXDTIPHTRTTIKEDPA 300
FVLGLFLMPLKREOEYIEKKRVDCRETPTNCPHSGENTEXDTIPHTRTTIKEDPA 300
FVLGLFLMPLKREOEYIEKKRVDCRETPTNCPHSGENTEXDTIPHTRTTIKEDPA 300
FVLGLFLMPLKREOEYIEKKRVDCRETPTNCPHSGENTEXDTIPHTRTTIKEDPA 300
NTVYSTVEIPKQENPHSLTMDPTPLFAVENYI 335
NTVYSTVEIPKQENPHSLTMDPTPLFAVENYI 335
NTVYSTVEIPKQENPHSLTMDPTPLFAVENYI 335
NTVYSTVEIPKQENPHSLTMDPTPLFAVENYI 335

RESULT 5
US-09-513-999C-4472
; Sequence 4472, Application US/09513999C

```
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 4472
LENGTH: 97
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -22...-1
OTHER INFORMATION: score 5.9
OTHER INFORMATION: seq LYLIMQLTGSAA/SG
US-09-513-999C-4472
```

```
Query Match          29.0%; Score 97; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.6e-85;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MAGSPCTLTITLITIMQLTGSAAAGPYVELVSGAVTFFPKSKYKQVDSITVMTENTPL 60
Db 1 MAGSPCTLTITLITIMQLTGSAAAGPYVELVSGAVTFFPKSKYKQVDSITVMTENTPL 60
Qy 61 VTIOPEGTTIVTONRNRERVPDGGYSLKSLK 97
Db 61 VTIOPEGTTIVTONRNRERVPDGGYSLKSLK 97
```

```
RESULT 6
US-09-466-778-8
Sequence 8, Application US/09466778
Patent No. 6872546
GENERAL INFORMATION:
APPLICANT: Hastings, Gregg et al.
TITLE OF INVENTION: No. 6872546e1 Hyaluronan-Binding Proteins and Encoding Genes
FILE REFERENCE: PF487
CURRENT APPLICATION NUMBER: US/09/466,778
CURRENT FILING DATE: 1999-12-20
EARLIER APPLICATION NUMBER: 60/113,871
EARLIER FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 289
TYPE: PRT
ORGANISM: Homo sapiens
US-09-466-778-8
```

```
Query Match          2.4%; Score 8; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 231 LLVPLLL 238
Db 4 LLVPLLL 11
```

```
RESULT 7
US-09-907-794A-213
Sequence 213, Application US/0990794A
Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
```

```
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsens, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 213
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-794A-213
```

```
Query Match          2.4%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 231 LLLVPLLL 238
Db 4 LLLVPLLL 11

RESULT 8

US-09-905-125A-213
; Sequence 213, Application US/0905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Macher, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905.125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 213
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-213

Query Match 2.4%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 231 LLLVPLLL 238
Db 4 LLLVPLLL 11

RESULT 9

US-09-902-775A-213
; Sequence 213, Application US/0902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Macher, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902.775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29

```
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 213
;; LENGTH: 360
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-902-775A-213

Query Match      2.4%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      231 LLLVPLLL 238
Db      4 LLLVPLLL 11

RESULT 10
US-09-906-700-213
; Sequence 213, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Macher, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906, 700
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143, 048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145, 698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146, 222
; PRIOR FILING DATE: 1999-07-28
```

```
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 213
;; LENGTH: 360
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-906-700-213

Query Match      2.4%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      231 LLLVPLLL 238
Db      4 LLLVPLLL 11

RESULT 11
US-09-903-603A-213
; Sequence 213, Application US/09903603A
; Patent No. 676795
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Macher, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
```

```

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903.603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 213
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-903-603A-213

Query Match      2.4%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 24;
Matches      8; Conservative 0; Mismatches      0; Indels      0; Gaps      0;

Oy      231  LLLVPLLL 238
Db      4  LLLVPLLL 11

RESULT 12
US-09-904-920A-213
; Sequence 213, Application US/09904920A
; Patent No. 6606352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deemoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

```

; APPLICANT: Gurney, Austen L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavain, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904.920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 213
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-904-920A-213

Query Match      2.4%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 24;
Matches      8; Conservative 0; Mismatches      0; Indels      0; Gaps      0;

Oy      231  LLLVPLLL 238
Db      4  LLLVPLLL 11

RESULT 13
US-09-909-064-213
; Sequence 213, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
```


APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Balon, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OR INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 213
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-909-064-213

Query March 2.4%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. NO. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 LLLVPLL 238
Db 4 LLLVPLL 11
RESULT 14
US-09-905-381A-213
Sequence 213, Application US/09905381A
Patent No. 6818746
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Balon, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OR INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,381A
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219

```
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 213
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-381A-213

Query Match      2.4%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      231 LLLVPLLL 238
DB      4 LLLVPLLL 11

RESULT 15
US-09-906-618-213
; Sequence 213, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: US/09/906,618
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
```

```
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 213
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-618-213

Query Match      2.4%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      231 LLLVPLLL 238
DB      4 LLLVPLLL 11
```

Search completed: December 16, 2005, 12:01:29
Job time : 49 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 11:36:44 ; Search time 13 Seconds
(without alignments)
173.601 Million cell updates/sec

Perfect score: 335
1 MAGSPCTLTITLIMQUTS.....PHSLTMPTRPLFAYENV1 335

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 51470 seqs, 6736768 residues

Word size: 0

Total number of hits satisfying chosen parameters: 51470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database :

1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	335	100.0	335	7 US-11-102-240-46	Sequence 46, Appl
2	7	2.1	75	6 US-10-667-295-53	Sequence 53, Appl
3	7	2.1	104	6 US-10-689-742-206	Sequence 206, Appl
4	7	2.1	539	7 US-11-069-642-16	Sequence 16, Appl
5	7	2.1	540	6 US-10-770-726-80	Sequence 80, Appl
6	6	1.8	33	7 US-11-069-642-146	Sequence 146, Appl
7	6	1.8	33	7 US-11-198-847-3	Sequence 3, Appl
8	6	1.8	33	7 US-11-198-847-237	Sequence 237, Appl
9	6	1.8	51	6 US-10-467-657-2114	Sequence 2114, Appl
10	6	1.8	83	7 US-11-198-847-2	Sequence 2, Appl
11	6	1.8	86	7 US-11-123-896-230	Sequence 230, Appl
12	6	1.8	101	7 US-11-053-076-157	Sequence 157, Appl
13	6	1.8	140	7 US-10-467-657-2486	Sequence 2486, Appl
14	6	1.8	168	7 US-11-108-172-631	Sequence 631, Appl
15	6	1.8	169	6 US-10-467-657-1526	Sequence 1526, Appl
16	6	1.8	176	7 US-11-102-240-146	Sequence 146, Appl
17	6	1.8	209	7 US-11-196-475-12	Sequence 32, Appl
18	6	1.8	212	7 US-11-196-475-14	Sequence 14, Appl
19	6	1.8	222	6 US-10-821-234-4117	Sequence 1417, Appl
20	6	1.8	232	7 US-11-173-564-2	Sequence 2, Appl
21	6	1.8	237	6 US-10-793-626-162	Sequence 162, Appl
22	6	1.8	252	7 US-11-054-515-1994	Sequence 1994, Appl
23	6	1.8	256	7 US-11-137-465-34	Sequence 34, Appl
24	6	1.8	265	6 US-10-689-742-188	Sequence 188, Appl
25	6	1.8	280	6 US-10-467-657-4208	Sequence 4208, Appl
26	6	1.8	286	7 US-11-194-246-320	Sequence 320, Appl

27	6	1.8	288	6 US-10-821-234-1062	Sequence 1062, Appl
28	6	1.8	307	6 US-10-467-657-6016	Sequence 6016, Appl
29	6	1.8	308	6 US-10-793-626-1072	Sequence 1072, Appl
30	6	1.8	308	6 US-10-793-626-2706	Sequence 2706, Appl
31	6	1.8	317	6 US-10-485-517-196	Sequence 196, Appl
32	6	1.8	339	6 US-10-467-657-4318	Sequence 4318, Appl
33	6	1.8	350	7 US-11-102-240-8	Sequence 8, Appl
34	6	1.8	355	6 US-10-503-051-2	Sequence 2, Appl
35	6	1.8	358	6 US-10-485-517-227	Sequence 227, Appl
36	6	1.8	358	6 US-10-793-626-18	Sequence 18, Appl
37	6	1.8	360	7 US-11-082-389-90	Sequence 90, Appl
38	6	1.8	360	7 US-11-082-389-92	Sequence 92, Appl
39	6	1.8	364	6 US-10-995-561-783	Sequence 783, Appl
40	6	1.8	371	6 US-10-821-234-1010	Sequence 1010, Appl
41	6	1.8	377	6 US-10-793-626-2926	Sequence 2926, Appl
42	6	1.8	380	6 US-10-793-626-1402	Sequence 1402, Appl
43	6	1.8	403	6 US-10-793-626-1522	Sequence 1522, Appl
44	6	1.8	443	7 US-11-196-475-166	Sequence 166, Appl
45	6	1.8	446	7 US-11-143-980-39	Sequence 39, Appl
46	6	1.8	447	6 US-10-467-657-364	Sequence 364, Appl
47	6	1.8	468	6 US-10-957-569-28	Sequence 28, Appl
48	6	1.8	468	6 US-10-995-561-907	Sequence 907, Appl
49	6	1.8	468	7 US-11-076-187-2	Sequence 2, Appl
50	6	1.8	468	7 US-11-055-822-68	Sequence 68, Appl
51	6	1.8	480	7 US-11-074-176-2	Sequence 2, Appl
52	6	1.8	484	7 US-11-078-735-43	Sequence 43, Appl
53	6	1.8	497	6 US-10-821-234-1358	Sequence 1358, Appl
54	6	1.8	525	6 US-10-467-657-5462	Sequence 5462, Appl
55	6	1.8	543	7 US-11-113-324-6	Sequence 6, Appl
56	6	1.8	557	6 US-10-821-234-1593	Sequence 1593, Appl
57	6	1.8	553	7 US-11-113-424-18	Sequence 18, Appl
58	6	1.8	567	6 US-10-503-051-5	Sequence 5, Appl
59	6	1.8	635	6 US-10-467-657-2076	Sequence 2076, Appl
60	6	1.8	635	6 US-10-467-657-6374	Sequence 6374, Appl
61	6	1.8	671	7 US-11-029-003-6	Sequence 6, Appl
62	6	1.8	684	6 US-10-714-781A-55	Sequence 55, Appl
63	6	1.8	684	6 US-10-714-781A-57	Sequence 57, Appl
64	6	1.8	684	6 US-10-714-781A-61	Sequence 61, Appl
65	6	1.8	686	6 US-10-714-781A-59	Sequence 59, Appl
66	6	1.8	723	7 US-11-078-735-17	Sequence 17, Appl
67	6	1.8	723	6 US-10-821-234-1147	Sequence 1147, Appl
68	6	1.8	745	7 US-11-135-855-37	Sequence 37, Appl
69	6	1.8	794	6 US-10-793-626-1050	Sequence 1050, Appl
70	6	1.8	816	7 US-11-143-980-67	Sequence 67, Appl
71	6	1.8	827	6 US-10-821-234-1685	Sequence 1685, Appl
72	6	1.8	827	6 US-10-995-561-1899	Sequence 899, Appl
73	6	1.8	833	6 US-10-645-441-7	Sequence 7, Appl
74	6	1.8	843	6 US-10-645-441-8	Sequence 8, Appl
75	6	1.8	843	6 US-11-137-465-35	Sequence 35, Appl
76	6	1.8	897	7 US-11-113-424-35	Sequence 35, Appl
77	6	1.8	964	7 US-11-137-465-58	Sequence 58, Appl
78	6	1.8	965	7 US-11-113-424-2	Sequence 2, Appl
79	6	1.8	965	7 US-11-147-047-51	Sequence 51, Appl
80	6	1.8	993	7 US-11-137-465-36	Sequence 36, Appl
81	6	1.8	1041	6 US-10-995-561-780	Sequence 780, Appl
82	6	1.8	1041	6 US-10-995-561-782	Sequence 782, Appl
83	6	1.8	1097	6 US-10-995-561-781	Sequence 781, Appl
84	6	1.8	1468	6 US-10-467-657-1088	Sequence 1088, Appl
85	6	1.8	1468	6 US-10-995-561-911	Sequence 911, Appl
86	6	1.8	1767	6 US-10-995-561-914	Sequence 912, Appl
87	6	1.8	1806	6 US-10-995-561-912	Sequence 910, Appl
88	6	1.8	1806	6 US-10-995-561-915	Sequence 915, Appl
89	6	1.8	1818	6 US-10-995-561-910	Sequence 913, Appl
90	6	1.8	1818	6 US-10-995-561-913	Sequence 913, Appl
91	6	1.8	3433	6 US-10-714-781A-67	Sequence 67, Appl
92	6	1.8	5712	7 US-11-143-980-47	Sequence 47, Appl
93	6	1.8	7102	7 US-11-143-980-48	Sequence 48, Appl
94	6	1.8	7968	7 US-11-143-980-49	Sequence 49, Appl
95	6	1.8	8	7 US-11-119-098-15	Sequence 15, Appl
96	6	1.8	8	7 US-11-045-024-1583	Sequence 1583, Appl
97	6	1.5	8	7 US-11-045-024-5290	Sequence 5290, Appl
98	6	1.5	8	7 US-11-045-024-7575	Sequence 7575, Appl
99	6	1.5	8	7 US-11-045-024-7575	Sequence 7575, Appl
100	6	1.5	8	7 US-11-045-024-7575	Sequence 7575, Appl
101	6	1.5	8	7 US-11-045-024-7575	Sequence 7575, Appl
102	6	1.5	8	7 US-11-045-024-7575	Sequence 7575, Appl

103	5	1.5	9	7	US-11-045-024-4424	Sequence 4424, Ap	176	5	1.5	59	6	US-10-667-295-170	Sequence 170, App
104	5	1.5	9	7	US-11-045-024-5817	Sequence 5817, Ap	177	5	1.5	59	6	US-10-667-657-1236	Sequence 1236, Ap
105	5	1.5	9	7	US-11-045-024-12723	Sequence 12723, A	178	5	1.5	59	6	US-10-467-657-5178	Sequence 5178, Ap
106	5	1.5	9	7	US-11-045-024-13889	Sequence 13889, A	179	5	1.5	59	7	US-11-068-717-14	Sequence 14, Appl
107	5	1.5	9	7	US-11-045-024-13905	Sequence 13905, A	180	5	1.5	64	7	US-11-000-463-262	Sequence 262, App
108	5	1.5	10	6	US-10-491-096-6	Sequence 6, Appl1	181	5	1.5	64	7	US-11-000-463-734	Sequence 734, App
109	5	1.5	10	6	US-10-491-096-69	Sequence 69, Appl1	182	5	1.5	66	6	US-10-467-657-2614	Sequence 2614, Ap
110	5	1.5	10	6	US-10-491-096-101	Sequence 101, App	183	5	1.5	66	6	US-10-995-561-801	Sequence 801, App
111	5	1.5	10	6	US-10-491-096-166	Sequence 166, App	184	5	1.5	66	7	US-11-000-463-419	Sequence 419, App
112	5	1.5	10	7	US-11-045-024-2018	Sequence 2018, App	185	5	1.5	66	7	US-11-000-463-891	Sequence 891, App
113	5	1.5	10	7	US-11-045-024-2020	Sequence 2020, App	186	5	1.5	66	7	US-11-068-717-13	Sequence 13, Appl1
114	5	1.5	10	7	US-11-045-024-4573	Sequence 4573, Ap	187	5	1.5	69	6	US-10-467-657-7568	Sequence 7568, Ap
115	5	1.5	10	7	US-11-045-024-7583	Sequence 7583, Ap	188	5	1.5	70	6	US-10-467-657-4268	Sequence 4268, Ap
116	5	1.5	10	7	US-11-045-024-7660	Sequence 7660, App	189	5	1.5	70	7	US-11-000-463-265	Sequence 265, App
117	5	1.5	11	7	US-11-045-024-2249	Sequence 2249, App	190	5	1.5	70	7	US-11-000-463-737	Sequence 737, App
118	5	1.5	11	7	US-11-045-024-2251	Sequence 2251, App	191	5	1.5	73	7	US-11-102-240-140	Sequence 148, App
119	5	1.5	11	7	US-11-045-024-3360	Sequence 3360, App	192	5	1.5	74	7	US-11-000-463-420	Sequence 420, App
120	5	1.5	11	7	US-11-045-024-4726	Sequence 4726, App	193	5	1.5	74	7	US-11-000-463-892	Sequence 892, App
121	5	1.5	11	7	US-11-045-024-4727	Sequence 4727, App	194	5	1.5	74	7	US-11-123-896-380	Sequence 380, App
122	5	1.5	11	7	US-11-045-024-4729	Sequence 4729, App	195	5	1.5	76	6	US-10-467-657-8532	Sequence 8532, App
123	5	1.5	11	7	US-11-045-024-6621	Sequence 6621, App	196	5	1.5	76	7	US-11-123-896-263	Sequence 263, App
124	5	1.5	11	7	US-11-045-024-9736	Sequence 9736, App	197	5	1.5	76	7	US-11-123-896-404	Sequence 404, App
125	5	1.5	11	7	US-11-045-024-11724	Sequence 11724, A	198	5	1.5	77	7	US-11-102-240-56	Sequence 56, Appl1
126	5	1.5	11	7	US-11-045-024-12701	Sequence 12701, A	199	5	1.5	77	7	US-11-123-896-371	Sequence 371, App
127	5	1.5	12	6	US-10-467-657-1386	Sequence 1386, Ap	200	5	1.5	78	7	US-11-102-240-66	Sequence 66, Appl
128	5	1.5	12	6	US-10-467-657-7526	Sequence 7526, App	201	5	1.5	79	6	US-10-467-657-1146	Sequence 1146, Ap
129	5	1.5	14	7	US-11-054-515-2768	Sequence 2768, App	202	5	1.5	79	6	US-10-467-657-5402	Sequence 5402, Ap
130	5	1.5	14	7	US-11-054-515-2815	Sequence 2815, App	204	5	1.5	82	7	US-11-123-896-287	Sequence 287, App
131	5	1.5	15	7	US-11-106-932-134	Sequence 134, App	205	5	1.5	85	6	US-10-485-517-205	Sequence 205, App
132	5	1.5	15	7	US-11-045-024-13233	Sequence 13233, A	206	5	1.5	85	6	US-10-485-517-237	Sequence 237, App
133	5	1.5	15	7	US-11-045-024-13249	Sequence 13249, A	207	5	1.5	86	7	US-11-123-896-227	Sequence 227, App
134	5	1.5	15	7	US-11-045-024-13267	Sequence 13267, A	208	5	1.5	86	7	US-11-123-896-233	Sequence 233, App
135	5	1.5	19	6	US-10-503-575-330	Sequence 330, App	210	5	1.5	87	7	US-11-184-574-8	Sequence 8, Appl1
136	5	1.5	19	6	US-10-503-575-332	Sequence 332, App	219	5	1.5	89	6	US-10-467-657-2164	Sequence 2164, Ap
137	5	1.5	19	6	US-10-503-575-333	Sequence 333, App	211	5	1.5	95	6	US-10-467-657-4134	Sequence 4134, Ap
138	5	1.5	19	6	US-10-503-575-334	Sequence 334, App	212	5	1.5	96	6	US-10-467-657-8706	Sequence 8706, Ap
139	5	1.5	19	6	US-10-503-575-340	Sequence 340, App	213	5	1.5	97	7	US-11-144-248-36	Sequence 36, Appl
140	5	1.5	20	6	US-10-509-170-6	Sequence 6, Appl1	214	5	1.5	97	7	US-11-144-248-44	Sequence 44, Appl
141	5	1.5	20	6	US-11-094-142-24	Sequence 24, Appl1	215	5	1.5	97	7	US-11-053-076-126	Sequence 126, App
142	5	1.5	21	6	US-10-986-501-260	Sequence 260, App	216	5	1.5	97	7	US-11-054-669-40	Sequence 40, Appl1
143	5	1.5	22	7	US-11-108-185-43	Sequence 43, Appl	217	5	1.5	97	7	US-11-054-669-42	Sequence 42, Appl1
144	5	1.5	22	7	US-11-108-185-44	Sequence 44, Appl	218	5	1.5	97	7	US-11-054-669-49	Sequence 49, Appl1
145	5	1.5	22	7	US-11-108-185-45	Sequence 45, Appl	219	5	1.5	97	7	US-11-054-669-51	Sequence 51, Appl1
146	5	1.5	22	7	US-11-108-185-48	Sequence 48, Appl1	220	5	1.5	97	7	US-11-054-669-52	Sequence 52, Appl1
147	5	1.5	25	7	US-11-058-735-58	Sequence 58, Appl1	221	5	1.5	97	7	US-11-054-669-53	Sequence 53, Appl1
148	5	1.5	27	7	US-11-098-674-9	Sequence 9, Appl1	222	5	1.5	97	7	US-11-084-554-53	Sequence 53, Appl1
149	5	1.5	30	6	US-10-467-657-1044	Sequence 1044, App	223	5	1.5	97	7	US-11-084-554-54	Sequence 54, Appl1
150	5	1.5	30	7	US-11-106-932-18	Sequence 18, Appl	224	5	1.5	98	6	US-10-816-768-43	Sequence 43, Appl
151	5	1.5	30	7	US-11-106-932-43	Sequence 43, Appl	225	5	1.5	98	6	US-10-816-768-44	Sequence 44, Appl
152	5	1.5	30	7	US-11-106-932-44	Sequence 44, Appl	226	5	1.5	98	7	US-11-144-248-34	Sequence 34, Appl
153	5	1.5	34	6	US-10-816-768-32	Sequence 32, Appl	227	5	1.5	98	7	US-11-012-353-74	Sequence 74, Appl
154	5	1.5	34	6	US-10-816-768-33	Sequence 33, Appl	228	5	1.5	98	7	US-11-054-669-34	Sequence 34, Appl1
155	5	1.5	34	6	US-10-990-877-1	Sequence 1, Appl1	229	5	1.5	98	7	US-11-054-669-35	Sequence 35, Appl1
156	5	1.5	36	6	US-10-467-657-7060	Sequence 7060, App	230	5	1.5	98	7	US-11-054-669-44	Sequence 44, Appl
157	5	1.5	37	6	US-10-821-234-1693	Sequence 1693, App	231	5	1.5	98	7	US-11-084-554-49	Sequence 49, Appl
158	5	1.5	37	6	US-11-069-642-147	Sequence 147, App	232	5	1.5	98	7	US-11-084-554-51	Sequence 51, Appl1
159	5	1.5	37	6	US-11-006-031-18	Sequence 18, Appl1	233	5	1.5	99	7	US-11-054-669-36	Sequence 36, Appl1
160	5	1.5	38	6	US-10-816-768-20	Sequence 20, Appl1	234	5	1.5	99	7	US-11-054-669-37	Sequence 37, Appl1
161	5	1.5	39	6	US-10-485-517-259	Sequence 259, App	235	5	1.5	99	7	US-11-054-669-38	Sequence 38, Appl1
162	5	1.5	39	6	US-10-467-657-4216	Sequence 4216, App	236	5	1.5	99	7	US-11-054-669-39	Sequence 39, Appl1
163	5	1.5	42	6	US-10-532-480-33	Sequence 33, App	237	5	1.5	99	7	US-11-054-669-41	Sequence 41, Appl1
164	5	1.5	43	6	US-10-982-545-10	Sequence 10, Appl1	238	5	1.5	99	7	US-11-054-669-43	Sequence 43, Appl1
165	5	1.5	43	6	US-10-957-8878-91	Sequence 91, Appl1	239	5	1.5	99	7	US-11-084-554-50	Sequence 50, Appl1
166	5	1.5	45	6	US-10-467-657-6976	Sequence 6976, App	240	5	1.5	99	7	US-11-084-554-52	Sequence 52, Appl1
167	5	1.5	47	6	US-10-467-657-6650	Sequence 6650, App	241	5	1.5	99	7	US-11-084-554-55	Sequence 55, Appl1
168	5	1.5	48	6	US-10-467-657-4322	Sequence 4322, App	242	5	1.5	99	7	US-11-186-284-87	Sequence 87, Appl1
169	5	1.5	51	6	US-10-467-657-4506	Sequence 4506, App	243	5	1.5	100	6	US-10-793-626-2158	Sequence 2158, App
170	5	1.5	51	6	US-10-467-657-7160	Sequence 7160, App	244	5	1.5	100	6	US-10-793-626-2550	Sequence 2550, App
171	5	1.5	51	7	US-11-069-642-145	Sequence 145, App	245	5	1.5	100	7	US-11-084-554-46	Sequence 46, Appl1
172	5	1.5	53	6	US-10-467-657-2666	Sequence 2666, App	246	5	1.5	104	6	US-10-793-626-92	Sequence 92, Appl1
173	5	1.5	53	6	US-10-467-657-3714	Sequence 3714, App	247	5	1.5	104	6	US-10-793-626-2232	Sequence 2232, App
174	5	1.5	53	6	US-10-467-657-1942	Sequence 1942, App	248	5	1.5	104	6	US-10-793-626-2380	Sequence 2380, App
175	5	1.5	58	6	US-10-467-657-3828	Sequence 3828, App	249	5	1.5	105	6	US-10-816-768-61	Sequence 61, Appl1

250	5	1.5	107	6	US-10-467-657-1054	Sequence 1054, Ap	323	5	1.5	152	7	US-11-174-398-9	Sequence 9, Appl1
251	5	1.5	107	7	US-11-000-463-300	Sequence 300, App	324	5	1.5	153	6	US-10-467-657-3392	Sequence 3392, Ap
252	5	1.5	107	7	US-11-124-215-12	Sequence 12, Appl	325	5	1.5	155	6	US-10-467-657-2674	Sequence 2674, Ap
253	5	1.5	108	6	US-10-793-626-592	Sequence 592, App	326	5	1.5	165	6	US-10-467-657-6012	Sequence 6012, Ap
254	5	1.5	108	6	US-10-999-866-6	Sequence 6, Appl1	327	5	1.5	165	6	US-10-878-556A-22	Sequence 22, Appl
255	5	1.5	108	6	US-10-925-366A-146	Sequence 146, App	328	5	1.5	165	7	US-11-082-389-68	Sequence 68, Appl
256	5	1.5	108	6	US-10-925-366A-166	Sequence 166, App	329	5	1.5	166	6	US-10-821-234-1293	Sequence 1293, Ap
257	5	1.5	108	6	US-10-925-366A-204	Sequence 204, App	330	5	1.5	166	6	US-10-878-556A-20	Sequence 20, Appl
258	5	1.5	108	7	US-11-061-821-6	Sequence 6, Appl1	331	5	1.5	168	6	US-10-793-626-724	Sequence 724, App
259	5	1.5	108	7	US-11-053-076-210	Sequence 210, App	332	5	1.5	170	6	US-10-467-657-104	Sequence 104, App
260	5	1.5	112	6	US-10-967-457-76	Sequence 76, Appl	333	5	1.5	170	6	US-10-467-657-8078	Sequence 8078, Ap
261	5	1.5	112	6	US-10-392-234A-44	Sequence 44, Appl	334	5	1.5	172	6	US-10-667-295-2	Sequence 2838, Ap
262	5	1.5	113	7	US-11-144-248-70	Sequence 20, Appl	335	5	1.5	174	6	US-10-667-295-2	Sequence 2, Appl1
263	5	1.5	113	7	US-11-073-605-8	Sequence 8, Appl1	336	5	1.5	175	6	US-10-793-626-1336	Sequence 1336, Ap
264	5	1.5	114	6	US-10-793-626-2298	Sequence 2298, App	337	5	1.5	176	7	US-11-055-822-1084	Sequence 1084, Ap
265	5	1.5	114	6	US-10-995-561-836	Sequence 836, App	338	5	1.5	177	7	US-11-068-717-8	Sequence 8, Appl1
266	5	1.5	114	7	US-11-186-284-47	Sequence 47, Appl	339	5	1.5	177	6	US-10-522-883-17	Sequence 17, Appl
267	5	1.5	115	7	US-11-129-817-2	Sequence 2, Appl1	340	5	1.5	179	6	US-10-522-883-21	Sequence 21, Appl
268	5	1.5	116	6	US-10-793-626-1680	Sequence 1680, App	341	5	1.5	179	6	US-10-821-234-1265	Sequence 1265, Ap
269	5	1.5	116	7	US-11-054-669-112	Sequence 112, App	342	5	1.5	179	6	US-10-467-657-6542	Sequence 6542, Ap
270	5	1.5	116	7	US-11-125-837-35	Sequence 35, Appl	343	5	1.5	179	6	US-10-467-657-7772	Sequence 7772, Ap
271	5	1.5	117	7	US-11-012-353-72	Sequence 72, Appl	344	5	1.5	180	6	US-10-821-234-1552	Sequence 1552, Ap
272	5	1.5	117	7	US-11-012-353-75	Sequence 75, Appl	345	5	1.5	180	6	US-10-467-657-2	Sequence 2, Appl1
273	5	1.5	117	7	US-11-012-353-79	Sequence 79, Appl	346	5	1.5	180	6	US-10-467-657-3732	Sequence 3732, Ap
274	5	1.5	117	7	US-11-012-353-83	Sequence 83, Appl	347	5	1.5	180	6	US-10-665-455-8	Sequence 8, Appl1
275	5	1.5	117	7	US-11-075-184A-2	Sequence 182, App	348	5	1.5	180	6	US-10-665-455-9	Sequence 9, Appl1
276	5	1.5	117	7	US-11-012-353-162	Sequence 2, Appl1	349	5	1.5	180	6	US-10-665-455-10	Sequence 10, Appl
277	5	1.5	120	6	US-10-507-662-23	Sequence 23, Appl	350	5	1.5	180	6	US-10-665-455-11	Sequence 11, Appl
278	5	1.5	120	6	US-10-507-662-24	Sequence 24, Appl	351	5	1.5	180	6	US-10-665-455-12	Sequence 12, Appl
279	5	1.5	120	6	US-11-102-201-1	Sequence 1, Appl1	352	5	1.5	180	6	US-10-665-455-13	Sequence 13, Appl
280	5	1.5	121	6	US-10-485-517-363	Sequence 363, App	353	5	1.5	180	7	US-11-157-049-9-12	Sequence 12, Appl
281	5	1.5	126	6	US-10-793-626-2766	Sequence 2766, App	354	5	1.5	181	6	US-10-467-657-8206	Sequence 8206, Ap
282	5	1.5	129	6	US-10-967-527A-11	Sequence 11, Appl	355	5	1.5	182	6	US-10-485-517-269	Sequence 269, App
283	5	1.5	131	6	US-11-194-246-415	Sequence 415, App	356	5	1.5	182	6	US-10-793-626-620	Sequence 620, App
284	5	1.5	131	6	US-10-689-742-192	Sequence 192, App	357	5	1.5	184	6	US-10-742-634-9	Sequence 9, Appl1
285	5	1.5	131	7	US-11-084-591-3	Sequence 3, Appl1	358	5	1.5	184	6	US-10-967-527A-8	Sequence 8, Appl1
286	5	1.5	133	6	US-10-667-295-221	Sequence 221, App	359	5	1.5	185	7	US-11-147-047-41	Sequence 41, Appl
287	5	1.5	133	6	US-10-793-626-1106	Sequence 1106, App	360	5	1.5	186	7	US-11-044-899-24	Sequence 24, Appl
288	5	1.5	133	7	US-11-128-420-13	Sequence 13, Appl	361	5	1.5	186	7	US-11-044-899-25	Sequence 25, Appl
289	5	1.5	135	6	US-10-821-234-1018	Sequence 1018, App	362	5	1.5	187	6	US-10-980-388-39	Sequence 39, Appl
290	5	1.5	135	7	US-11-012-353-77	Sequence 77, Appl	363	5	1.5	187	6	US-10-980-388-98	Sequence 98, Appl
291	5	1.5	135	7	US-11-012-353-81	Sequence 81, Appl	365	5	1.5	188	6	US-10-821-234-1316	Sequence 1316, App
292	5	1.5	135	7	US-11-012-353-85	Sequence 85, Appl	366	5	1.5	188	6	US-10-467-657-3332	Sequence 3332, App
293	5	1.5	138	6	US-10-789-273-4	Sequence 4, Appl1	367	5	1.5	189	6	US-10-793-626-2976	Sequence 2976, App
294	5	1.5	138	6	US-10-667-295-176	Sequence 176, App	368	5	1.5	189	6	US-10-793-626-3000	Sequence 3000, App
295	5	1.5	138	7	US-11-008-227-2	Sequence 2, Appl1	370	5	1.5	193	6	US-10-793-626-1240	Sequence 1240, App
296	5	1.5	138	7	US-11-055-822-1074	Sequence 1074, App	371	5	1.5	193	6	US-10-967-527A-28	Sequence 28, Appl
297	5	1.5	139	7	US-11-125-837-24	Sequence 24, Appl	372	5	1.5	193	7	US-11-144-889A-4	Sequence 4, Appl1
298	5	1.5	140	7	US-11-083-800-7	Sequence 7, Appl1	373	5	1.5	194	6	US-10-995-561-784	Sequence 784, App
299	5	1.5	140	7	US-11-084-591-4	Sequence 4, Appl1	374	5	1.5	194	7	US-11-108-172-1126	Sequence 1126, App
300	5	1.5	140	7	US-11-193-512-23	Sequence 23, Appl	375	5	1.5	196	6	US-10-793-626-2014	Sequence 2014, App
301	5	1.5	141	7	US-11-044-899-32	Sequence 32, Appl	376	5	1.5	197	6	US-10-467-657-4944	Sequence 4944, App
302	5	1.5	141	7	US-11-000-463-435	Sequence 435, App	377	5	1.5	201	7	US-11-069-642-25	Sequence 25, Appl
303	5	1.5	142	6	US-10-467-657-5116	Sequence 5116, App	378	5	1.5	201	1	US-09-940-308-5	Sequence 5, Appl1
304	5	1.5	146	6	US-10-721-763-17	Sequence 17, Appl	379	5	1.5	202	6	US-11-055-822-166	Sequence 166, App
305	5	1.5	146	6	US-10-721-763-21	Sequence 21, Appl	380	5	1.5	202	6	US-10-980-388-109	Sequence 109, App
306	5	1.5	147	7	US-11-128-420-14	Sequence 14, Appl	381	5	1.5	203	7	US-11-074-176-366	Sequence 366, App
307	5	1.5	150	6	US-10-793-626-3228	Sequence 3228, App	383	5	1.5	204	7	US-11-128-440-7	Sequence 7, Appl1
308	5	1.5	151	6	US-10-821-234-1378	Sequence 1378, App	384	5	1.5	205	7	US-11-082-389-374	Sequence 374, Appl
309	5	1.5	151	6	US-10-528-031-9	Sequence 9, Appl1	385	5	1.5	205	7	US-11-082-389-378	Sequence 378, App
310	5	1.5	152	6	US-10-793-626-1122	Sequence 1122, App	386	5	1.5	207	6	US-10-793-626-3290	Sequence 3290, App
311	5	1.5	153	6	US-10-793-626-1838	Sequence 1838, App	387	5	1.5	208	6	US-10-793-626-1124	Sequence 124, App
312	5	1.5	153	6	US-10-467-657-4546	Sequence 4546, App	388	5	1.5	208	6	US-10-467-657-6666	Sequence 6666, App
313	5	1.5	154	6	US-10-721-763-35	Sequence 35, Appl	389	5	1.5	209	6	US-10-793-626-688	Sequence 688, App
314	5	1.5	154	6	US-10-821-234-1366	Sequence 1366, App	390	5	1.5	209	6	US-10-793-626-2236	Sequence 2236, App
315	5	1.5	155	6	US-10-793-626-2704	Sequence 2704, App	391	5	1.5	209	6	US-10-467-657-4090	Sequence 4090, App
316	5	1.5	155	7	US-11-069-642-97	Sequence 97, Appl	392	5	1.5	211	6	US-10-858-730-102	Sequence 102, App
317	5	1.5	155	7	US-11-097-632-8	Sequence 8, Appl1	393	5	1.5	211	7	US-11-098-662-16	Sequence 16, Appl
318	5	1.5	157	6	US-10-793-626-1168	Sequence 1168, App	394	5	1.5	211	7	US-11-165-141-21	Sequence 21, Appl
319	5	1.5	158	7	US-11-097-622-10	Sequence 10, Appl	395	5	1.5	212	6	US-10-467-657-5486	Sequence 5486, App
320	5	1.5	161	6	US-10-467-962B-67	Sequence 67, Appl	396	5	1.5	212	6	US-10-467-657-7404	Sequence 7404, App
321	5	1.5	161	6	US-10-510-386-80	Sequence 80, Appl	397	5	1.5	213	6	US-10-467-657-8566	Sequence 8566, App
322	5	1.5	162	6	US-10-516-768-21	Sequence 21, Appl	398	5	1.5	214	6	US-10-467-657-7796	Sequence 7796, App

399	5	1.5	216	6	US-10-821-234-1483	Sequence 1483, Ap	472	5	1.5	246	7	US-11-054-515-2075	Sequence 2075, Ap
400	5	1.5	216	6	US-10-878-556A-191	Sequence 191, App	473	5	1.5	247	7	US-11-054-515-1651	Sequence 1651, Ap
401	5	1.5	219	6	US-10-467-657-446	Sequence 446, App	474	5	1.5	247	7	US-11-113-424-76	Sequence 76, Appl
402	5	1.5	220	7	US-11-174-150-32	Sequence 32, Appl	475	5	1.5	248	6	US-10-793-626-2982	Sequence 2982, Ap
403	5	1.5	221	6	US-10-485-517-142	Sequence 142, App	476	5	1.5	248	7	US-11-054-515-1198	Sequence 1198, Ap
404	5	1.5	221	6	US-10-793-626-2778	Sequence 2778, App	477	5	1.5	248	7	US-11-054-515-1660	Sequence 1660, Ap
405	5	1.5	223	6	US-10-467-657-2382	Sequence 2382, App	478	5	1.5	249	6	US-10-467-657-1938	Sequence 1938, Ap
406	5	1.5	223	6	US-10-793-626-3266	Sequence 3266, App	479	5	1.5	249	7	US-11-054-515-946	Sequence 946, App
407	5	1.5	224	6	US-10-884-730-379	Sequence 5, Appl	480	5	1.5	249	7	US-11-054-515-957	Sequence 957, App
408	5	1.5	225	7	US-11-000-463-379	Sequence 26, Appl	481	5	1.5	249	7	US-11-054-515-1138	Sequence 1138, Ap
409	5	1.5	225	6	US-10-467-657-26	Sequence 1734, Ap	482	5	1.5	249	7	US-11-054-515-1442	Sequence 1442, Ap
410	5	1.5	226	6	US-10-793-626-1734	Sequence 1301, Ap	483	5	1.5	249	7	US-11-054-515-1618	Sequence 1618, Ap
411	5	1.5	227	6	US-10-821-234-1301	Sequence 1424, Ap	484	5	1.5	249	7	US-11-054-515-1629	Sequence 1629, Ap
412	5	1.5	228	6	US-10-467-657-1242	Sequence 5176, Ap	485	5	1.5	249	7	US-11-054-515-1730	Sequence 1730, Ap
413	5	1.5	228	6	US-10-467-657-5176	Sequence 370, App	486	5	1.5	249	7	US-11-054-515-2065	Sequence 2065, App
414	5	1.5	230	6	US-10-884-730-370	Sequence 371, App	487	5	1.5	250	6	US-10-821-234-987	Sequence 987, App
415	5	1.5	230	6	US-10-884-730-371	Sequence 372, App	488	5	1.5	250	7	US-11-054-515-993	Sequence 993, App
416	5	1.5	230	6	US-10-884-730-372	Sequence 373, App	490	5	1.5	250	7	US-11-054-515-1413	Sequence 1413, Ap
417	5	1.5	230	6	US-10-884-730-373	Sequence 374, App	491	5	1.5	250	7	US-11-054-515-1548	Sequence 1548, Ap
418	5	1.5	230	6	US-10-884-730-374	Sequence 375, App	492	5	1.5	250	7	US-11-054-515-1548	Sequence 1548, Ap
419	5	1.5	230	6	US-10-884-730-375	Sequence 376, App	493	5	1.5	250	7	US-11-054-515-1110	Sequence 1110, App
420	5	1.5	230	6	US-10-884-730-376	Sequence 377, App	494	5	1.5	251	6	US-10-467-657-2306	Sequence 2306, Ap
421	5	1.5	230	6	US-10-884-730-377	Sequence 377, App	495	5	1.5	251	7	US-11-054-515-990	Sequence 990, App
422	5	1.5	231	7	US-10-688-742-132	Sequence 132, App	496	5	1.5	251	7	US-11-054-515-1152	Sequence 1152, Ap
423	5	1.5	231	7	US-11-000-463-745	Sequence 745, App	497	5	1.5	251	7	US-11-054-515-1316	Sequence 1316, Ap
424	5	1.5	232	7	US-10-467-657-3352	Sequence 3352, Ap	498	5	1.5	251	7	US-11-054-515-1510	Sequence 1510, Ap
425	5	1.5	232	7	US-11-100-183-38	Sequence 38, Appl	499	5	1.5	252	7	US-11-054-515-1223	Sequence 1223, Ap
426	5	1.5	232	7	US-11-170-653-64	Sequence 64, Appl	500	5	1.5	252	7	US-11-054-515-1329	Sequence 1329, Ap
427	5	1.5	233	7	US-10-793-626-1380	Sequence 1380, Ap	501	5	1.5	252	7	US-11-055-822-22	Sequence 22, Appl
428	5	1.5	233	7	US-11-074-176-272	Sequence 272, App	502	5	1.5	253	6	US-10-485-517-373	Sequence 373, App
429	5	1.5	236	6	US-10-467-657-3480	Sequence 3480, Ap	503	5	1.5	253	7	US-11-054-515-954	Sequence 954, App
430	5	1.5	236	6	US-10-878-556A-33	Sequence 33, Appl	504	5	1.5	253	7	US-11-054-515-1333	Sequence 1333, App
431	5	1.5	236	7	US-11-000-463-378	Sequence 378, App	505	5	1.5	253	7	US-11-054-515-1545	Sequence 1545, Ap
432	5	1.5	237	6	US-10-510-386-34	Sequence 34, Appl	506	5	1.5	253	7	US-11-054-515-1602	Sequence 1602, Ap
433	5	1.5	237	6	US-10-884-730-2	Sequence 2, Appli	507	5	1.5	253	7	US-11-054-515-1619	Sequence 1619, Ap
434	5	1.5	237	6	US-10-884-730-10	Sequence 10, Appl	508	5	1.5	254	6	US-10-467-657-1534	Sequence 1534, Ap
435	5	1.5	237	6	US-10-884-730-12	Sequence 12, Appl	509	5	1.5	254	7	US-11-054-515-1659	Sequence 1659, Ap
436	5	1.5	237	6	US-10-884-730-22	Sequence 22, Appl	510	5	1.5	255	7	US-11-054-515-1642	Sequence 1642, Ap
437	5	1.5	237	6	US-10-884-730-36	Sequence 36, Appl	511	5	1.5	255	7	US-11-185-111-36	Sequence 36, Appl
438	5	1.5	237	6	US-10-884-730-41	Sequence 41, Appl	512	5	1.5	256	7	US-11-054-515-1150	Sequence 1150, Ap
439	5	1.5	237	6	US-10-884-730-113	Sequence 113, App	513	5	1.5	256	7	US-11-054-515-1607	Sequence 1607, Ap
440	5	1.5	237	6	US-10-884-730-120	Sequence 120, App	514	5	1.5	256	7	US-11-083-800-6	Sequence 6, Appli
441	5	1.5	237	6	US-10-884-730-175	Sequence 175, App	515	5	1.5	257	6	US-10-821-234-1484	Sequence 1484, Ap
442	5	1.5	237	6	US-10-884-730-177	Sequence 177, App	516	5	1.5	257	6	US-10-467-657-2358	Sequence 2358, Ap
443	5	1.5	237	6	US-10-884-730-273	Sequence 273, App	517	5	1.5	257	7	US-11-054-515-1327	Sequence 1327, Ap
444	5	1.5	237	6	US-10-884-730-307	Sequence 307, App	518	5	1.5	257	7	US-11-135-855-42	Sequence 42, Appl
445	5	1.5	237	6	US-10-884-730-317	Sequence 317, App	519	5	1.5	258	6	US-10-995-561-583	Sequence 583, App
446	5	1.5	237	6	US-10-884-730-318	Sequence 318, App	520	5	1.5	258	6	US-11-055-822-390	Sequence 390, App
447	5	1.5	237	6	US-10-884-730-329	Sequence 329, App	521	5	1.5	259	6	US-10-995-561-883	Sequence 883, App
448	5	1.5	237	6	US-10-884-730-336	Sequence 336, App	522	5	1.5	259	7	US-11-075-185-24	Sequence 24, Appl
449	5	1.5	237	6	US-10-884-730-355	Sequence 355, App	523	5	1.5	260	6	US-10-467-657-4848	Sequence 4848, Ap
450	5	1.5	237	6	US-10-884-730-356	Sequence 356, App	524	5	1.5	261	6	US-10-467-657-3926	Sequence 3926, Ap
451	5	1.5	237	6	US-10-884-730-357	Sequence 357, App	525	5	1.5	262	6	US-10-884-730-289	Sequence 289, App
452	5	1.5	237	6	US-10-884-730-358	Sequence 358, App	526	5	1.5	262	6	US-10-793-626-516	Sequence 516, App
453	5	1.5	237	6	US-10-884-730-359	Sequence 359, App	527	5	1.5	263	6	US-10-793-626-876	Sequence 876, App
454	5	1.5	237	6	US-10-884-730-360	Sequence 360, App	528	5	1.5	263	6	US-10-512-184-29	Sequence 29, Appl
455	5	1.5	237	6	US-10-884-730-361	Sequence 362, App	529	5	1.5	263	6	US-10-467-657-6102	Sequence 6102, App
456	5	1.5	237	6	US-10-884-730-362	Sequence 9, Appli	530	5	1.5	263	7	US-11-040-638-2	Sequence 2, Appli
457	5	1.5	238	6	US-10-467-657-9954	Sequence 4954, Ap	531	5	1.5	263	7	US-11-042-889-2	Sequence 35, Appl
458	5	1.5	240	6	US-10-467-657-7890	Sequence 7890, Ap	532	5	1.5	264	6	US-10-884-730-35	Sequence 35, Appl
459	5	1.5	240	6	US-10-508-263-98	Sequence 98, Appl	533	5	1.5	264	7	US-11-188-743-24	Sequence 24, Appl
460	5	1.5	243	6	US-10-793-626-3066	Sequence 3066, Ap	534	5	1.5	264	7	US-11-188-743-25	Sequence 25, Appl
461	5	1.5	243	7	US-11-147-047-40	Sequence 40, Appl	535	5	1.5	265	7	US-11-082-389-190	Sequence 190, App
462	5	1.5	244	6	US-10-821-234-1264	Sequence 1264, Ap	536	5	1.5	266	6	US-10-884-730-4	Sequence 4, Appli
463	5	1.5	244	7	US-11-054-515-1210	Sequence 1210, Ap	537	5	1.5	266	6	US-10-884-730-31	Sequence 31, Appl
464	5	1.5	244	7	US-11-054-515-1214	Sequence 1214, Ap	538	5	1.5	266	6	US-10-884-730-33	Sequence 33, Appl
465	5	1.5	244	7	US-11-054-515-1371	Sequence 1371, Ap	539	5	1.5	266	6	US-10-884-730-38	Sequence 38, Appl
466	5	1.5	244	7	US-11-054-515-1372	Sequence 1372, Ap	540	5	1.5	266	6	US-10-884-730-47	Sequence 47, Appl
467	5	1.5	244	7	US-11-054-515-1377	Sequence 1507, App	541	5	1.5	266	6	US-10-884-730-79	Sequence 79, Appl
468	5	1.5	246	7	US-11-054-515-1300	Sequence 1300, Ap	542	5	1.5	266	6	US-10-884-730-85	Sequence 85, Appl
469	5	1.5	246	7	US-11-054-515-1300	Sequence 1655, Ap	543	5	1.5	266	6	US-10-884-730-114	Sequence 114, App
470	5	1.5	246	7	US-11-054-515-1655	Sequence 1702, Ap	544	5	1.5	266	6	US-10-884-730-116	Sequence 116, App
471	5	1.5	246	7	US-11-054-515-1702		545	5	1.5	266	6	US-10-884-730-121	Sequence 121, App

546	5	1.5	266	6	US-10-884-730-165	Sequence 165, App	621	5	1.5	305	6	US-10-995-561-582	Sequence 582, App
547	5	1.5	266	6	US-10-884-730-166	Sequence 166, App	622	5	1.5	307	6	US-10-467-657-2792	Sequence 2792, App
548	5	1.5	266	6	US-10-884-730-270	Sequence 270, App	623	5	1.5	307	6	US-10-467-657-6738	Sequence 6738, App
549	5	1.5	266	6	US-10-884-730-285	Sequence 285, App	624	5	1.5	307	7	US-11-000-463-244	Sequence 244, App
550	5	1.5	266	6	US-10-884-730-287	Sequence 287, App	625	5	1.5	308	6	US-10-467-657-4192	Sequence 4192, App
551	5	1.5	266	6	US-10-884-730-295	Sequence 295, App	626	5	1.5	308	6	US-10-995-561-814	Sequence 814, App
552	5	1.5	266	6	US-10-884-730-296	Sequence 296, App	627	5	1.5	308	7	US-11-074-176-254	Sequence 254, App
553	5	1.5	266	6	US-10-884-730-306	Sequence 306, App	628	5	1.5	308	7	US-11-092-140-37	Sequence 37, App
554	5	1.5	266	6	US-10-884-730-326	Sequence 326, App	629	5	1.5	309	6	US-10-467-657-666	Sequence 666, App
555	5	1.5	266	6	US-10-884-730-328	Sequence 328, App	630	5	1.5	310	6	US-10-467-657-1590	Sequence 1590, App
556	5	1.5	266	6	US-10-884-730-330	Sequence 330, App	631	5	1.5	311	6	US-10-980-388-111	Sequence 111, App
557	5	1.5	266	6	US-10-884-730-334	Sequence 334, App	632	5	1.5	311	6	US-10-980-388-113	Sequence 113, App
558	5	1.5	266	6	US-10-884-730-345	Sequence 345, App	633	5	1.5	311	6	US-10-467-657-2334	Sequence 2334, App
559	5	1.5	266	6	US-10-884-730-381	Sequence 381, App	634	5	1.5	312	6	US-10-995-561-700	Sequence 700, App
560	5	1.5	266	7	US-11-000-463-381	Sequence 853, App	635	5	1.5	312	7	US-11-129-143-94	Sequence 94, App
561	5	1.5	267	7	US-11-000-463-381	Sequence 853, App	636	5	1.5	314	6	US-10-485-517-230	Sequence 230, App
562	5	1.5	267	7	US-11-194-246-290	Sequence 290, App	637	5	1.5	314	7	US-11-055-822-410	Sequence 410, App
563	5	1.5	269	6	US-10-972-587-16	Sequence 16, App	638	5	1.5	314	7	US-11-143-880-56	Sequence 56, App
564	5	1.5	271	7	US-11-091-100-17	Sequence 17, App	639	5	1.5	316	6	US-10-467-657-5040	Sequence 4040, App
565	5	1.5	271	7	US-11-112-882-74	Sequence 74, App	640	5	1.5	317	6	US-10-674-767-2	Sequence 2, App
566	5	1.5	272	6	US-10-986-501-120	Sequence 120, App	641	5	1.5	317	6	US-10-995-561-798	Sequence 798, App
567	5	1.5	272	6	US-10-467-657-410	Sequence 40, App	642	5	1.5	317	7	US-11-129-143-67	Sequence 67, App
568	5	1.5	273	6	US-10-467-657-6782	Sequence 6782, App	643	5	1.5	318	6	US-10-821-234-1590	Sequence 1590, App
569	5	1.5	273	6	US-10-467-657-7462	Sequence 7462, App	644	5	1.5	318	7	US-11-186-284-69	Sequence 69, App
570	5	1.5	273	7	US-11-196-475-7	Sequence 7, App	645	5	1.5	318	7	US-11-194-246-294	Sequence 294, App
571	5	1.5	273	7	US-11-196-475-13	Sequence 13, App	646	5	1.5	319	6	US-10-793-626-1844	Sequence 1844, App
572	5	1.5	273	7	US-11-196-475-95	Sequence 95, App	647	5	1.5	320	6	US-10-793-626-2988	Sequence 2988, App
573	5	1.5	273	7	US-11-196-475-98	Sequence 98, App	648	5	1.5	320	6	US-10-858-730-111	Sequence 111, App
574	5	1.5	273	7	US-11-196-475-101	Sequence 101, App	649	5	1.5	320	7	US-11-074-176-216	Sequence 216, App
575	5	1.5	273	7	US-11-196-475-104	Sequence 104, App	650	5	1.5	320	7	US-11-000-463-354	Sequence 354, App
576	5	1.5	273	7	US-11-196-475-144	Sequence 144, App	651	5	1.5	321	6	US-10-793-626-2816	Sequence 2816, App
577	5	1.5	273	7	US-11-196-475-186	Sequence 186, App	652	5	1.5	321	7	US-11-102-240-181	Sequence 181, App
578	5	1.5	274	6	US-10-495-597-7	Sequence 7, App	653	5	1.5	322	7	US-11-074-176-36	Sequence 36, App
579	5	1.5	274	7	US-11-196-475-9	Sequence 9, App	654	5	1.5	323	6	US-10-467-657-7180	Sequence 7180, App
580	5	1.5	274	7	US-11-196-475-86	Sequence 86, App	655	5	1.5	324	7	US-11-092-140-34	Sequence 34, App
581	5	1.5	274	7	US-11-196-475-138	Sequence 138, App	656	5	1.5	325	1	US-09-940-308-8	Sequence 8, App
582	5	1.5	276	6	US-10-467-657-8460	Sequence 8460, App	657	5	1.5	325	6	US-10-821-234-1261	Sequence 1261, App
583	5	1.5	276	7	US-11-186-284-95	Sequence 95, App	658	5	1.5	326	6	US-10-467-657-7224	Sequence 7224, App
584	5	1.5	277	6	US-10-793-626-314	Sequence 314, App	660	5	1.5	326	6	US-10-821-234-1671	Sequence 1671, App
585	5	1.5	277	6	US-10-793-626-2178	Sequence 2178, App	661	5	1.5	328	6	US-10-995-561-884	Sequence 884, App
586	5	1.5	277	6	US-11-102-240-28	Sequence 28, App	662	5	1.5	329	6	US-10-793-626-1460	Sequence 1460, App
587	5	1.5	279	7	US-11-074-176-100	Sequence 100, App	663	5	1.5	331	7	US-11-102-240-36	Sequence 36, App
588	5	1.5	281	7	US-11-082-389-58	Sequence 58, App	664	5	1.5	332	7	US-11-113-424-55	Sequence 55, App
589	5	1.5	282	6	US-10-353-783-56	Sequence 56, App	665	5	1.5	333	6	US-10-793-626-2890	Sequence 2890, App
591	5	1.5	286	6	US-10-858-730-199	Sequence 199, App	666	5	1.5	334	7	US-11-055-822-980	Sequence 980, App
592	5	1.5	286	6	US-11-082-389-196	Sequence 196, App	667	5	1.5	334	7	US-11-055-822-1072	Sequence 1072, App
593	5	1.5	287	6	US-10-793-626-1146	Sequence 1146, App	668	5	1.5	334	7	US-11-113-424-80	Sequence 80, App
594	5	1.5	287	7	US-11-174-150-30	Sequence 30, App	669	5	1.5	335	6	US-10-995-561-866	Sequence 866, App
595	5	1.5	289	7	US-11-060-008-12	Sequence 12, App	670	5	1.5	335	7	US-11-182-946-7	Sequence 7, App
597	5	1.5	290	7	US-11-113-424-77	Sequence 77, App	671	5	1.5	336	6	US-10-793-626-1858	Sequence 1858, App
598	5	1.5	292	6	US-10-858-730-127	Sequence 127, App	672	5	1.5	336	6	US-10-980-388-120	Sequence 120, App
599	5	1.5	292	6	US-10-467-657-3590	Sequence 3590, App	673	5	1.5	336	7	US-11-113-424-83	Sequence 83, App
600	5	1.5	292	7	US-11-129-143-95	Sequence 95, App	674	5	1.5	337	6	US-10-467-657-97	Sequence 97, App
601	5	1.5	294	6	US-10-467-657-934	Sequence 934, App	675	5	1.5	337	6	US-10-793-626-444	Sequence 444, App
602	5	1.5	294	6	US-10-467-657-2876	Sequence 2876, App	676	5	1.5	337	6	US-10-875-716-2	Sequence 2, App
603	5	1.5	295	6	US-10-995-561-581	Sequence 581, App	677	5	1.5	337	7	US-11-102-240-74	Sequence 74, App
604	5	1.5	295	7	US-11-091-100-2	Sequence 2, App	678	5	1.5	338	6	US-10-467-657-3178	Sequence 3178, App
605	5	1.5	295	7	US-11-055-822-62	Sequence 62, App	679	5	1.5	338	6	US-10-467-657-8208	Sequence 8208, App
606	5	1.5	296	6	US-10-793-626-866	Sequence 866, App	680	5	1.5	338	6	US-10-467-657-8384	Sequence 8384, App
607	5	1.5	296	6	US-10-965-972-8	Sequence 8, App	681	5	1.5	338	7	US-11-000-463-445	Sequence 445, App
608	5	1.5	296	6	US-11-196-475-22	Sequence 22, App	682	5	1.5	339	6	US-10-467-657-8034	Sequence 8034, App
609	5	1.5	297	6	US-10-858-730-115	Sequence 115, App	683	5	1.5	344	6	US-10-967-5274-24	Sequence 24, App
610	5	1.5	297	6	US-10-858-730-116	Sequence 116, App	684	5	1.5	344	7	US-11-082-389-288	Sequence 288, App
611	5	1.5	298	6	US-10-498-715-6	Sequence 6, App	685	5	1.5	344	5	US-11-000-463-917	Sequence 917, App
612	5	1.5	298	6	US-10-793-626-1298	Sequence 1298, App	686	5	1.5	345	6	US-10-995-561-871	Sequence 871, App
613	5	1.5	298	6	US-11-138-949-9	Sequence 9, App	687	5	1.5	346	6	US-10-467-657-5946	Sequence 5946, App
614	5	1.5	299	7	US-11-112-882-30	Sequence 30, App	688	5	1.5	347	6	US-10-793-626-462	Sequence 462, App
615	5	1.5	301	7	US-11-074-176-362	Sequence 362, App	689	5	1.5	347	6	US-10-793-626-1268	Sequence 1268, App
616	5	1.5	301	7	US-11-000-463-380	Sequence 380, App	690	5	1.5	347	6	US-10-793-626-3326	Sequence 3326, App
617	5	1.5	301	7	US-11-000-463-752	Sequence 752, App	691	5	1.5	347	6	US-10-467-657-2014	Sequence 2014, App
618	5	1.5	302	6	US-10-878-556A-61	Sequence 61, App	692	5	1.5	347	7	US-11-066-648A-2	Sequence 2, App
619	5	1.5	303	7	US-11-102-240-166	Sequence 166, App	693	5	1.5	347	7	US-11-066-648A-12	Sequence 12, App
620	5	1.5	304	7	US-11-000-463-315	Sequence 315, App	694	5	1.5	347	7	US-11-066-648A-14	Sequence 14, App

695	5	1.5	348	6	US-10-674-767-4	Sequence 4, Appli	771	5	1.5	392	6	US-10-793-626-194	Sequence 124, App
696	5	1.5	348	6	US-10-793-626-2866	Sequence 2466, Ap	772	5	1.5	392	6	US-10-467-657-5724	Sequence 5724, Ap
698	5	1.5	349	6	US-11-028-922A-2	Sequence 2, Appl1	773	5	1.5	393	1	US-09-940-308-7	Sequence 7, Appl1
699	5	1.5	350	6	US-10-467-657-1972	Sequence 1972, Ap	774	5	1.5	393	7	US-11-100-352-3	Sequence 3, Appl1
700	5	1.5	350	6	US-10-467-657-3256	Sequence 3256, Ap	775	5	1.5	393	7	US-11-196-475-114	Sequence 114, Appl
701	5	1.5	350	6	US-10-467-657-3588	Sequence 3588, Ap	776	5	1.5	396	7	US-11-061-869-11	Sequence 11, Appl
702	5	1.5	351	6	US-10-793-626-338	Sequence 338, App	777	5	1.5	396	7	US-11-061-869-17	Sequence 17, Appl
703	5	1.5	351	6	US-10-467-657-5088	Sequence 5088, Ap	778	5	1.5	399	7	US-11-077-386-18	Sequence 18, Appl
704	5	1.5	351	6	US-10-467-657-5272	Sequence 5272, Ap	779	5	1.5	400	7	US-11-117-169-2	Sequence 2, Appl1
705	5	1.5	351	6	US-10-467-657-8320	Sequence 8320, Ap	780	5	1.5	400	7	US-11-117-169-4	Sequence 4, Appl1
706	5	1.5	351	7	US-11-108-528-52	Sequence 52, Appl	781	5	1.5	401	6	US-11-134-795-28	Sequence 28, Appl
707	5	1.5	352	7	US-11-055-822-666	Sequence 666, App	782	5	1.5	402	6	US-10-821-234-1581	Sequence 1581, Ap
708	5	1.5	354	6	US-10-467-657-3080	Sequence 3080, Ap	783	5	1.5	402	6	US-10-995-561-719	Sequence 719, App
709	5	1.5	354	6	US-10-995-561-717	Sequence 717, App	784	5	1.5	403	6	US-10-485-517-165	Sequence 165, App
710	5	1.5	355	6	US-10-793-626-3172	Sequence 3172, Ap	785	5	1.5	403	6	US-10-858-730-27	Sequence 27, Appl
711	5	1.5	355	6	US-10-967-527A-22	Sequence 22, Appl	786	5	1.5	403	6	US-10-858-730-28	Sequence 28, Appl
712	5	1.5	359	7	US-11-080-091-1	Sequence 1, Appl1	787	5	1.5	403	6	US-10-523-477-11	Sequence 11, Appl
713	5	1.5	359	7	US-11-116-939-15	Sequence 15, Appl	788	5	1.5	403	6	US-10-770-726-83	Sequence 83, Appl
714	5	1.5	359	7	US-11-129-143-71	Sequence 71, Appl	789	5	1.5	403	6	US-10-770-726-85	Sequence 85, Appl
715	5	1.5	360	7	US-11-084-408-3	Sequence 3, Appl1	790	5	1.5	403	6	US-11-109-156-12	Sequence 12, Appl
716	5	1.5	361	6	US-10-995-561-701	Sequence 701, App	791	5	1.5	403	7	US-11-055-822-776	Sequence 776, App
717	5	1.5	361	7	US-11-012-762-54	Sequence 54, Appl	792	5	1.5	407	6	US-10-793-626-886	Sequence 886, App
718	5	1.5	362	6	US-10-858-730-123	Sequence 123, App	793	5	1.5	407	6	US-10-613-744-14	Sequence 14, Appl
720	5	1.5	364	6	US-10-984-376-5	Sequence 5, Appl1	794	5	1.5	407	6	US-10-995-561-811	Sequence 811, App
721	5	1.5	364	6	US-10-984-376-6	Sequence 6, Appl1	795	5	1.5	409	6	US-10-627-633-4	Sequence 4, Appl1
722	5	1.5	364	7	US-10-995-561-699	Sequence 699, App	796	5	1.5	409	6	US-10-467-657-342	Sequence 342, App
723	5	1.5	364	7	US-11-091-334-2	Sequence 2, Appl1	797	5	1.5	410	6	US-10-793-626-3258	Sequence 3258, Ap
724	5	1.5	365	6	US-10-995-561-545	Sequence 545, App	798	5	1.5	410	6	US-10-467-657-4864	Sequence 4864, Ap
725	5	1.5	366	6	US-10-432-483-24	Sequence 24, Appl	799	5	1.5	410	7	US-11-055-822-6	Sequence 6, Appl1
726	5	1.5	366	7	US-11-000-463-410	Sequence 410, App	800	5	1.5	410	7	US-11-055-822-306	Sequence 306, App
727	5	1.5	366	7	US-11-000-463-457	Sequence 457, App	801	5	1.5	410	7	US-11-055-822-332	Sequence 332, App
728	5	1.5	366	7	US-11-000-463-882	Sequence 882, App	802	5	1.5	410	7	US-11-055-822-520	Sequence 520, App
729	5	1.5	367	6	US-10-821-234-1058	Sequence 1058, Ap	803	5	1.5	411	6	US-10-793-626-3236	Sequence 3236, Ap
730	5	1.5	367	6	US-10-858-730-205	Sequence 205, App	804	5	1.5	411	6	US-10-467-657-4076	Sequence 4076, Ap
731	5	1.5	368	6	US-10-793-626-742	Sequence 742, App	805	5	1.5	411	7	US-11-061-869-12	Sequence 12, Appl
732	5	1.5	368	6	US-10-467-657-4756	Sequence 4756, Ap	806	5	1.5	414	6	US-10-821-234-1170	Sequence 1170, Ap
733	5	1.5	369	6	US-10-793-626-1390	Sequence 1390, Ap	807	5	1.5	414	6	US-10-467-657-4316	Sequence 4316, Ap
734	5	1.5	369	6	US-10-793-626-1610	Sequence 1610, Ap	808	5	1.5	414	7	US-11-102-240-102	Sequence 102, Appl
735	5	1.5	370	7	US-11-129-143-58	Sequence 8, Appl	809	5	1.5	415	6	US-10-627-633-2	Sequence 2, Appl1
736	5	1.5	371	6	US-10-467-657-1166	Sequence 1166, Ap	810	5	1.5	415	6	US-10-821-234-936	Sequence 936, Appl
737	5	1.5	374	7	US-10-467-657-3088	Sequence 3088, Ap	811	5	1.5	416	7	US-11-061-869-18	Sequence 18, Appl
738	5	1.5	374	7	US-11-051-267-8	Sequence 8, Appl1	812	5	1.5	417	6	US-10-821-234-1536	Sequence 1536, Ap
739	5	1.5	375	7	US-11-051-267-20	Sequence 20, Appl	813	5	1.5	418	6	US-10-878-556A-53	Sequence 53, Appl
740	5	1.5	375	6	US-10-793-626-1840	Sequence 1840, Ap	814	5	1.5	418	6	US-10-995-561-753	Sequence 753, App
741	5	1.5	375	7	US-11-051-267-2	Sequence 2, Appl1	815	5	1.5	418	6	US-10-995-561-754	Sequence 754, App
742	5	1.5	375	7	US-11-051-267-10	Sequence 10, Appl	816	5	1.5	418	6	US-10-995-561-755	Sequence 755, App
743	5	1.5	375	7	US-11-051-267-12	Sequence 12, Appl	817	5	1.5	418	6	US-10-995-561-756	Sequence 756, App
744	5	1.5	375	7	US-11-051-267-14	Sequence 14, Appl	818	5	1.5	418	6	US-10-995-561-757	Sequence 757, App
745	5	1.5	375	7	US-11-051-267-16	Sequence 16, Appl	819	5	1.5	418	6	US-10-995-561-758	Sequence 758, App
746	5	1.5	375	7	US-11-051-267-18	Sequence 18, Appl	820	5	1.5	418	6	US-10-995-561-759	Sequence 759, App
747	5	1.5	376	6	US-10-793-626-490	Sequence 490, App	821	5	1.5	418	7	US-11-074-176-328	Sequence 328, App
748	5	1.5	376	6	US-10-793-626-2260	Sequence 2260, Ap	822	5	1.5	419	6	US-10-821-234-1556	Sequence 1556, Ap
749	5	1.5	376	7	US-11-051-267-4	Sequence 4, Appl1	823	5	1.5	419	6	US-10-821-234-1564	Sequence 1564, Ap
750	5	1.5	376	7	US-11-051-267-6	Sequence 6, Appl1	824	5	1.5	422	7	US-11-055-822-626	Sequence 626, App
751	5	1.5	377	6	US-10-467-657-7508	Sequence 7508, Ap	825	5	1.5	424	7	US-11-137-850-7	Sequence 7, Appl1
752	5	1.5	377	6	US-10-467-657-8228	Sequence 8228, Ap	826	5	1.5	424	7	US-11-137-850-8	Sequence 8, Appl1
753	5	1.5	377	7	US-11-055-822-448	Sequence 448, App	827	5	1.5	424	7	US-11-137-850-9	Sequence 9, Appl1
754	5	1.5	378	6	US-10-467-657-734	Sequence 734, App	828	5	1.5	426	6	US-10-467-657-1548	Sequence 1548, Ap
755	5	1.5	378	6	US-11-129-143-49	Sequence 49, Appl	829	5	1.5	426	6	US-10-467-657-2120	Sequence 2120, Ap
756	5	1.5	379	7	US-11-055-822-446	Sequence 446, App	830	5	1.5	427	6	US-11-182-946-5	Sequence 5, Appl1
757	5	1.5	379	7	US-11-129-143-66	Sequence 66, Appl	831	5	1.5	427	7	US-11-112-882-1	Sequence 1, Appl1
759	5	1.5	380	7	US-11-116-939-2	Sequence 2, Appl1	832	5	1.5	428	7	US-11-029-003-24	Sequence 24, Appl
760	5	1.5	380	7	US-11-196-475-118	Sequence 118, App	833	5	1.5	428	7	US-10-467-657-1622	Sequence 1622, Ap
761	5	1.5	381	6	US-10-510-386-168	Sequence 168, App	834	5	1.5	430	6	US-10-992-577-8	Sequence 8, Appl1
762	5	1.5	381	6	US-10-821-234-1342	Sequence 1342, Ap	835	5	1.5	430	6	US-11-194-246-438	Sequence 438, App
763	5	1.5	381	6	US-10-467-657-3226	Sequence 3226, Ap	836	5	1.5	431	6	US-10-821-234-1065	Sequence 1065, Ap
764	5	1.5	384	6	US-10-467-657-508	Sequence 508, App	837	5	1.5	431	7	US-11-069-642-1	Sequence 1, Appl1
765	5	1.5	387	7	US-11-055-822-112	Sequence 112, App	839	5	1.5	432	6	US-10-793-626-2942	Sequence 2942, Ap
766	5	1.5	387	7	US-11-082-822-472	Sequence 472, App	840	5	1.5	432	6	US-10-992-577-2	Sequence 2, Appl1
767	5	1.5	389	7	US-11-188-743-33	Sequence 23, Appl	841	5	1.5	433	7	US-11-196-475-180	Sequence 180, App
768	5	1.5	391	6	US-10-878-556A-86	Sequence 86, Appl	842	5	1.5	434	6	US-10-821-234-1680	Sequence 1680, Ap
769	5	1.5	392	6	US-10-392-234A-50	Sequence 50, Appl	843	5	1.5	434	7	US-11-055-822-794	Sequence 794, App

844	5	1.5	434	7	US-11-196-475-164	Sequence 164, App	921	5	1.5	466	7	US-11-196-475-110	Sequence 110, App
845	5	1.5	435	7	US-11-077-386-19	Sequence 2, App1	922	5	1.5	467	7	US-11-000-463-452	Sequence 452, App
847	5	1.5	437	6	US-10-521-536-2	Sequence 19, App1	923	5	1.5	467	7	US-11-000-463-924	Sequence 924, App
848	5	1.5	437	6	US-10-821-234-1392	Sequence 1392, Ap	924	5	1.5	467	7	US-11-000-463-925	Sequence 925, App
849	5	1.5	437	6	US-10-525-710-18	Sequence 18, App1	925	5	1.5	468	6	US-10-763-712A-3	Sequence 3, App1
850	5	1.5	437	7	US-11-069-642-92	Sequence 92, App1	926	5	1.5	470	6	US-10-485-517-119	Sequence 319, App
851	5	1.5	437	7	US-11-199-124-2	Sequence 2, App1	927	5	1.5	470	7	US-11-008-727-20	Sequence 20, App1
852	5	1.5	438	6	US-10-793-626-508	Sequence 508, App	928	5	1.5	472	6	US-10-467-657-2268	Sequence 2268, Ap
853	5	1.5	438	7	US-11-069-642-47	Sequence 47, App1	929	5	1.5	473	7	US-11-075-185-12	Sequence 12, App1
854	5	1.5	438	7	US-11-069-642-49	Sequence 49, App1	930	5	1.5	474	6	US-10-793-626-946	Sequence 946, App
855	5	1.5	438	7	US-11-069-642-51	Sequence 51, App1	931	5	1.5	475	7	US-11-061-869-15	Sequence 15, App1
856	5	1.5	438	7	US-11-069-642-53	Sequence 53, App1	932	5	1.5	477	6	US-10-793-626-3250	Sequence 3250, Ap
857	5	1.5	438	7	US-11-069-642-55	Sequence 55, App1	933	5	1.5	479	7	US-11-147-047-14	Sequence 44, App1
858	5	1.5	438	7	US-11-069-642-57	Sequence 57, App1	934	5	1.5	479	7	US-11-024-251-33	Sequence 33, App1
859	5	1.5	438	7	US-11-069-642-59	Sequence 59, App1	935	5	1.5	479	7	US-11-194-246-110	Sequence 310, App
860	5	1.5	438	7	US-11-069-642-61	Sequence 61, App1	936	5	1.5	480	6	US-10-510-386-12	Sequence 12, App1
861	5	1.5	438	7	US-11-069-642-63	Sequence 63, App1	937	5	1.5	480	6	US-10-336-263A-8	Sequence 8, App1
862	5	1.5	438	7	US-11-090-439-31	Sequence 31, App1	938	5	1.5	480	6	US-10-821-234-886	Sequence 886, App
863	5	1.5	438	7	US-11-196-475-168	Sequence 168, App	939	5	1.5	480	7	US-11-080-991-76	Sequence 76, App1
864	5	1.5	438	7	US-11-199-124-10	Sequence 10, App1	940	5	1.5	481	7	US-11-116-939-14	Sequence 14, App1
865	5	1.5	439	6	US-10-467-657-3034	Sequence 3034, Ap	941	5	1.5	482	6	US-10-878-556A-139	Sequence 139, App1
866	5	1.5	439	7	US-11-082-389-80	Sequence 80, App1	942	5	1.5	482	7	US-11-055-822-20	Sequence 20, App1
867	5	1.5	440	7	US-11-196-475-178	Sequence 178, App	943	5	1.5	485	6	US-10-204-029-7	Sequence 7, App1
868	5	1.5	441	7	US-11-196-475-120	Sequence 120, App	944	5	1.5	485	6	US-10-467-657-326	Sequence 326, App
869	5	1.5	442	6	US-10-821-234-1594	Sequence 1594, App	945	5	1.5	485	6	US-10-467-657-4512	Sequence 4512, Ap
870	5	1.5	443	6	US-10-793-626-1598	Sequence 1598, Ap	946	5	1.5	485	7	US-11-055-822-18	Sequence 18, App1
871	5	1.5	444	6	US-10-467-657-362	Sequence 362, App	947	5	1.5	486	7	US-11-000-463-373	Sequence 273, App
872	5	1.5	445	7	US-11-102-240-32	Sequence 32, App1	948	5	1.5	487	7	US-11-113-424-56	Sequence 56, App1
873	5	1.5	445	7	US-11-115-564-2	Sequence 2, App1	949	5	1.5	487	7	US-11-113-424-57	Sequence 57, App1
874	5	1.5	446	7	US-11-196-475-150	Sequence 150, App	950	5	1.5	488	6	US-10-984-376-1	Sequence 1, App1
875	5	1.5	446	7	US-11-196-475-154	Sequence 154, App	951	5	1.5	488	6	US-10-984-376-4	Sequence 4, App1
876	5	1.5	446	7	US-11-196-475-158	Sequence 158, App	952	5	1.5	488	6	US-10-995-561-860	Sequence 860, App
877	5	1.5	447	6	US-10-884-730-379	Sequence 379, App	953	5	1.5	491	6	US-10-793-626-1798	Sequence 1798, App
878	5	1.5	447	7	US-11-055-822-978	Sequence 978, App	954	5	1.5	491	7	US-11-098-662-14	Sequence 14, App1
879	5	1.5	447	7	US-11-196-475-162	Sequence 162, App	955	5	1.5	491	7	US-11-165-141-2	Sequence 2, App1
880	5	1.5	448	7	US-11-112-882-24	Sequence 24, App1	956	5	1.5	492	6	US-10-467-657-4326	Sequence 4326, Ap
881	5	1.5	448	7	US-11-112-882-67	Sequence 67, App1	957	5	1.5	492	6	US-10-467-657-7112	Sequence 7112, App
883	5	1.5	449	6	US-10-858-730-26	Sequence 26, App1	958	5	1.5	494	6	US-10-467-657-4376	Sequence 4376, Ap
884	5	1.5	449	6	US-10-525-710-4	Sequence 4, App1	959	5	1.5	496	7	US-11-067-121-3	Sequence 3, App1
886	5	1.5	450	6	US-10-995-561-815	Sequence 815, App	960	5	1.5	496	7	US-11-067-121-12	Sequence 12, App1
887	5	1.5	450	7	US-11-077-386-20	Sequence 20, App1	961	5	1.5	496	7	US-11-110-082-31	Sequence 31, App1
888	5	1.5	450	7	US-11-196-475-148	Sequence 148, App	962	5	1.5	496	7	US-11-186-284-103	Sequence 103, App
889	5	1.5	452	6	US-10-467-657-3312	Sequence 3312, Ap	963	5	1.5	499	6	US-10-508-263-94	Sequence 94, App1
890	5	1.5	453	7	US-11-196-475-146	Sequence 146, App	964	5	1.5	500	6	US-10-467-657-48	Sequence 48, App1
891	5	1.5	453	7	US-11-196-475-152	Sequence 152, App	966	5	1.5	502	6	US-10-689-742-148	Sequence 148, App
892	5	1.5	453	7	US-11-196-475-156	Sequence 156, App	967	5	1.5	502	6	US-10-821-234-1554	Sequence 1554, App
893	5	1.5	454	7	US-11-089-551A-35	Sequence 35, App1	968	5	1.5	502	7	US-11-102-240-158	Sequence 158, App
894	5	1.5	454	7	US-11-196-475-116	Sequence 116, App	969	5	1.5	504	7	US-11-155-492-33	Sequence 73, App1
895	5	1.5	454	7	US-11-196-475-160	Sequence 160, App	970	5	1.5	505	6	US-11-063-343-8	Sequence 38, App1
896	5	1.5	456	6	US-10-467-657-5786	Sequence 5786, Ap	971	5	1.5	506	6	US-10-485-517-344	Sequence 344, App
897	5	1.5	456	7	US-11-055-822-4	Sequence 4, App1	972	5	1.5	510	7	US-11-194-246-442	Sequence 442, App
898	5	1.5	456	7	US-11-055-822-304	Sequence 304, App	974	5	1.5	511	7	US-11-152-747-4	Sequence 4, App1
899	5	1.5	456	7	US-11-055-822-330	Sequence 330, App	975	5	1.5	512	7	US-11-032-236-6	Sequence 6, App1
900	5	1.5	456	7	US-11-055-822-518	Sequence 518, App	977	5	1.5	513	6	US-10-821-234-1112	Sequence 1112, Ap
901	5	1.5	456	7	US-11-069-642-15	Sequence 15, App1	978	5	1.5	513	7	US-11-102-240-124	Sequence 124, App
903	5	1.5	457	6	US-10-995-561-797	Sequence 797, App	979	5	1.5	513	7	US-11-000-463-358	Sequence 358, App
904	5	1.5	457	7	US-11-194-246-326	Sequence 326, App	980	5	1.5	514	6	US-10-957-569-48	Sequence 48, App1
905	5	1.5	459	6	US-10-821-234-896	Sequence 896, App	981	5	1.5	514	7	US-11-186-284-228	Sequence 228, App
906	5	1.5	459	6	US-11-186-284-12	Sequence 12, App1	982	5	1.5	516	6	US-10-508-263-26	Sequence 26, App1
907	5	1.5	461	6	US-10-509-464-7	Sequence 7, App1	983	5	1.5	518	6	US-10-821-234-1165	Sequence 1165, Ap
908	5	1.5	461	6	US-10-467-657-6794	Sequence 6794, App	984	5	1.5	518	6	US-10-467-657-1124	Sequence 1124, App
909	5	1.5	462	6	US-10-467-657-622	Sequence 622, App	985	5	1.5	519	7	US-11-099-691-10	Sequence 10, App1
910	5	1.5	462	6	US-10-467-657-4348	Sequence 4348, App	986	5	1.5	520	6	US-10-467-657-3948	Sequence 3948, App
911	5	1.5	462	6	US-10-467-657-7636	Sequence 7636, App	987	5	1.5	520	6	US-10-995-561-532	Sequence 532, App
912	5	1.5	463	6	US-10-510-386-186	Sequence 186, App	988	5	1.5	520	7	US-11-098-662-12	Sequence 12, App1
913	5	1.5	463	6	US-10-467-657-4228	Sequence 4228, App	989	5	1.5	520	7	US-11-165-141-19	Sequence 19, App1
914	5	1.5	464	6	US-10-763-712A-46	Sequence 46, App1	990	5	1.5	521	6	US-10-821-234-1546	Sequence 1546, App
915	5	1.5	465	6	US-10-967-648A-6	Sequence 6, App1	991	5	1.5	522	6	US-10-467-657-7238	Sequence 7238, App
916	5	1.5	465	6	US-10-793-626-1576	Sequence 1576, App	992	5	1.5	527	7	US-10-821-234-1574	Sequence 1574, App
917	5	1.5	465	6	US-10-821-234-1550	Sequence 1550, App	993	5	1.5	527	7	US-11-113-424-81	Sequence 81, App1
918	5	1.5	465	7	US-11-037-829A-14	Sequence 14, App1	994	5	1.5	528	6	US-10-467-657-1042	Sequence 1042, App
919	5	1.5	466	7	US-11-102-240-104	Sequence 104, App	995	5	1.5	528	6	US-10-467-657-6354	Sequence 6354, App
920	5	1.5	466	7	US-11-196-475-107	Sequence 107, App	996	5	1.5	528	6	US-10-878-556A-77	Sequence 77, App1

997	5	1.5	529	7	US-11-113-424-82	Sequence 82, Appl	1074	5	1.5	628	7	US-11-147-047-45	Sequence 45, Appl
998	5	1.5	530	6	US-10-858-730-332	Sequence 232, App	1075	5	1.5	633	7	US-11-119-683-3	Sequence 3, Appl1
999	5	1.5	531	6	US-10-980-388-52	Sequence 62, Appl	1076	5	1.5	634	7	US-11-137-465-63	Sequence 63, Appl1
1000	5	1.5	532	6	US-10-878-556A-70	Sequence 70, Appl	1077	5	1.5	638	6	US-10-793-626-1468	Sequence 1468, Ap
1001	5	1.5	533	6	US-10-821-234-918	Sequence 918, App	1079	5	1.5	641	6	US-10-821-234-1519	Sequence 1519, Ap
1002	5	1.5	533	6	US-10-467-657-8	Sequence 8, Appl1	1080	5	1.5	641	6	US-10-491-096-189	Sequence 189, App
1003	5	1.5	533	6	US-10-467-657-8	Sequence 2668, Ap	1081	5	1.5	643	6	US-11-074-176-318	Sequence 318, App
1004	5	1.5	534	6	US-10-858-730-66	Sequence 66, Appl	1082	5	1.5	644	6	US-10-467-657-5958	Sequence 5958, Ap
1005	5	1.5	534	7	US-11-082-389-348	Sequence 348, App	1083	5	1.5	645	6	US-10-510-386-32	Sequence 3, Appl
1006	5	1.5	534	7	US-11-075-185-17	Sequence 17, Appl	1084	5	1.5	645	6	US-10-821-234-1409	Sequence 1409, Ap
1007	5	1.5	539	6	US-10-467-657-7736	Sequence 7736, Ap	1085	5	1.5	646	6	US-10-491-096-190	Sequence 12, App
1008	5	1.5	541	7	US-11-112-882-34	Sequence 34, Appl	1086	5	1.5	647	7	US-11-080-991-32	Sequence 32, Appl
1009	5	1.5	544	6	US-10-467-657-468	Sequence 468, App	1087	5	1.5	648	6	US-10-501-039-6	Sequence 6, Appl1
1010	5	1.5	546	6	US-10-821-234-902	Sequence 902, App	1088	5	1.5	652	6	US-10-821-234-1016	Sequence 1016, Ap
1011	5	1.5	547	6	US-10-770-726-87	Sequence 87, Appl	1089	5	1.5	654	6	US-10-770-726-82	Sequence 82, Appl
1012	5	1.5	548	6	US-10-995-561-810	Sequence 810, App	1090	5	1.5	654	7	US-11-110-082-24	Sequence 24, Appl
1013	5	1.5	549	7	US-11-194-246-431	Sequence 431, App	1091	5	1.5	656	6	US-10-995-661-871	Sequence 871, App
1014	5	1.5	550	7	US-11-184-380-14	Sequence 14, Appl	1092	5	1.5	657	7	US-11-109-156-27	Sequence 27, Appl
1015	5	1.5	551	7	US-11-000-463-346	Sequence 346, App	1093	5	1.5	658	6	US-10-467-657-4782	Sequence 4782, Ap
1016	5	1.5	554	6	US-10-793-626-1414	Sequence 1414, Ap	1094	5	1.5	662	7	US-11-090-439-9	Sequence 9, Appl1
1017	5	1.5	554	6	US-10-763-712A-33	Sequence 33, Appl	1095	5	1.5	667	6	US-10-793-626-198	Sequence 198, App
1018	5	1.5	554	6	US-11-055-822-998	Sequence 998, App	1096	5	1.5	667	7	US-11-074-176-64	Sequence 64, Appl
1019	5	1.5	555	6	US-10-763-712A-119	Sequence 119, App	1097	5	1.5	668	6	US-10-467-657-4238	Sequence 4238, Ap
1020	5	1.5	562	6	US-10-467-657-4346	Sequence 4346, Ap	1098	5	1.5	668	7	US-11-113-424-12	Sequence 12, Appl
1021	5	1.5	562	6	US-10-508-263-24	Sequence 24, Appl	1099	5	1.5	669	7	US-11-076-187-3	Sequence 3, Appl1
1022	5	1.5	564	6	US-10-485-517-298	Sequence 298, App	1100	5	1.5	669	7	US-11-119-683-2	Sequence 2, Appl1
1023	5	1.5	564	7	US-11-082-389-78	Sequence 78, Appl	1101	5	1.5	670	6	US-10-821-234-879	Sequence 879, App
1024	5	1.5	567	6	US-10-467-657-4328	Sequence 4328, Ap	1102	5	1.5	672	6	US-10-467-657-5126	Sequence 5126, Ap
1026	5	1.5	567	6	US-10-995-561-813	Sequence 813, App	1103	5	1.5	673	6	US-11-102-240-16	Sequence 16, Appl
1027	5	1.5	569	6	US-10-821-234-664	Sequence 864, App	1104	5	1.5	675	6	US-10-467-657-3802	Sequence 3802, Ap
1028	5	1.5	573	7	US-11-196-475-112	Sequence 112, App	1105	5	1.5	677	6	US-10-982-545-12	Sequence 12, Appl
1029	5	1.5	574	6	US-10-507-275-7	Sequence 7, Appl1	1106	5	1.5	678	7	US-11-102-240-34	Sequence 34, Appl
1030	5	1.5	574	6	US-10-763-712A-1	Sequence 1, Appl1	1107	5	1.5	679	6	US-10-995-561-872	Sequence 872, App
1031	5	1.5	574	6	US-10-763-712A-102	Sequence 102, App	1108	5	1.5	687	6	US-11-099-691-9	Sequence 9, Appl1
1032	5	1.5	574	6	US-10-770-726-50	Sequence 50, Appl	1109	5	1.5	687	6	US-10-485-517-274	Sequence 274, App
1033	5	1.5	576	6	US-11-137-465-64	Sequence 64, Appl	1110	5	1.5	687	7	US-11-117-169-6	Sequence 6, Appl1
1034	5	1.5	580	6	US-10-995-561-987	Sequence 987, App	1111	5	1.5	688	7	US-11-113-424-48	Sequence 48, Appl
1035	5	1.5	582	7	US-11-074-176-110	Sequence 110, App	1112	5	1.5	689	7	US-11-113-424-46	Sequence 46, Appl
1036	5	1.5	583	6	US-10-793-626-1358	Sequence 1358, Ap	1113	5	1.5	689	7	US-11-113-424-47	Sequence 47, Appl
1037	5	1.5	585	6	US-10-510-386-30	Sequence 20, Appl	1114	5	1.5	692	7	US-11-038-284-33	Sequence 33, Appl
1038	5	1.5	585	7	US-11-012-762-6	Sequence 6, Appl1	1115	5	1.5	692	7	US-11-045-802-26	Sequence 26, Appl
1039	5	1.5	585	7	US-11-074-176-190	Sequence 190, App	1116	5	1.5	697	7	US-11-074-176-62	Sequence 62, Appl
1040	5	1.5	588	6	US-10-650-3268-7	Sequence 7, Appl1	1117	5	1.5	703	7	US-11-069-642-113	Sequence 113, App
1041	5	1.5	588	6	US-11-196-475-122	Sequence 122, App	1118	5	1.5	706	6	US-10-485-517-146	Sequence 146, App
1042	5	1.5	589	7	US-11-074-176-196	Sequence 196, App	1119	5	1.5	708	7	US-11-196-475-76	Sequence 76, Appl
1043	5	1.5	590	1	US-09-940-308-2	Sequence 2, Appl1	1120	5	1.5	709	6	US-10-821-234-1138	Sequence 1138, Ap
1044	5	1.5	594	6	US-10-510-386-38	Sequence 38, Appl	1121	5	1.5	709	7	US-11-074-176-158	Sequence 158, App
1045	5	1.5	594	6	US-10-467-657-3952	Sequence 3952, Ap	1122	5	1.5	711	6	US-10-821-234-1017	Sequence 1017, Ap
1046	5	1.5	594	7	US-11-012-762-4	Sequence 4, Appl1	1123	5	1.5	711	7	US-11-087-100-18	Sequence 18, Appl
1047	5	1.5	599	6	US-10-995-561-812	Sequence 812, App	1124	5	1.5	711	7	US-11-087-084-18	Sequence 18, Appl
1048	5	1.5	609	6	US-10-606-302-3	Sequence 3, Appl1	1125	5	1.5	721	7	US-11-087-085-18	Sequence 18, Appl
1049	5	1.5	602	7	US-11-055-822-74	Sequence 74, Appl	1126	5	1.5	721	7	US-11-060-920-5	Sequence 5, Appl1
1050	5	1.5	604	6	US-10-995-561-839	Sequence 839, App	1128	5	1.5	724	6	US-10-793-626-968	Sequence 968, Appl
1051	5	1.5	607	7	US-11-167-856-18	Sequence 18, Appl	1129	5	1.5	727	6	US-10-793-626-2862	Sequence 2862, Ap
1054	5	1.5	607	7	US-11-176-863-2	Sequence 2, Appl1	1130	5	1.5	727	6	US-10-995-561-864	Sequence 864, App
1055	5	1.5	609	7	US-11-058-555-2	Sequence 5, Appl1	1131	5	1.5	728	6	US-11-117-169-8	Sequence 8, Appl1
1056	5	1.5	609	7	US-11-062-225-3	Sequence 3, Appl1	1132	5	1.5	728	6	US-10-467-657-1742	Sequence 1442, Ap
1057	5	1.5	609	7	US-11-062-225-4	Sequence 4, Appl1	1133	5	1.5	728	6	US-10-467-657-8376	Sequence 8376, Ap
1058	5	1.5	609	7	US-11-062-225-5	Sequence 5, Appl1	1134	5	1.5	734	6	US-10-652-893-2	Sequence 2, Appl1
1059	5	1.5	609	7	US-11-062-225-6	Sequence 6, Appl1	1135	5	1.5	734	6	US-10-995-561-1770	Sequence 770, App
1060	5	1.5	609	7	US-11-062-225-7	Sequence 7, Appl1	1136	5	1.5	736	6	US-11-137-465-65	Sequence 65, Appl
1061	5	1.5	610	6	US-10-606-302-1	Sequence 1, Appl1	1137	5	1.5	736	6	US-10-467-657-4780	Sequence 4780, Ap
1063	5	1.5	610	6	US-10-606-302-1	Sequence 8, Appl1	1138	5	1.5	747	7	US-11-018-018-1	Sequence 1, Appl1
1064	5	1.5	610	7	US-11-184-380-3	Sequence 3, Appl1	1139	5	1.5	747	7	US-11-047-757-1	Sequence 1, Appl1
1065	5	1.5	614	6	US-10-821-224-1041	Sequence 1041, Ap	1140	5	1.5	750	6	US-10-689-742-86	Sequence 86, Appl
1066	5	1.5	614	6	US-11-155-492-107	Sequence 107, App	1141	5	1.5	753	6	US-10-485-517-173	Sequence 173, App
1067	5	1.5	616	7	US-11-083-800-4	Sequence 4, Appl1	1142	5	1.5	753	7	US-11-137-465-51	Sequence 51, Appl
1068	5	1.5	617	7	US-11-143-980-35	Sequence 35, Appl1	1143	5	1.5				
1069	5	1.5	620	6	US-10-467-657-5892	Sequence 5892, Ap	1145	5	1.5				
1070	5	1.5	622	7	US-11-199-124-12	Sequence 12, Appl	1147	5	1.5				
1071	5	1.5	625	7	US-11-021-441-37	Sequence 37, Appl	1148	5	1.5				
1072	5	1.5	626	6	US-10-467-657-1196	Sequence 1196, Ap	1149	5	1.5				
1073	5	1.5	626	7	US-11-010-748A-1	Sequence 1, Appl1	1149	5	1.5				

1150	5	1.5	757	7	US-11-110-082-35	Sequence 35, Appl	1225	5	1.5	919	7	US-11-074-176-284	Sequence 284, App
1151	5	1.5	758	6	US-10-467-962B-12	Sequence 12, Appl	1226	5	1.5	932	7	US-11-057-058-59	Sequence 59, Appl
1152	5	1.5	761	7	US-11-110-082-34	Sequence 34, Appl	1227	5	1.5	932	7	US-11-071-581-1	Sequence 1, Appl
1153	5	1.5	769	6	US-10-467-657-3280	Sequence 3280, Ap	1228	5	1.5	934	6	US-10-858-730-8	Sequence 8, Appl
1154	5	1.5	773	6	US-10-821-234-1134	Sequence 1134, Ap	1229	5	1.5	934	7	US-11-188-743-19	Sequence 19, Appl
1155	5	1.5	773	6	US-10-995-561-852	Sequence 852, App	1230	5	1.5	943	6	US-10-467-657-5508	Sequence 5508, Ap
1156	5	1.5	774	7	US-11-000-463-459	Sequence 459, App	1231	5	1.5	944	6	US-10-793-626-3324	Sequence 3324, Ap
1157	5	1.5	774	7	US-11-077-886-34	Sequence 34, Appl	1232	5	1.5	948	6	US-10-485-517-131	Sequence 131, App
1158	5	1.5	777	6	US-10-821-234-1658	Sequence 1658, Ap	1233	5	1.5	948	6	US-10-523-477-14	Sequence 14, Appl
1159	5	1.5	779	7	US-11-128-420-12	Sequence 12, Appl	1234	5	1.5	950	6	US-10-467-657-854	Sequence 854, App
1160	5	1.5	781	7	US-11-194-246-344	Sequence 344, App	1235	5	1.5	952	6	US-11-174-166-18	Sequence 18, Appl
1161	5	1.5	782	6	US-10-793-626-3352	Sequence 2352, Ap	1236	5	1.5	963	7	US-11-174-166-20	Sequence 20, Appl
1162	5	1.5	782	6	US-10-821-234-1592	Sequence 1592, Ap	1237	5	1.5	977	7	US-11-093-274-39	Sequence 39, Appl
1163	5	1.5	782	6	US-10-972-053-2	Sequence 2, Appl	1238	5	1.5	966	6	US-10-821-334-1310	Sequence 1310, Ap
1164	5	1.5	782	6	US-10-972-053-8	Sequence 8, Appl	1239	5	1.5	1005	7	US-11-113-424-63	Sequence 63, Appl
1165	5	1.5	782	6	US-10-995-561-861	Sequence 861, App	1240	5	1.5	1008	7	US-11-055-822-312	Sequence 312, App
1166	5	1.5	783	7	US-11-082-389-354	Sequence 354, App	1241	5	1.5	1015	6	US-10-957-569-51	Sequence 51, Appl
1167	5	1.5	784	6	US-10-972-053-10	Sequence 10, Appl	1242	5	1.5	1022	7	US-11-186-284-163	Sequence 163, App
1169	5	1.5	790	6	US-11-080-991-82	Sequence 82, Appl	1243	5	1.5	1029	6	US-10-857-780-22	Sequence 22, Appl
1170	5	1.5	791	6	US-10-972-053-4	Sequence 4, Appl	1244	5	1.5	1031	6	US-10-857-780-22	Sequence 2, Appl
1171	5	1.5	791	6	US-10-467-657-5014	Sequence 5014, Ap	1245	5	1.5	1044	7	US-11-110-204-2	Sequence 10, App
1172	5	1.5	792	6	US-10-972-053-12	Sequence 12, Appl	1248	5	1.5	1045	7	US-11-055-822-100	Sequence 54, Appl
1173	5	1.5	792	6	US-10-467-657-6026	Sequence 6026, Ap	1249	5	1.5	1045	7	US-11-113-424-54	Sequence 200, App
1174	5	1.5	792	6	US-10-467-657-7528	Sequence 7528, Ap	1250	5	1.5	1047	6	US-10-510-386-200	Sequence 18, Appl
1175	5	1.5	797	6	US-10-995-561-802	Sequence 802, App	1251	5	1.5	1048	6	US-10-392-234-14	Sequence 14, Appl
1176	5	1.5	805	6	US-10-518-599-2	Sequence 2, Appl	1252	5	1.5	1048	6	US-10-392-234-18	Sequence 18, Appl
1177	5	1.5	805	6	US-10-518-599-4	Sequence 4, Appl	1253	5	1.5	1048	6	US-10-392-234-20	Sequence 20, Appl
1178	5	1.5	805	6	US-10-518-599-24	Sequence 24, Appl	1254	5	1.5	1049	7	US-11-137-465-42	Sequence 42, Appl
1179	5	1.5	805	6	US-10-467-657-8246	Sequence 8246, Ap	1255	5	1.5	1059	6	US-10-467-657-3992	Sequence 3992, Ap
1180	5	1.5	808	7	US-10-878-556A-80	Sequence 80, Appl	1256	5	1.5	1052	7	US-10-467-657-3992	Sequence 5, Appl
1181	5	1.5	808	7	US-11-110-082-58	Sequence 38, Appl	1257	5	1.5	1059	6	US-11-062	Sequence 4, Appl
1182	5	1.5	814	6	US-10-878-556A-161	Sequence 161, App	1258	5	1.5	1062	7	US-11-137-465-43	Sequence 2804, Ap
1183	5	1.5	816	7	US-11-090-439-48	Sequence 48, Appl	1259	5	1.5	1068	6	US-10-467-657-2904	Sequence 5230, Ap
1184	5	1.5	817	7	US-11-012-762-2	Sequence 2, Appl	1260	5	1.5	1073	6	US-10-467-657-5230	Sequence 23, Appl
1185	5	1.5	826	6	US-10-878-556A-68	Sequence 68, Appl	1261	5	1.5	1075	7	US-11-089-551A-23	Sequence 8, Appl
1186	5	1.5	826	6	US-10-501-039-2	Sequence 2, Appl	1262	5	1.5	1084	7	US-11-062	Sequence 1097, Ap
1187	5	1.5	833	6	US-10-667-295-102	Sequence 102, App	1263	5	1.5	1094	6	US-10-821-334-1097	Sequence 27, Appl
1188	5	1.5	833	7	US-11-076-187-5	Sequence 5, Appl	1264	5	1.5	1114	6	US-10-857-780-27	Sequence 236, App
1190	5	1.5	839	7	US-10-667-295-101	Sequence 101, App	1265	5	1.5	1116	6	US-10-485-517-238	Sequence 206, App
1191	5	1.5	839	7	US-11-076-431-2	Sequence 2, Appl	1266	5	1.5	1117	6	US-10-485-517-206	Sequence 1657, Ap
1192	5	1.5	839	7	US-11-076-431-4	Sequence 4, Appl	1267	5	1.5	1122	6	US-10-821-334-1657	Sequence 12, Appl
1193	5	1.5	839	7	US-11-076-431-6	Sequence 6, Appl	1268	5	1.5	1124	6	US-10-858-730-12	Sequence 3, Appl
1194	5	1.5	839	7	US-11-076-431-8	Sequence 8, Appl	1269	5	1.5	1126	5	US-11-075-185-3	Sequence 13, Appl
1195	5	1.5	840	6	US-10-645-441-1	Sequence 1, Appl	1270	5	1.5	1127	6	US-10-858-730-13	Sequence 119, Ap
1196	5	1.5	840	6	US-11-108-172-1102	Sequence 1102, Ap	1271	5	1.5	1133	6	US-10-821-334-1219	Sequence 4, Appl
1197	5	1.5	841	6	US-10-624-932-6	Sequence 6, Appl	1272	5	1.5	1137	6	US-10-499-715-4	Sequence 1009, Ap
1198	5	1.5	841	6	US-10-624-932-8	Sequence 8, Appl	1273	5	1.5	1141	6	US-10-995-561-1009	Sequence 1010, Ap
1199	5	1.5	842	6	US-10-645-441-2	Sequence 2, Appl	1274	5	1.5	1141	6	US-10-995-561-1010	Sequence 73, Appl
1200	5	1.5	842	6	US-11-038-284-38	Sequence 38, Appl	1275	5	1.5	1142	7	US-11-044-051-73	Sequence 1820, App
1201	5	1.5	845	7	US-11-147-047-46	Sequence 46, Appl	1276	5	1.5	1144	6	US-10-467-657-1820	Sequence 308, App
1202	5	1.5	847	6	US-10-995-561-863	Sequence 863, App	1277	5	1.5	1152	7	US-11-055-822-308	Sequence 6, Appl
1203	5	1.5	847	7	US-10-995-561-865	Sequence 865, App	1278	5	1.5	1156	7	US-11-075-646-6	Sequence 2, Appl
1204	5	1.5	847	7	US-11-038-284-42	Sequence 42, App	1279	5	1.5	1163	7	US-11-044-899-2	Sequence 30, Appl
1205	5	1.5	852	6	US-10-467-657-5004	Sequence 5004, Ap	1280	5	1.5	1163	7	US-11-044-899-30	Sequence 6, Appl
1206	5	1.5	852	6	US-10-645-441-15	Sequence 15, Appl	1281	5	1.5	1167	6	US-10-942-072-6	Sequence 6, Appl
1207	5	1.5	853	6	US-10-420-192-6	Sequence 6, Appl	1282	5	1.5	1168	6	US-10-942-072-13	Sequence 11, Appl
1208	5	1.5	858	6	US-10-645-441-18	Sequence 18, Appl	1283	5	1.5	1170	6	US-10-942-072-11	Sequence 2, Appl
1209	5	1.5	858	6	US-10-645-441-20	Sequence 20, Appl	1284	5	1.5	1170	6	US-10-831-997-2	Sequence 554, App
1210	5	1.5	858	6	US-10-645-441-23	Sequence 23, Appl	1285	5	1.5	1170	6	US-10-995-561-594	Sequence 555, App
1211	5	1.5	858	6	US-10-645-441-25	Sequence 25, Appl	1286	5	1.5	1170	6	US-10-995-561-595	Sequence 556, App
1212	5	1.5	858	6	US-10-878-556A-113	Sequence 113, App	1287	5	1.5	1170	6	US-10-995-561-596	Sequence 557, App
1213	5	1.5	858	6	US-10-995-561-854	Sequence 854, App	1288	5	1.5	1170	7	US-11-046-456-28	Sequence 28, Appl
1214	5	1.5	862	7	US-11-128-420-11	Sequence 11, Appl	1289	5	1.5	1170	7	US-11-046-644-28	Sequence 28, Appl
1215	5	1.5	873	7	US-11-038-284-35	Sequence 35, Appl	1290	5	1.5	1178	6	US-10-995-561-851	Sequence 851, App
1216	5	1.5	874	6	US-10-510-386-28	Sequence 28, Appl	1291	5	1.5	1178	7	US-11-044-899-29	Sequence 29, Appl
1217	5	1.5	877	6	US-10-821-234-960	Sequence 960, App	1292	5	1.5	1179	7	US-11-087-125-1	Sequence 1, Appl
1218	5	1.5	885	7	US-10-467-657-2302	Sequence 2302, Ap	1293	5	1.5	1189	7	US-11-074-176-134	Sequence 134, App
1219	5	1.5	889	6	US-11-038-284-15	Sequence 15, Appl	1295	5	1.5	1192	6	US-10-667-295-259	Sequence 259, App
1220	5	1.5	892	6	US-10-507-275-3	Sequence 3, Appl	1296	5	1.5	1196	6	US-10-667-295-100	Sequence 100, App
1221	5	1.5	898	7	US-11-099-691-7	Sequence 7, Appl	1297	5	1.5	1196	6	US-10-995-561-921	Sequence 921, App
1222	5	1.5	914	7	US-11-108-172-1066	Sequence 1066, Ap	1298	5	1.5	1211	7	US-11-186-284-4	Sequence 4, Appl
1223	5	1.5	914	7	US-11-148-108-41	Sequence 41, Appl	1299	5	1.5	1218	7	US-11-078-735-20	Sequence 20, Appl
1224	5	1.5	919	6	US-10-821-234-1144	Sequence 1144, Ap	1300	5	1.5	1234	6	US-10-667-295-260	Sequence 260, App

1301	5	1.5	1234	6	US-10-995-561-870	Sequence 870, Appl	1374	5	1.5	3704	6	US-10-513-786-1	Sequence 1, Appl
1302	5	1.5	1250	7	US-11-137-465-62	Sequence 62, Appl	1375	5	1.5	3803	6	US-10-995-561-773	Sequence 773, Appl
1303	5	1.5	1263	7	US-11-076-163-3	Sequence 3, Appl	1376	5	1.5	3960	6	US-10-995-561-771	Sequence 771, Appl
1304	5	1.5	1271	6	US-10-770-726-46	Sequence 46, Appl	1377	5	1.5	4128	6	US-10-770-726-46	Sequence 77, Appl
1305	5	1.5	1279	6	US-10-793-626-1188	Sequence 3188, Ap	1378	5	1.5	4346	6	US-10-995-561-671	Sequence 671, Appl
1306	5	1.5	1299	6	US-10-821-234-1145	Sequence 1145, Ap	1379	5	1.5	4347	6	US-10-995-561-670	Sequence 670, Appl
1307	5	1.5	1342	6	US-10-770-726-63	Sequence 63, Appl	1380	5	1.5	4374	7	US-11-128-572-2	Sequence 2, Appl
1308	5	1.5	1342	7	US-11-113-202-12	Sequence 12, Appl	1381	5	1.5	4384	6	US-10-821-234-1120	Sequence 1120, Ap
1309	5	1.5	1342	7	US-11-113-202-14	Sequence 14, Appl	1382	5	1.5	4419	6	US-10-821-234-1155	Sequence 1155, Ap
1310	5	1.5	1346	7	US-11-060-005-2	Sequence 2, Appl	1383	5	1.5	5335	6	US-10-995-561-777	Sequence 777, Appl
1311	5	1.5	1360	7	US-11-188-743-22	Sequence 22, Appl	1384	5	1.5	5405	7	US-11-108-172-1116	Sequence 1116, Ap
1312	5	1.5	1365	6	US-10-995-561-867	Sequence 867, Appl	1385	5	1.5	5415	6	US-10-995-561-779	Sequence 779, Appl
1313	5	1.5	1366	6	US-10-995-561-868	Sequence 868, Appl	1386	5	1.5	5464	6	US-10-995-561-775	Sequence 775, Appl
1314	5	1.5	1375	6	US-10-995-561-809	Sequence 809, Appl	1387	5	1.5	5935	6	US-10-995-561-776	Sequence 776, Appl
1315	5	1.5	1377	6	US-10-821-234-1070	Sequence 1070, Ap	1388	4	1.2	4	7	US-11-016-503-35	Sequence 35, Appl
1316	5	1.5	1381	6	US-10-467-657-178	Sequence 178, Appl	1389	4	1.2	5	6	US-10-467-657-6796	Sequence 6796, Appl
1317	5	1.5	1381	6	US-10-467-657-3726	Sequence 3726, Ap	1390	4	1.2	5	7	US-11-178-737-14	Sequence 14, Appl
1318	5	1.5	1402	6	US-10-971-982-2	Sequence 2, Appl	1391	4	1.2	5	7	US-11-127-601-16	Sequence 16, Appl
1319	5	1.5	1404	6	US-10-995-561-526	Sequence 526, Appl	1392	4	1.2	5	7	US-11-062-186-72	Sequence 72, Appl
1320	5	1.5	1411	6	US-10-995-561-869	Sequence 869, Appl	1393	4	1.2	6	7	US-11-009-939-23	Sequence 23, Appl
1321	5	1.5	1411	7	US-11-077-550-110	Sequence 110, Appl	1394	4	1.2	6	7	US-11-167-710-10	Sequence 10, Appl
1322	5	1.5	1437	7	US-11-074-176-96	Sequence 96, Appl	1395	4	1.2	6	7	US-10-509-170-4	Sequence 4, Appl
1323	5	1.5	1458	7	US-11-096-274-2	Sequence 2, Appl	1396	4	1.2	7	6	US-10-981-873-35	Sequence 35, Appl
1324	5	1.5	1463	6	US-10-971-982-3	Sequence 3, Appl	1397	4	1.2	7	6	US-10-467-657-8713	Sequence 8713, Ap
1325	5	1.5	1510	7	US-11-055-822-72	Sequence 72, Appl	1398	4	1.2	7	6	US-10-467-657-8863	Sequence 8863, Ap
1326	5	1.5	1581	7	US-11-090-439-24	Sequence 24, Appl	1399	4	1.2	7	6	US-10-925-366A-35	Sequence 35, Appl
1327	5	1.5	1581	7	US-11-090-439-26	Sequence 26, Appl	1400	4	1.2	7	6	US-10-925-366A-50	Sequence 50, Appl
1328	5	1.5	1588	6	US-10-995-561-527	Sequence 527, Appl	1401	4	1.2	7	6	US-10-925-366A-65	Sequence 65, Appl
1329	5	1.5	1596	7	US-11-060-005-4	Sequence 4, Appl	1402	4	1.2	7	6	US-10-925-366A-68	Sequence 68, Appl
1330	5	1.5	1614	7	US-11-108-528-82	Sequence 82, Appl	1403	4	1.2	7	7	US-11-096-706-89	Sequence 89, Appl
1331	5	1.5	1615	7	US-11-108-528-80	Sequence 80, Appl	1404	4	1.2	7	7	US-11-033-365-25	Sequence 25, Appl
1332	5	1.5	1618	6	US-10-984-645-2	Sequence 2, Appl	1405	4	1.2	7	7	US-11-101-287-89	Sequence 89, Appl
1333	5	1.5	1637	6	US-10-821-234-1204	Sequence 1204, Ap	1406	4	1.2	7	7	US-11-115-922-89	Sequence 89, Appl
1334	5	1.5	1734	7	US-11-192-967-6	Sequence 6, Appl	1407	4	1.2	7	7	US-11-115-922-160	Sequence 160, Appl
1335	5	1.5	1734	7	US-11-193-715-6	Sequence 6, Appl	1408	4	1.2	7	7	US-11-135-414-3	Sequence 3, Appl
1336	5	1.5	1804	6	US-10-513-786-2	Sequence 2, Appl	1409	4	1.2	8	6	US-11-055-163-23	Sequence 23, Appl
1337	5	1.5	1857	7	US-11-057-058-60	Sequence 60, Appl	1410	4	1.2	8	6	US-10-467-657-8959	Sequence 8959, Ap
1338	5	1.5	1857	7	US-11-057-058-61	Sequence 61, Appl	1411	4	1.2	8	7	US-11-011-666-6	Sequence 6, Appl
1339	5	1.5	1874	6	US-10-821-234-1182	Sequence 1182, Ap	1412	4	1.2	8	7	US-11-054-515-1157	Sequence 3157, Appl
1340	5	1.5	1889	7	US-11-102-476-46	Sequence 46, Appl	1413	4	1.2	8	7	US-11-045-024-1116	Sequence 1116, Appl
1341	5	1.5	1892	7	US-11-075-185-6	Sequence 6, Appl	1414	4	1.2	8	7	US-11-045-024-1104	Sequence 1104, Appl
1342	5	1.5	1933	6	US-10-523-912-2	Sequence 2, Appl	1415	4	1.2	8	7	US-11-045-024-1105	Sequence 1105, Appl
1343	5	1.5	2080	6	US-10-821-234-1640	Sequence 1640, Ap	1416	4	1.2	8	7	US-11-045-024-1584	Sequence 1584, Ap
1344	5	1.5	2102	6	US-10-995-561-990	Sequence 990, Appl	1417	4	1.2	8	7	US-11-045-024-1614	Sequence 1614, Ap
1345	5	1.5	2108	6	US-10-995-561-989	Sequence 989, Appl	1418	4	1.2	8	7	US-11-045-024-1657	Sequence 1657, Appl
1346	5	1.5	2157	6	US-10-995-561-991	Sequence 991, Appl	1419	4	1.2	8	7	US-11-045-024-1937	Sequence 1937, Appl
1347	5	1.5	2197	7	US-11-075-185-8	Sequence 8, Appl	1420	4	1.2	8	7	US-11-045-024-4016	Sequence 4016, Appl
1348	5	1.5	2280	7	US-11-022-562-211	Sequence 211, Appl	1421	4	1.2	8	7	US-11-045-024-4359	Sequence 4359, Appl
1349	5	1.5	2283	7	US-11-096-281-13	Sequence 13, Appl	1422	4	1.2	8	7	US-11-045-024-5291	Sequence 5291, Appl
1350	5	1.5	2339	7	US-11-096-281-11	Sequence 11, Appl	1423	4	1.2	8	7	US-11-045-024-5463	Sequence 5463, Appl
1351	5	1.5	2376	7	US-11-096-051-4	Sequence 4, Appl	1424	4	1.2	8	7	US-11-045-024-5464	Sequence 5464, Appl
1352	5	1.5	2491	6	US-10-995-561-769	Sequence 769, Appl	1425	4	1.2	8	7	US-11-045-024-5471	Sequence 5471, Appl
1353	5	1.5	2515	7	US-11-113-424-53	Sequence 53, Appl	1426	4	1.2	8	7	US-11-045-024-5625	Sequence 5625, Appl
1354	5	1.5	2516	6	US-10-647-956A-2	Sequence 2, Appl	1427	4	1.2	8	7	US-11-045-024-5761	Sequence 5761, Appl
1355	5	1.5	2715	7	US-11-096-051-2	Sequence 2, Appl	1428	4	1.2	8	7	US-11-045-024-5979	Sequence 5979, Appl
1356	5	1.5	2715	7	US-11-113-424-51	Sequence 51, Appl	1429	4	1.2	8	7	US-11-045-024-7316	Sequence 7316, Appl
1357	5	1.5	2725	7	US-11-096-051-10	Sequence 10, Appl	1430	4	1.2	8	7	US-11-045-024-7517	Sequence 7517, Appl
1358	5	1.5	2725	7	US-11-096-051-8	Sequence 8, Appl	1431	4	1.2	8	7	US-11-045-024-7641	Sequence 7641, Appl
1359	5	1.5	2725	7	US-11-113-424-52	Sequence 52, Appl	1432	4	1.2	8	7	US-11-045-024-9035	Sequence 9035, Appl
1360	5	1.5	2763	7	US-11-113-424-14	Sequence 14, Appl	1433	4	1.2	8	7	US-11-045-024-9149	Sequence 9149, Appl
1361	5	1.5	2828	7	US-11-080-991-54	Sequence 54, Appl	1434	4	1.2	8	7	US-11-045-024-9188	Sequence 9188, Appl
1362	5	1.5	2828	7	US-11-186-284-49	Sequence 49, Appl	1435	4	1.2	8	7	US-11-045-024-1133	Sequence 1133, A
1363	5	1.5	2828	6	US-10-499-715-2	Sequence 2, Appl	1436	4	1.2	8	7	US-11-045-024-9204	Sequence 9204, Appl
1364	5	1.5	2910	7	US-11-087-100-2	Sequence 2, Appl	1437	4	1.2	8	7	US-11-045-024-10113	Sequence 10113, A
1365	5	1.5	2910	7	US-11-087-084-2	Sequence 2, Appl	1438	4	1.2	8	7	US-11-045-024-10266	Sequence 10266, A
1366	5	1.5	2910	7	US-11-087-085-2	Sequence 2, Appl	1439	4	1.2	8	7	US-11-045-024-10286	Sequence 10286, A
1367	5	1.5	3011	6	US-10-985-205-3	Sequence 3, Appl	1440	4	1.2	8	7	US-11-045-024-11331	Sequence 11331, A
1368	5	1.5	3056	6	US-11-109-156-20	Sequence 20, Appl	1441	4	1.2	8	7	US-11-045-024-11351	Sequence 11351, A
1369	5	1.5	3073	7	US-11-143-980-50	Sequence 50, Appl	1442	4	1.2	8	7	US-11-045-024-12002	Sequence 12002, A
1370	5	1.5	3144	7	US-11-055-035-1	Sequence 1, Appl	1443	4	1.2	8	7	US-11-045-024-12116	Sequence 12116, A
1371	5	1.5	3588	6	US-10-995-561-672	Sequence 672, Appl	1444	4	1.2	9	6	US-10-984-376-15	Sequence 15, Appl
1372	5	1.5	3623	6	US-10-995-561-593	Sequence 593, Appl	1445	4	1.2	9	6	US-10-981-873-22	Sequence 22, Appl
1373	5	1.5	3655	7	US-11-075-185-5	Sequence 5, Appl	1446	4	1.2	9	6	US-10-952-535A-44	Sequence 44, Appl

1447	4	1.2	9	6	US-10-623-155-226	Sequence 226, App
1448	4	1.2	9	6	US-10-491-096-66	Sequence 66, App1
1449	4	1.2	9	6	US-10-491-096-68	Sequence 68, App1
1450	4	1.2	9	6	US-10-491-096-100	Sequence 100, App
1451	4	1.2	9	6	US-10-491-096-165	Sequence 165, App
1452	4	1.2	9	7	US-11-010-748A-102	Sequence 102, App
1453	4	1.2	9	7	US-11-010-748A-103	Sequence 103, App
1454	4	1.2	9	7	US-11-010-748A-105	Sequence 105, App
1455	4	1.2	9	7	US-11-010-748A-106	Sequence 106, App
1456	4	1.2	9	7	US-11-010-748A-107	Sequence 107, App
1457	4	1.2	9	7	US-11-010-748A-109	Sequence 109, App
1458	4	1.2	9	7	US-11-010-748A-110	Sequence 110, App
1459	4	1.2	9	7	US-11-010-748A-111	Sequence 111, App
1460	4	1.2	9	7	US-11-010-748A-113	Sequence 113, App
1461	4	1.2	9	7	US-11-010-748A-114	Sequence 114, App
1462	4	1.2	9	7	US-11-010-748A-115	Sequence 115, App
1463	4	1.2	9	7	US-11-010-748A-151	Sequence 151, App
1464	4	1.2	9	7	US-11-010-748A-153	Sequence 153, App
1465	4	1.2	9	7	US-11-010-748A-155	Sequence 155, App
1466	4	1.2	9	7	US-11-010-748A-156	Sequence 156, App
1467	4	1.2	9	7	US-11-010-748A-157	Sequence 157, App
1468	4	1.2	9	7	US-11-010-748A-159	Sequence 159, App
1469	4	1.2	9	7	US-11-010-748A-160	Sequence 160, App
1470	4	1.2	9	7	US-11-010-748A-161	Sequence 161, App
1471	4	1.2	9	7	US-11-010-748A-163	Sequence 163, App
1472	4	1.2	9	7	US-11-010-748A-164	Sequence 164, App
1473	4	1.2	9	7	US-11-010-748A-165	Sequence 165, App
1474	4	1.2	9	7	US-11-010-748A-257	Sequence 257, App
1475	4	1.2	9	7	US-11-010-748A-258	Sequence 258, App
1476	4	1.2	9	7	US-11-010-748A-520	Sequence 520, App
1477	4	1.2	9	7	US-11-010-748A-521	Sequence 521, App
1478	4	1.2	9	7	US-11-010-748A-523	Sequence 523, App
1479	4	1.2	9	7	US-11-010-748A-524	Sequence 524, App
1480	4	1.2	9	7	US-11-010-748A-525	Sequence 525, App
1481	4	1.2	9	7	US-11-010-748A-526	Sequence 526, App
1482	4	1.2	9	7	US-11-010-748A-715	Sequence 715, App
1483	4	1.2	9	7	US-11-010-748A-716	Sequence 716, App
1484	4	1.2	9	7	US-11-010-748A-717	Sequence 717, App
1485	4	1.2	9	7	US-11-010-748A-718	Sequence 718, App
1486	4	1.2	9	7	US-11-010-748A-720	Sequence 720, App
1487	4	1.2	9	7	US-11-010-748A-722	Sequence 722, App
1488	4	1.2	9	7	US-11-010-748A-726	Sequence 726, App
1489	4	1.2	9	7	US-11-010-748A-727	Sequence 727, App
1490	4	1.2	9	7	US-11-010-748A-729	Sequence 729, App
1491	4	1.2	9	7	US-11-010-748A-730	Sequence 730, App
1492	4	1.2	9	7	US-11-010-748A-731	Sequence 731, App
1493	4	1.2	9	7	US-11-010-748A-732	Sequence 732, App
1494	4	1.2	9	7	US-11-010-748A-734	Sequence 734, App
1495	4	1.2	9	7	US-11-010-748A-738	Sequence 738, App
1496	4	1.2	9	7	US-11-010-748A-739	Sequence 739, App
1497	4	1.2	9	7	US-11-010-748A-740	Sequence 740, App
1498	4	1.2	9	7	US-11-010-748A-742	Sequence 742, App
1499	4	1.2	9	7	US-11-010-748A-743	Sequence 743, App
1500	4	1.2	9	7	US-11-010-748A-744	Sequence 744, App

Search completed: December 16, 2005, 11:49:50
Job time : 15 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 11:35:44 / Search time 164 Seconds
(without alignments)
853.493 Million cell updates/sec

Perfect score: 335
Sequence: 1 MAGSPCTLTLYILMQLTGS.....PHSLTWPDPRLPAYENVYI 335

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 4178293326 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database :
1: /cgn2_6/ptodaca/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodaca/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodaca/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodaca/1/pubpaa/US10_PUBCOMB.pep:*
5: /cgn2_6/ptodaca/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodaca/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	335	100.0	335	3	US-09-732-524-2
8	335	100.0	335	3	US-09-745-605-4
29	335	100.0	335	3	US-09-997-428-253
540	335	100.0	335	4	US-10-021-741A-2
565	335	100.0	335	4	US-10-174-587-192
629	335	100.0	335	4	US-10-063-742-46
739	335	100.0	335	4	US-10-262-839-110
745	335	100.0	335	5	US-10-842-011-2
746	335	100.0	335	5	US-10-972-317-46
748	335	100.0	335	5	US-10-950-374-253
751	312	93.1	312	3	US-09-732-524-4
752	312	69.9	312	3	US-10-104-943-5
753	234	69.9	335	4	US-10-436-523-60
754	234	69.9	335	4	US-10-408-765A-1405
755	217	64.8	348	4	US-10-262-839-112
761	110	32.8	110	5	US-10-143-050-125
762	92	27.5	684	5	US-10-960-251-125
763	92	27.5	684	5	US-10-450-763-42056
764	91	27.2	91	3	US-09-864-761-41706
765	33	9.9	33	3	US-09-984-245-244
766	33	9.9	33	3	US-09-966-262-244
767	33	9.9	33	3	US-09-983-966-244
768	33	9.9	33	4	US-10-059-395-244

769	33	9.9	33	4	US-10-143-090-244	Sequence 244, App
770	33	9.9	33	5	US-10-960-251-244	Sequence 244, App
771	27	8.1	28	3	US-09-984-245-243	Sequence 243, App
772	27	8.1	28	3	US-09-966-262-243	Sequence 243, App
773	27	8.1	28	3	US-09-983-966-243	Sequence 243, App
774	27	8.1	28	4	US-10-059-395-243	Sequence 243, App
775	27	8.1	28	4	US-10-143-090-243	Sequence 243, App
776	27	8.1	28	5	US-10-960-251-243	Sequence 243, App
777	9	2.7	456	5	US-10-450-763-55384	Sequence 55384, A
778	9	2.4	59	4	US-10-424-599-229784	Sequence 229784, A
779	8	2.4	130	5	US-10-739-930-9038	Sequence 9038, Ap
780	8	2.4	152	4	US-10-767-701-56635	Sequence 56635, A
781	8	2.4	159	4	US-10-767-701-38620	Sequence 38620, A
782	8	2.4	191	4	US-10-767-701-40580	Sequence 40580, A
783	8	2.4	200	4	US-10-767-701-36759	Sequence 36759, A
784	8	2.4	224	4	US-10-767-701-45460	Sequence 45460, A
785	8	2.4	289	5	US-10-960-275-8	Sequence 8, Appl1
786	8	2.4	306	4	US-10-282-122A-52432	Sequence 52432, A
787	8	2.4	310	4	US-10-094-749-3057	Sequence 3057, Ap
790	8	2.4	360	3	US-09-905-291A-213	Sequence 213, App
1321	8	2.4	360	4	US-10-174-587-28	Sequence 28, Appl1
1356	8	2.4	360	4	US-10-299-976-213	Sequence 213, App
1358	8	2.4	360	4	US-10-298-937-213	Sequence 213, App
1363	8	2.4	360	4	US-10-298-933-213	Sequence 213, App
1373	8	2.4	360	4	US-10-448-923-213	Sequence 213, App
1374	8	2.4	360	4	US-10-449-656-213	Sequence 213, App
1375	8	2.4	360	4	US-10-448-713-213	Sequence 213, App
1377	8	2.4	360	4	US-10-425-447-213	Sequence 213, App
1385	8	2.4	360	4	US-10-215-371-213	Sequence 213, App
1386	8	2.4	360	4	US-10-797-366-213	Sequence 213, App
1387	8	2.4	360	4	US-10-771-187-213	Sequence 213, App
1388	8	2.4	360	5	US-10-963-467-213	Sequence 213, App
1389	8	2.4	360	5	US-10-978-255-213	Sequence 213, App
1393	8	2.4	360	5	US-10-970-823-213	Sequence 213, App
1394	8	2.4	404	5	US-10-739-930-10928	Sequence 10928, A
1395	8	2.4	419	4	US-10-425-114-44960	Sequence 44960, A
1396	8	2.4	428	4	US-10-425-114-51066	Sequence 51066, A
1397	8	2.4	452	4	US-10-425-114-65803	Sequence 65803, A
1398	8	2.4	466	4	US-10-106-698-5687	Sequence 5687, Ap
1399	8	2.4	530	4	US-10-425-115-239773	Sequence 239773, A
1400	8	2.4	543	4	US-10-437-963-193432	Sequence 193432, A
1401	8	2.4	568	4	US-10-425-115-188428	Sequence 188428, A
1402	8	2.4	575	4	US-10-425-115-188427	Sequence 188427, A
1403	8	2.4	585	4	US-10-173-519-4	Sequence 4, Appl1
1404	8	2.4	671	4	US-10-156-763-13998	Sequence 13998, A
1405	8	2.4	808	5	US-10-450-763-4064	Sequence 4064, A
1406	8	2.4	868	6	US-11-097-143-18507	Sequence 18507, A
1407	8	2.4	1117	4	US-10-788-792-238	Sequence 238, App
1408	8	2.4	1117	5	US-10-756-149-5461	Sequence 5461, Ap
1409	8	2.4	1138	3	US-09-909-5678-42	Sequence 42, Appl1
1410	8	2.4	1280	5	US-10-450-763-40643	Sequence 40643, A
1411	8	2.4	1311	4	US-10-262-839-92	Sequence 92, Appl1
1412	8	2.4	1311	4	US-10-103-377C-6	Sequence 6, Appl1
1413	8	2.4	1311	4	US-10-391-364-91	Sequence 91, Appl1
1414	7	2.1	24	5	US-10-808-187-1895	Sequence 1895, Ap
1415	7	2.1	24	5	US-10-807-807-1895	Sequence 1895, Ap
1416	7	2.1	47	4	US-10-724-972-13642	Sequence 13642, Ap
1417	7	2.1	51	4	US-10-425-115-193003	Sequence 193003, A
1418	7	2.1	52	4	US-10-424-599-207050	Sequence 207050, A
1419	7	2.1	55	4	US-10-424-599-172010	Sequence 172010, A
1420	7	2.1	57	4	US-10-425-115-278083	Sequence 278083, A
1421	7	2.1	58	4	US-10-424-599-214301	Sequence 214301, A
1422	7	2.1	63	4	US-10-425-115-357958	Sequence 357958, A
1423	7	2.1	69	4	US-10-425-115-287665	Sequence 287665, A
1424	7	2.1	72	3	US-09-864-761-41706	Sequence 41706, A
1425	7	2.1	75	4	US-10-425-115-296274	Sequence 296274, A
1426	7	2.1	82	4	US-10-425-115-291093	Sequence 291093, A
1427	7	2.1	85	3	US-09-864-761-41706	Sequence 41706, A
1428	7	2.1	85	4	US-10-424-599-192252	Sequence 192252, A
1429	7	2.1	85	4	US-10-424-599-240190	Sequence 240190, A
1430	7	2.1	86	4	US-10-425-115-197457	Sequence 197457, A
1431	7	2.1	86	4	US-10-425-115-328955	Sequence 328955, A
1432	7	2.1	89	4	US-10-425-115-365198	Sequence 365198, A

1433	7	2.1	91	4	US-10-425-115-203677
1434	7	2.1	94	4	US-10-425-115-300034
1435	7	2.1	97	3	US-09-886-319A-29
1436	7	2.1	97	4	US-10-376-564-29
1437	7	2.1	97	4	US-10-437-963-117092
1438	7	2.1	97	4	US-10-425-115-201843
1439	7	2.1	98	2	US-08-927-939-50
1440	7	2.1	98	2	US-08-927-939-83
1441	7	2.1	98	3	US-09-261-201A-4
1442	7	2.1	98	3	US-09-834-795A-25
1443	7	2.1	98	3	US-09-872-611A-2
1444	7	2.1	98	3	US-09-834-794A-25
1445	7	2.1	98	4	US-10-164-621-4
1446	7	2.1	98	4	US-10-125-451-4
1447	7	2.1	98	4	US-10-263-139-4
1448	7	2.1	98	4	US-10-295-027-1221
1449	7	2.1	98	4	US-10-646-770-4
1450	7	2.1	98	5	US-10-723-860-3704
1451	7	2.1	98	5	US-10-893-995-4
1452	7	2.1	98	5	US-10-847-824-25
1453	7	2.1	98	5	US-10-756-149-5640
1454	7	2.1	100	3	US-09-864-761-41304
1455	7	2.1	101	4	US-10-156-761-9397
1456	7	2.1	104	3	US-09-746-783-206
1457	7	2.1	104	4	US-10-425-115-198566
1458	7	2.1	106	5	US-10-450-763-43931
1459	7	2.1	108	4	US-10-437-963-113045
1460	7	2.1	109	4	US-10-424-599-284058
1461	7	2.1	119	4	US-10-425-115-185689
1462	7	2.1	120	6	US-11-097-143-34971
1463	7	2.1	125	5	US-10-732-923-20384
1464	7	2.1	126	4	US-10-437-963-122526
1465	7	2.1	129	4	US-10-437-963-148643
1466	7	2.1	130	4	US-10-424-599-253767
1467	7	2.1	135	5	US-10-450-763-31521
1468	7	2.1	139	4	US-10-767-701-51966
1469	7	2.1	143	4	US-10-335-977-7863
1470	7	2.1	144	4	US-10-437-963-108977
1471	7	2.1	148	4	US-10-437-963-165913
1472	7	2.1	150	4	US-10-437-963-134615
1473	7	2.1	150	4	US-10-425-115-323439
1474	7	2.1	153	3	US-09-925-298-646
1475	7	2.1	153	4	US-10-102-806-646
1476	7	2.1	163	4	US-10-437-963-161121
1477	7	2.1	163	5	US-10-650-274-135
1478	7	2.1	168	4	US-10-425-115-291050
1479	7	2.1	174	4	US-10-424-599-149243
1480	7	2.1	179	4	US-10-283-122A-51667
1481	7	2.1	179	4	US-10-767-701-42327
1482	7	2.1	189	4	US-10-425-115-345243
1483	7	2.1	192	4	US-10-267-682-107
1484	7	2.1	192	4	US-10-267-748-107
1485	7	2.1	196	4	US-10-767-701-40509
1486	7	2.1	197	4	US-10-335-977-7864
1487	7	2.1	201	3	US-09-864-761-37006
1488	7	2.1	202	4	US-10-425-115-346967
1489	7	2.1	202	5	US-10-200-545-78
1490	7	2.1	208	4	US-10-156-275-72
1491	7	2.1	208	4	US-10-437-963-138752
1492	7	2.1	211	5	US-10-450-763-43932
1493	7	2.1	225	4	US-10-437-963-167884
1494	7	2.1	227	5	US-10-733-930-8104
1495	7	2.1	233	4	US-10-156-761-12450
1496	7	2.1	234	4	US-10-425-115-251727
1497	7	2.1	235	5	US-10-450-763-55476
1498	7	2.1	236	4	US-10-767-701-56113
1499	7	2.1	237	4	US-10-425-114-38444
1500	7	2.1	240	4	US-10-437-963-166170

Sequence 203677,
Sequence 300034,
Sequence 29, Appl
Sequence 29, Appl
Sequence 117092,
Sequence 201843,
Sequence 50, Appl
Sequence 83, Appl
Sequence 4, Appl
Sequence 25, Appl
Sequence 2, Appl
Sequence 25, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 1221, Ap
Sequence 4, Appl
Sequence 3704, Ap
Sequence 4, Appl
Sequence 25, Appl
Sequence 5640, Ap
Sequence 41304, A
Sequence 9397, Ap
Sequence 206, App
Sequence 188566, A
Sequence 43931, A
Sequence 113045,
Sequence 284058,
Sequence 185689,
Sequence 34971, A
Sequence 20384, A
Sequence 122526,
Sequence 148643,
Sequence 253767,
Sequence 31521, A
Sequence 51966, A
Sequence 7863, Ap
Sequence 108977,
Sequence 165913,
Sequence 134615,
Sequence 323439,
Sequence 646, App
Sequence 646, App
Sequence 161121,
Sequence 135, App
Sequence 291050,
Sequence 149243,
Sequence 42327, A
Sequence 345243,
Sequence 107, App
Sequence 40509, A
Sequence 7864, Ap
Sequence 37006, A
Sequence 346967,
Sequence 78, Appl
Sequence 72, Appl
Sequence 138752,
Sequence 43932, A
Sequence 167884,
Sequence 8104, Ap
Sequence 12450, A
Sequence 251727,
Sequence 55476, A
Sequence 56113, A
Sequence 38444, A
Sequence 166170,